(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
4 October 2001 (04.10.2001)

PCT

(10) International Publication Number
WO 01/72295 A2

(51) International Patent Classification[7]: A61K 31/00

(21) International Application Number: PCT/US01/09991

(22) International Filing Date: 28 March 2001 (28.03.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

09/538,037	29 March 2000 (29.03.2000)	US
09/588,937	5 June 2000 (05.06.2000)	US
09/640,878	18 August 2000 (18.08.2000)	US
60/234,517	22 September 2000 (22.09.2000)	US
09/704,512	1 November 2000 (01.11.2000)	US
09/738,973	14 December 2000 (14.12.2000)	US

(71) Applicant *(for all designated States except US)*: **CORIXA CORPORATION** [US/US]; 1124 Columbia Street, Suite 200, Seattle, WA 98104 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **REED, Steven, G.** [US/US]; 2843 122nd Place N.E., Bellevue, WA 98005 (US). **LODES, Michael, J.** [US/US]; 9223 36th Avenue S.W., Seattle, WA 98126 (US). **MOHAMATH, Raodoh** [US/US]; 4205 South Morgan, Seattle, WA 98118 (US). **SECRIST, Heather** [US/US]; 3844 35th Avenue W., Seattle, WA 98199 (US). **BENSON, Darin, R.** [US/US]; 723 N. 48th Street, Seattle, WA 98103 (US). **INDIRIAS, Carol, Yoseph** [US/US]; 1541 N.W. 52nd Street, Seattle, WA 98107 (US). **HENDERSON, Robert, A.** [US/US]; 8904 192nd Street S.W., Edmonds, WA 98026 (US). **FLING, Steven, P.** [US/US]; 11414 Pinyon Avenue Northeast, Bainbridge Island, WA 98110 (US). **ALGATE, Paul, A.** [GB/US]; 580 Kalmia Place N.W., Issaquah, WA 98027 (US). **ELLIOT, Mark** [US/US]; 10800 26th Avenue S.W., Seattle, WA 98146 (US). **MANNION, Jane** [US/US]; 8904 192nd Street S.W., Edmonds, WA 98026 (US). **KALOS, Michael, D.** [US/US]; 8116 Dayton Ave. N., Seattle, WA 98103 (US).

(74) Agents: **POTTER, Jane, E., R.** et al.; Seed Intellectual Property Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/72295 A2

(54) **Title:** COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER

(57) **Abstract:** Compositions and methods for the therapy and diagnosis of cancer, particularly lung cancer, are disclosed. Illustrative compositions comprise one or more lung tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly lung cancer.

COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER

TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of cancer, such as lung cancer. The invention is more specifically related to polypeptides, comprising at least a portion of a lung tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides are useful in pharmaceutical compositions, *e.g.*, vaccines, and other compositions for the diagnosis and treatment of lung cancer.

BACKGROUND OF THE INVENTION

Lung cancer is the primary cause of cancer death among both men and women in the U.S., with an estimated 172,000 new cases being reported in 1994. The five-year survival rate among all lung cancer patients, regardless of the stage of disease at diagnosis, is only 13%. This contrasts with a five-year survival rate of 46% among cases detected while the disease is still localized. However, only 16% of lung cancers are discovered before the disease has spread.

Early detection is difficult since clinical symptoms are often not seen until the disease has reached an advanced stage. Currently, diagnosis is aided by the use of chest x-rays, analysis of the type of cells contained in sputum and fiberoptic examination of the bronchial passages. Treatment regimens are determined by the type and stage of the cancer, and include surgery, radiation therapy and/or chemotherapy. In spite of considerable research into therapies for the disease, lung cancer remains difficult to treat.

Accordingly, there remains a need in the art for improved vaccines, treatment methods and diagnostic techniques for lung cancer.

SUMMARY OF THE INVENTION

In one aspect, the present invention provides polynucleotide compositions comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583;

(b) complements of the sequences provided in SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583;

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583, under moderately stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583; and

(g) degenerate variants of a sequence provided in SEQ ID NO: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583.

In one preferred embodiment, the polynucleotide compositions of the invention are expressed in at least about 20%, more preferably in at least about 30%, and most preferably in at least about 50% of lung tumors samples tested, at a level that is at least about 2-fold, preferably at least about 5-fold, and most preferably at least about 10-fold higher than that for normal tissues.

The present invention, in another aspect, provides polypeptide compositions comprising an amino acid sequence that is encoded by a polynucleotide sequence described above.

In specific embodiments, the present invention provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 391, 393, 395, 397, 421, 425-427, 434-439 and 584-587.

In certain preferred embodiments, the polypeptides and/or polynucleotides of the present invention are immunogenic, *i.e.*, they are capable of

eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.

The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the fragments, variants and/or derivatives preferably have a level of immunogenic activity of at least about 50%, preferably at least about 70% and more preferably at least about 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID NOs: 391, 393, 395, 397, 421, 425-427, 434-439 and 584-587 or a polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583.

The present invention further provides polynucleotides that encode a polypeptide described above, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, the pharmaceutical compositions, *e.g.*, vaccine compositions, are provided for prophylactic or therapeutic applications. Such compositions generally comprise an immunogenic polypeptide or polynucleotide of the invention and an immunostimulant, such as an adjuvant.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier and/or an immunostimulant. The fusions proteins may comprise multiple immunogenic polypeptides or portions/variants thereof, as described herein, and may further comprise one or more polypeptide segments for facilitating the expression, purification and/or immunogenicity of the polypeptide(s).

Within further aspects, the present invention provides methods for stimulating an immune response in a patient, preferably a T cell response in a human patient, comprising administering a pharmaceutical composition described herein. The patient may be afflicted with lung cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition as recited above. The patient may be afflicted with lung cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating $CD4^+$ and/or $CD8^+$ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer, preferably a lung cancer, in a patient comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time

with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

SEQUENCE IDENTIFIERS

SEQ ID NO: 1 is the determined cDNA sequence for L363C1.cons

SEQ ID NO: 2 is the determined cDNA sequence for L263C2.cons

SEQ ID NO: 3 is the determined cDNA sequence for L263C2c

SEQ ID NO: 4 is the determined cDNA sequence for L263C1.cons

SEQ ID NO: 5 is the determined cDNA sequence for L263C1b

SEQ ID NO: 6 is the determined cDNA sequence for L164C2.cons

SEQ ID NO: 7 is the determined cDNA sequence for L164C1.cons

SEQ ID NO: 8 is the determined cDNA sequence for L366C1a

SEQ ID NO: 9 is the determined cDNA sequence for L260C1.cons

SEQ ID NO: 10 is the determined cDNA sequence for L163C1c

SEQ ID NO: 11 is the determined cDNA sequence for L163C1b

SEQ ID NO: 12 is the determined cDNA sequence for L255C1.cons

SEQ ID NO: 13 is the determined cDNA sequence for L255C1b

SEQ ID NO: 14 is the determined cDNA sequence for L355C1.cons

SEQ ID NO: 15 is the determined cDNA sequence for L366C1.cons

SEQ ID NO: 16 is the determined cDNA sequence for L163C1a

SEQ ID NO: 17 is the determined cDNA sequence for LT86-1

SEQ ID NO: 18 is the determined cDNA sequence for LT86-2

SEQ ID NO: 19 is the determined cDNA sequence for LT86-3

SEQ ID NO: 20 is the determined cDNA sequence for LT86-4

SEQ ID NO: 21 is the determined cDNA sequence for LT86-5
SEQ ID NO: 22 is the determined cDNA sequence for LT86-6
SEQ ID NO: 23 is the determined cDNA sequence for LT86-7
SEQ ID NO: 24 is the determined cDNA sequence for LT86-8
SEQ ID NO: 25 is the determined cDNA sequence for LT86-9
SEQ ID NO: 26 is the determined cDNA sequence for LT86-10
SEQ ID NO: 27 is the determined cDNA sequence for LT86-11
SEQ ID NO: 28 is the determined cDNA sequence for LT86-12
SEQ ID NO: 29 is the determined cDNA sequence for LT86-13
SEQ ID NO: 30 is the determined cDNA sequence for LT86-14
SEQ ID NO: 31 is the determined cDNA sequence for LT86-15
SEQ ID NO: 32 is the predicted amino acid sequence for LT86-1
SEQ ID NO: 33 is the predicted amino acid sequence for LT86-2
SEQ ID NO: 34 is the predicted amino acid sequence for LT86-3
SEQ ID NO: 35 is the predicted amino acid sequence for LT86-4
SEQ ID NO: 36 is the predicted amino acid sequence for LT86-5
SEQ ID NO: 37 is the predicted amino acid sequence for LT86-6
SEQ ID NO: 38 is the predicted amino acid sequence for LT86-7
SEQ ID NO: 39 is the predicted amino acid sequence for LT86-8
SEQ ID NO: 40 is the predicted amino acid sequence for LT86-9
SEQ ID NO: 41 is the predicted amino acid sequence for LT86-10
SEQ ID NO: 42 is the predicted amino acid sequence for LT86-11
SEQ ID NO: 43 is the predicted amino acid sequence for LT86-12
SEQ ID NO: 44 is the predicted amino acid sequence for LT86-13
SEQ ID NO: 45 is the predicted amino acid sequence for LT86-14
SEQ ID NO: 46 is the predicted amino acid sequence for LT86-15
SEQ ID NO: 47 is a $(dT)_{12}AG$ primer
SEQ ID NO: 48 is a primer
SEQ ID NO: 49 is the determined 5′ cDNA sequence for L86S-3
SEQ ID NO: 50 is the determined 5′ cDNA sequence for L86S-12

SEQ ID NO: 51 is the determined 5′ cDNA sequence for L86S-16

SEQ ID NO: 52 is the determined 5′ cDNA sequence for L86S-25

SEQ ID NO: 53 is the determined 5′ cDNA sequence for L86S-36

SEQ ID NO: 54 is the determined 5′ cDNA sequence for L86S-40

SEQ ID NO: 55 is the determined 5′ cDNA sequence for L86S-46

SEQ ID NO: 56 is the predicted amino acid sequence for L86S-3

SEQ ID NO: 57 is the predicted amino acid sequence for L86S-12

SEQ ID NO: 58 is the predicted amino acid sequence for L86S-16

SEQ ID NO: 59 is the predicted amino acid sequence for L86S-25

SEQ ID NO: 60 is the predicted amino acid sequence for L86S-36

SEQ ID NO: 61 is the predicted amino acid sequence for L86S-40

SEQ ID NO: 62 is the predicted amino acid sequence for L86S-46

SEQ ID NO: 63 is the determined 5′ cDNA sequence for L86S-30

SEQ ID NO: 64 is the determined 5′ cDNA sequence for L86S-41

SEQ ID NO: 65 is the predicted amino acid sequence from the 5′ end of LT86-9

SEQ ID NO: 66 is the determined extended cDNA sequence for LT86-4

SEQ ID NO: 67 is the predicted extended amino acid sequence for LT86-4

SEQ ID NO: 68 is the determined 5′ cDNA sequence for LT86-20

SEQ ID NO: 69 is the determined 3′ cDNA sequence for LT86-21

SEQ ID NO: 70 is the determined 5′ cDNA sequence for LT86-22

SEQ ID NO: 71 is the determined 5′ cDNA sequence for LT86-26

SEQ ID NO: 72 is the determined 5′ cDNA sequence for LT86-27

SEQ ID NO: 73 is the predicted amino acid sequence for LT86-20

SEQ ID NO: 74 is the predicted amino acid sequence for LT86-21

SEQ ID NO: 75 is the predicted amino acid sequence for LT86-22

SEQ ID NO: 76 is the predicted amino acid sequence for LT86-26

SEQ ID NO: 77 is the predicted amino acid sequence for LT86-27

SEQ ID NO: 78 is the determined extended cDNA sequence for L86S-12

SEQ ID NO: 79 is the determined extended cDNA sequence for L86S-36

SEQ ID NO: 80 is the determined extended cDNA sequence for L86S-46

SEQ ID NO: 81 is the predicted extended amino acid sequence for L86S-12

SEQ ID NO: 82 is the predicted extended amino acid sequence for L86S-36

SEQ ID NO: 83 is the predicted extended amino acid sequence for L86S-46

SEQ ID NO: 84 is the determined 5′cDNA sequence for L86S-6

SEQ ID NO: 85 is the determined 5′cDNA sequence for L86S-11

SEQ ID NO: 86 is the determined 5′cDNA sequence for L86S-14

SEQ ID NO: 87 is the determined 5′cDNA sequence for L86S-29

SEQ ID NO: 88 is the determined 5′cDNA sequence for L86S-34

SEQ ID NO: 89 is the determined 5′cDNA sequence for L86S-39

SEQ ID NO: 90 is the determined 5′cDNA sequence for L86S-47

SEQ ID NO: 91 is the determined 5′cDNA sequence for L86S-49

SEQ ID NO: 92 is the determined 5′cDNA sequence for L86S-51

SEQ ID NO: 93 is the predicted amino acid sequence for L86S-6

SEQ ID NO: 94 is the predicted amino acid sequence for L86S-11

SEQ ID NO: 95 is the predicted amino acid sequence for L86S-14

SEQ ID NO: 96 is the predicted amino acid sequence for L86S-29

SEQ ID NO: 97 is the predicted amino acid sequence for L86S-34

SEQ ID NO: 98 is the predicted amino acid sequence for L86S-39

SEQ ID NO: 99 is the predicted amino acid sequence for L86S-47

SEQ ID NO: 100 is the predicted amino acid sequence for L86S-49

SEQ ID NO: 101 is the predicted amino acid sequence for L86S-51

SEQ ID NO: 102 is the determined DNA sequence for SLT-T1

SEQ ID NO: 103 is the determined 5′ cDNA sequence for SLT-T2

SEQ ID NO: 104 is the determined 5′ cDNA sequence for SLT-T3

SEQ ID NO: 105 is the determined 5′ cDNA sequence for SLT-T5

SEQ ID NO: 106 is the determined 5′ cDNA sequence for SLT-T7

SEQ ID NO: 107 is the determined 5′ cDNA sequence for SLT-T9

SEQ ID NO: 108 is the determined 5′ cDNA sequence for SLT-T10

SEQ ID NO: 109 is the determined 5′ cDNA sequence for SLT-T11

SEQ ID NO: 110 is the determined 5′ cDNA sequence for SLT-T12

SEQ ID NO: 111 is the predicted amino acid sequence for SLT-T1

SEQ ID NO: 112 is the predicted amino acid sequence for SLT-T2

SEQ ID NO: 113 is the predicted amino acid sequence for SLT-T3

SEQ ID NO: 114 is the predicted amino acid sequence for SLT-T10

SEQ ID NO: 115 is the predicted amino acid sequence for SLT-T12

SEQ ID NO: 116 is the determined 5′ cDNA sequence for SALT-T3

SEQ ID NO: 117 is the determined 5′ cDNA sequence for SALT-T4

SEQ ID NO: 118 is the determined 5′ cDNA sequence for SALT-T7

SEQ ID NO: 119 is the determined 5′ cDNA sequence for SALT-T8

SEQ ID NO: 120 is the determined 5′ cDNA sequence for SALT-T9

SEQ ID NO: 121 is the predicted amino acid sequence for SALT-T3

SEQ ID NO: 122 is the predicted amino acid sequence for SALT-T4

SEQ ID NO: 123 is the predicted amino acid sequence for SALT-T7

SEQ ID NO: 124 is the predicted amino acid sequence for SALT-T8

SEQ ID NO: 125 is the predicted amino acid sequence for SALT-T9

SEQ ID NO: 126 is the determined cDNA sequence for PSLT-1

SEQ ID NO: 127 is the determined cDNA sequence for PSLT-2

SEQ ID NO: 128 is the determined cDNA sequence for PSLT-7

SEQ ID NO: 129 is the determined cDNA sequence for PSLT-13

SEQ ID NO: 130 is the determined cDNA sequence for PSLT-27

SEQ ID NO: 131 is the determined cDNA sequence for PSLT-28

SEQ ID NO: 132 is the determined cDNA sequence for PSLT-30

SEQ ID NO: 133 is the determined cDNA sequence for PSLT-40

SEQ ID NO: 134 is the determined cDNA sequence for PSLT-69

SEQ ID NO: 135 is the determined cDNA sequence for PSLT-71

SEQ ID NO: 136 is the determined cDNA sequence for PSLT-73
SEQ ID NO: 137 is the determined cDNA sequence for PSLT-79
SEQ ID NO: 138 is the determined cDNA sequence for PSLT-03
SEQ ID NO: 139 is the determined cDNA sequence for PSLT-09
SEQ ID NO: 140 is the determined cDNA sequence for PSLT-011
SEQ ID NO: 141 is the determined cDNA sequence for PSLT-041
SEQ ID NO: 142 is the determined cDNA sequence for PSLT-62
SEQ ID NO: 143 is the determined cDNA sequence for PSLT-6
SEQ ID NO: 144 is the determined cDNA sequence for PSLT-37
SEQ ID NO: 145 is the determined cDNA sequence for PSLT-74
SEQ ID NO: 146 is the determined cDNA sequence for PSLT-010
SEQ ID NO: 147 is the determined cDNA sequence for PSLT-012
SEQ ID NO: 148 is the determined cDNA sequence for PSLT-037
SEQ ID NO: 149 is the determined 5′ cDNA sequence for SAL-3
SEQ ID NO: 150 is the determined 5′ cDNA sequence for SAL-24
SEQ ID NO: 151 is the determined 5′ cDNA sequence for SAL-25
SEQ ID NO: 152 is the determined 5′ cDNA sequence for SAL-33
SEQ ID NO: 153 is the determined 5′ cDNA sequence for SAL-50
SEQ ID NO: 154 is the determined 5′ cDNA sequence for SAL-57
SEQ ID NO: 155 is the determined 5′ cDNA sequence for SAL-66
SEQ ID NO: 156 is the determined 5′ cDNA sequence for SAL-82
SEQ ID NO: 157 is the determined 5′ cDNA sequence for SAL-99
SEQ ID NO: 158 is the determined 5′ cDNA sequence for SAL-104
SEQ ID NO: 159 is the determined 5′ cDNA sequence for SAL-109
SEQ ID NO: 160 is the determined 5′ cDNA sequence for SAL-5
SEQ ID NO: 161 is the determined 5′ cDNA sequence for SAL-8
SEQ ID NO: 162 is the determined 5′ cDNA sequence for SAL-12
SEQ ID NO: 163 is the determined 5′ cDNA sequence for SAL-14
SEQ ID NO: 164 is the determined 5′ cDNA sequence for SAL-16
SEQ ID NO: 165 is the determined 5′ cDNA sequence for SAL-23

SEQ ID NO: 166 is the determined 5′ cDNA sequence for SAL-26

SEQ ID NO: 167 is the determined 5′ cDNA sequence for SAL-29

SEQ ID NO: 168 is the determined 5′ cDNA sequence for SAL-32

SEQ ID NO: 169 is the determined 5′ cDNA sequence for SAL-39

SEQ ID NO: 170 is the determined 5′ cDNA sequence for SAL-42

SEQ ID NO: 171 is the determined 5′ cDNA sequence for SAL-43

SEQ ID NO: 172 is the determined 5′ cDNA sequence for SAL-44

SEQ ID NO: 173 is the determined 5′ cDNA sequence for SAL-48

SEQ ID NO: 174 is the determined 5′ cDNA sequence for SAL-68

SEQ ID NO: 175 is the determined 5′ cDNA sequence for SAL-72

SEQ ID NO: 176 is the determined 5′ cDNA sequence for SAL-77

SEQ ID NO: 177 is the determined 5′ cDNA sequence for SAL-86

SEQ ID NO: 178 is the determined 5′ cDNA sequence for SAL-88

SEQ ID NO: 179 is the determined 5′ cDNA sequence for SAL-93

SEQ ID NO: 180 is the determined 5′ cDNA sequence for SAL-100

SEQ ID NO: 181 is the determined 5′ cDNA sequence for SAL-105

SEQ ID NO: 182 is the predicted amino acid sequence for SAL-3

SEQ ID NO: 183 is the predicted amino acid sequence for SAL-24

SEQ ID NO: 184 is a first predicted amino acid sequence for SAL-25

SEQ ID NO: 185 is a second predicted amino acid sequence for SAL-25

SEQ ID NO: 186 is the predicted amino acid sequence for SAL-33

SEQ ID NO: 187 is a first predicted amino acid sequence for SAL-50

SEQ ID NO: 188 is the predicted amino acid sequence for SAL-57

SEQ ID NO: 189 is a first predicted amino acid sequence for SAL-66

SEQ ID NO: 190 is a second predicted amino acid sequence for SAL-66

SEQ ID NO: 191 is the predicted amino acid sequence for SAL-82

SEQ ID NO: 192 is the predicted amino acid sequence for SAL-99

SEQ ID NO: 193 is the predicted amino acid sequence for SAL-104

SEQ ID NO: 194 is the predicted amino acid sequence for SAL-5

SEQ ID NO: 195 is the predicted amino acid sequence for SAL-8

SEQ ID NO: 196 is the predicted amino acid sequence for SAL-12

SEQ ID NO: 197 is the predicted amino acid sequence for SAL-14

SEQ ID NO: 198 is the predicted amino acid sequence for SAL-16

SEQ ID NO: 199 is the predicted amino acid sequence for SAL-23

SEQ ID NO: 200 is the predicted amino acid sequence for SAL-26

SEQ ID NO: 201 is the predicted amino acid sequence for SAL-29

SEQ ID NO: 202 is the predicted amino acid sequence for SAL-32

SEQ ID NO: 203 is the predicted amino acid sequence for SAL-39

SEQ ID NO: 204 is the predicted amino acid sequence for SAL-42

SEQ ID NO: 205 is the predicted amino acid sequence for SAL-43

SEQ ID NO: 206 is the predicted amino acid sequence for SAL-44

SEQ ID NO: 207 is the predicted amino acid sequence for SAL-48

SEQ ID NO: 208 is the predicted amino acid sequence for SAL-68

SEQ ID NO: 209 is the predicted amino acid sequence for SAL-72

SEQ ID NO: 210 is the predicted amino acid sequence for SAL-77

SEQ ID NO: 211 is the predicted amino acid sequence for SAL-86

SEQ ID NO: 212 is the predicted amino acid sequence for SAL-88

SEQ ID NO: 213 is the predicted amino acid sequence for SAL-93

SEQ ID NO: 214 is the predicted amino acid sequence for SAL-100

SEQ ID NO: 215 is the predicted amino acid sequence for SAL-105

SEQ ID NO: 216 is a second predicted amino acid sequence for SAL-50

SEQ ID NO: 217 is the determined cDNA sequence for SSLT-4

SEQ ID NO: 218 is the determined cDNA sequence for SSLT-9

SEQ ID NO: 219 is the determined cDNA sequence for SSLT-10

SEQ ID NO: 220 is the determined cDNA sequence for SSLT-12

SEQ ID NO: 221 is the determined cDNA sequence for SSLT-19

SEQ ID NO: 222 is the determined cDNA sequence for SSLT-31

SEQ ID NO: 223 is the determined cDNA sequence for SSLT-38

SEQ ID NO: 224 is the determined cDNA sequence for LT4690-2

SEQ ID NO: 225 is the determined cDNA sequence for LT4690-3

SEQ ID NO: 226 is the determined cDNA sequence for LT4690-22

SEQ ID NO: 227 is the determined cDNA sequence for LT4690-24

SEQ ID NO: 228 is the determined cDNA sequence for LT4690-37

SEQ ID NO: 229 is the determined cDNA sequence for LT4690-39

SEQ ID NO: 230 is the determined cDNA sequence for LT4690-40

SEQ ID NO: 231 is the determined cDNA sequence for LT4690-41

SEQ ID NO: 232 is the determined cDNA sequence for LT4690-49

SEQ ID NO: 233 is the determined 3′ cDNA sequence for LT4690-55

SEQ ID NO: 234 is the determined 5′ cDNA sequence for LT4690-55

SEQ ID NO: 235 is the determined cDNA sequence for LT4690-59

SEQ ID NO: 236 is the determined cDNA sequence for LT4690-63

SEQ ID NO: 237 is the determined cDNA sequence for LT4690-71

SEQ ID NO: 238 is the determined cDNA sequence for 2LT-3

SEQ ID NO: 239 is the determined cDNA sequence for 2LT-6

SEQ ID NO: 240 is the determined cDNA sequence for 2LT-22

SEQ ID NO: 241 is the determined cDNA sequence for 2LT-25

SEQ ID NO: 242 is the determined cDNA sequence for 2LT-26

SEQ ID NO: 243 is the determined cDNA sequence for 2LT-31

SEQ ID NO: 244 is the determined cDNA sequence for 2LT-36

SEQ ID NO: 245 is the determined cDNA sequence for 2LT-42

SEQ ID NO: 246 is the determined cDNA sequence for 2LT-44

SEQ ID NO: 247 is the determined cDNA sequence for 2LT-54

SEQ ID NO: 248 is the determined cDNA sequence for 2LT-55

SEQ ID NO: 249 is the determined cDNA sequence for 2LT-57

SEQ ID NO: 250 is the determined cDNA sequence for 2LT-58

SEQ ID NO: 251 is the determined cDNA sequence for 2LT-59

SEQ ID NO: 252 is the determined cDNA sequence for 2LT-62

SEQ ID NO: 253 is the determined cDNA sequence for 2LT-63

SEQ ID NO: 254 is the determined cDNA sequence for 2LT-65

SEQ ID NO: 255 is the determined cDNA sequence for 2LT-66

SEQ ID NO: 256 is the determined cDNA sequence for 2LT-70
SEQ ID NO: 257 is the determined cDNA sequence for 2LT-73
SEQ ID NO: 258 is the determined cDNA sequence for 2LT-74
SEQ ID NO: 259 is the determined cDNA sequence for 2LT-76
SEQ ID NO: 260 is the determined cDNA sequence for 2LT-77
SEQ ID NO: 261 is the determined cDNA sequence for 2LT-78
SEQ ID NO: 262 is the determined cDNA sequence for 2LT-80
SEQ ID NO: 263 is the determined cDNA sequence for 2LT-85
SEQ ID NO: 264 is the determined cDNA sequence for 2LT-87
SEQ ID NO: 265 is the determined cDNA sequence for 2LT-89
SEQ ID NO: 266 is the determined cDNA sequence for 2LT-94
SEQ ID NO: 267 is the determined cDNA sequence for 2LT-95
SEQ ID NO: 268 is the determined cDNA sequence for 2LT-98
SEQ ID NO: 269 is the determined cDNA sequence for 2LT-100
SEQ ID NO: 270 is the determined cDNA sequence for 2LT-103
SEQ ID NO: 271 is the determined cDNA sequence for 2LT-105
SEQ ID NO: 272 is the determined cDNA sequence for 2LT-107
SEQ ID NO: 273 is the determined cDNA sequence for 2LT-108
SEQ ID NO: 274 is the determined cDNA sequence for 2LT-109
SEQ ID NO: 275 is the determined cDNA sequence for 2LT-118
SEQ ID NO: 276 is the determined cDNA sequence for 2LT-120
SEQ ID NO: 277 is the determined cDNA sequence for 2LT-121
SEQ ID NO: 278 is the determined cDNA sequence for 2LT-122
SEQ ID NO: 279 is the determined cDNA sequence for 2LT-124
SEQ ID NO: 280 is the determined cDNA sequence for 2LT-126
SEQ ID NO: 281 is the determined cDNA sequence for 2LT-127
SEQ ID NO: 282 is the determined cDNA sequence for 2LT-128
SEQ ID NO: 283 is the determined cDNA sequence for 2LT-129
SEQ ID NO: 284 is the determined cDNA sequence for 2LT-133
SEQ ID NO: 285 is the determined cDNA sequence for 2LT-137

SEQ ID NO: 286 is the determined cDNA sequence for LT4690-71

SEQ ID NO: 287 is the determined cDNA sequence for LT4690-82

SEQ ID NO: 288 is the determined full-length cDNA sequence for SSLT-74

SEQ ID NO: 289 is the determined cDNA sequence for SSLT-78

SEQ ID NO: 290 is the determined cDNA sequence for SCC1-8.

SEQ ID NO: 291 is the determined cDNA sequence for SCC1-12.

SEQ ID NO: 292 is the determined cDNA sequence for SCC1-336

SEQ ID NO: 293 is the determined cDNA sequence for SCC1-344

SEQ ID NO: 294 is the determined cDNA sequence for SCC1-345

SEQ ID NO: 295 is the determined cDNA sequence for SCC1-346

SEQ ID NO: 296 is the determined cDNA sequence for SCC1-348

SEQ ID NO: 297 is the determined cDNA sequence for SCC1-350

SEQ ID NO: 298 is the determined cDNA sequence for SCC1-352

SEQ ID NO: 299 is the determined cDNA sequence for SCC1-354

SEQ ID NO: 300 is the determined cDNA sequence for SCC1-355

SEQ ID NO: 301 is the determined cDNA sequence for SCC1-356

SEQ ID NO: 302 is the determined cDNA sequence for SCC1-357

SEQ ID NO: 303 is the determined cDNA sequence for SCC1-501

SEQ ID NO: 304 is the determined cDNA sequence for SCC1-503

SEQ ID NO: 305 is the determined cDNA sequence for SCC1-513

SEQ ID NO: 306 is the determined cDNA sequence for SCC1-516

SEQ ID NO: 307 is the determined cDNA sequence for SCC1-518

SEQ ID NO: 308 is the determined cDNA sequence for SCC1-519

SEQ ID NO: 309 is the determined cDNA sequence for SCC1-522

SEQ ID NO: 310 is the determined cDNA sequence for SCC1-523

SEQ ID NO: 311 is the determined cDNA sequence for SCC1-525

SEQ ID NO: 312 is the determined cDNA sequence for SCC1-527

SEQ ID NO: 313 is the determined cDNA sequence for SCC1-529

SEQ ID NO: 314 is the determined cDNA sequence for SCC1-530

SEQ ID NO: 315 is the determined cDNA sequence for SCC1-531
SEQ ID NO: 316 is the determined cDNA sequence for SCC1-532
SEQ ID NO: 317 is the determined cDNA sequence for SCC1-533
SEQ ID NO: 318 is the determined cDNA sequence for SCC1-536
SEQ ID NO: 319 is the determined cDNA sequence for SCC1-538
SEQ ID NO: 320 is the determined cDNA sequence for SCC1-539
SEQ ID NO: 321 is the determined cDNA sequence for SCC1-541
SEQ ID NO: 322 is the determined cDNA sequence for SCC1-542
SEQ ID NO: 323 is the determined cDNA sequence for SCC1-546
SEQ ID NO: 324 is the determined cDNA sequence for SCC1-549
SEQ ID NO: 325 is the determined cDNA sequence for SCC1-551
SEQ ID NO: 326 is the determined cDNA sequence for SCC1-552
SEQ ID NO: 327 is the determined cDNA sequence for SCC1-554
SEQ ID NO: 328 is the determined cDNA sequence for SCC1-558
SEQ ID NO: 329 is the determined cDNA sequence for SCC1-559
SEQ ID NO: 330 is the determined cDNA sequence for SCC1-561
SEQ ID NO: 331 is the determined cDNA sequence for SCC1-562
SEQ ID NO: 332 is the determined cDNA sequence for SCC1-564
SEQ ID NO: 333 is the determined cDNA sequence for SCC1-565
SEQ ID NO: 334 is the determined cDNA sequence for SCC1-566
SEQ ID NO: 335 is the determined cDNA sequence for SCC1-567
SEQ ID NO: 336 is the determined cDNA sequence for SCC1-568
SEQ ID NO: 337 is the determined cDNA sequence for SCC1-570
SEQ ID NO: 338 is the determined cDNA sequence for SCC1-572
SEQ ID NO: 339 is the determined cDNA sequence for SCC1-575
SEQ ID NO: 340 is the determined cDNA sequence for SCC1-576
SEQ ID NO: 341 is the determined cDNA sequence for SCC1-577
SEQ ID NO: 342 is the determined cDNA sequence for SCC1-578
SEQ ID NO: 343 is the determined cDNA sequence for SCC1-582
SEQ ID NO: 344 is the determined cDNA sequence for SCC1-583

SEQ ID NO: 345 is the determined cDNA sequence for SCC1-586
SEQ ID NO: 346 is the determined cDNA sequence for SCC1-588
SEQ ID NO: 347 is the determined cDNA sequence for SCC1-590
SEQ ID NO: 348 is the determined cDNA sequence for SCC1-591
SEQ ID NO: 349 is the determined cDNA sequence for SCC1-592
SEQ ID NO: 350 is the determined cDNA sequence for SCC1-593
SEQ ID NO: 351 is the determined cDNA sequence for SCC1-594
SEQ ID NO: 352 is the determined cDNA sequence for SCC1-595
SEQ ID NO: 353 is the determined cDNA sequence for SCC1-596
SEQ ID NO: 354 is the determined cDNA sequence for SCC1-598
SEQ ID NO: 355 is the determined cDNA sequence for SCC1-599
SEQ ID NO: 356 is the determined cDNA sequence for SCC1-602
SEQ ID NO: 357 is the determined cDNA sequence for SCC1-604
SEQ ID NO: 358 is the determined cDNA sequence for SCC1-605
SEQ ID NO: 359 is the determined cDNA sequence for SCC1-606
SEQ ID NO: 360 is the determined cDNA sequence for SCC1-607
SEQ ID NO: 361 is the determined cDNA sequence for SCC1-608
SEQ ID NO: 362 is the determined cDNA sequence for SCC1-610
SEQ ID NO: 363 is the determined cDNA sequence for clone DMS79T1
SEQ ID NO: 364 is the determined cDNA sequence for clone DMS79T2
SEQ ID NO: 365 is the determined cDNA sequence for clone DMS79T3
SEQ ID NO: 366 is the determined cDNA sequence for clone DMS79T5
SEQ ID NO: 367 is the determined cDNA sequence for clone DMS79T6
SEQ ID NO: 368 is the determined cDNA sequence for clone DMS79T7
SEQ ID NO: 369 is the determined cDNA sequence for clone DMS79T9
SEQ ID NO: 370 is the determined cDNA sequence for clone DMS79T10
SEQ ID NO: 371 is the determined cDNA sequence for clone DMS79T11
SEQ ID NO: 372 is the determined cDNA sequence for clone 128T1

SEQ ID NO: 373 is the determined cDNA sequence for clone 128T2

SEQ ID NO: 374 is the determined cDNA sequence for clone 128T3

SEQ ID NO: 375 is the determined cDNA sequence for clone 128T4

SEQ ID NO: 376 is the determined cDNA sequence for clone 128T5

SEQ ID NO: 377 is the determined cDNA sequence for clone 128T7

SEQ ID NO: 378 is the determined cDNA sequence for clone 128T9

SEQ ID NO: 379 is the determined cDNA sequence for clone 128T10

SEQ ID NO: 380 is the determined cDNA sequence for clone 128T11

SEQ ID NO: 381 is the determined cDNA sequence for clone 128T12

SEQ ID NO: 382 is the determined cDNA sequence for clone NCIH69T3

SEQ ID NO: 383 is the determined cDNA sequence for clone NCIH69T5

SEQ ID NO: 384 is the determined cDNA sequence for clone NCIH69T6

SEQ ID NO: 385 is the determined cDNA sequence for clone NCIH69T7

SEQ ID NO: 386 is the determined cDNA sequence for clone NCIH69T9

SEQ ID NO: 387 is the determined cDNA sequence for clone NCIH69T10

SEQ ID NO: 388 is the determined cDNA sequence for clone NCIH69T11

SEQ ID NO: 389 is the determined cDNA sequence for clone NCIH69T12

SEQ ID NO: 390 is the full-length cDNA sequence for 128T1

SEQ ID NO: 391 is the amino acid sequence for 128T1

SEQ ID NO: 392 is the full-length cDNA sequence for 2LT-128

SEQ ID NO: 393 is the amino acid sequence for 2LT-128

SEQ ID NO: 394 is an extended cDNA sequence for clone SCC1-542

SEQ ID NO: 395 is the amino acid sequence corresponding to SEQ ID NO:394

SEQ ID NO: 396 is an extended cDNA sequence for clone SCC1-593

SEQ ID NO: 397 is the amino acid sequence corresponding to SEQ ID NO:396

SEQ ID NO:398 is the determined cDNA sequence for 55508.1

SEQ ID NO:399 is the determined cDNA sequence for 55509.1

SEQ ID NO:400 is the determined cDNA sequence for 54243.1

SEQ ID NO:401 is the determined cDNA sequence for 54251.1

SEQ ID NO:402 is the determined cDNA sequence for 54252.1

SEQ ID NO:403 is the determined cDNA sequence for 54253.1

SEQ ID NO:404 is the determined cDNA sequence for 55518.1

SEQ ID NO:405 is the determined cDNA sequence for 54258.1

SEQ ID NO:406 is the determined cDNA sequence for 54575.1

SEQ ID NO:407 is the determined cDNA sequence for 54577.1

SEQ ID NO:408 is the determined cDNA sequence for 54584.1

SEQ ID NO:409 is the determined cDNA sequence for 55521.1

SEQ ID NO:410 is the determined cDNA sequence for 54589.1

SEQ ID NO:411 is the determined cDNA sequence for 54592.1

SEQ ID NO:412 is the determined cDNA sequence for 55134.1

SEQ ID NO:413 is the determined cDNA sequence for 55137.1

SEQ ID NO:414 is the determined cDNA sequence for 55140.1

SEQ ID NO:415 is the determined cDNA sequence for 55531.1

SEQ ID NO:416 is the determined cDNA sequence for 55532.1

SEQ ID NO:417 is the determined cDNA sequence for 54621.1

SEQ ID NO:418 is the determined cDNA sequence for 55548.1

SEQ ID NO:419 is the determined cDNA sequence for 54623.1

SEQ ID NO:420 is the determined cDNA sequence for L39

SEQ ID NO:421 is the predicted amino acid sequence for L39

SEQ ID NO:422 is the determined cDNA sequence for SCC2-29

SEQ ID NO:423 is the determined cDNA sequence for SCC2-36

SEQ ID NO:424 is the determined cDNA sequence for SCC2-60

SEQ ID NO:425 is the predicted amino acid sequence for SCC2-29

SEQ ID NO:426 is the predicted amino acid sequence for SCC2-36

SEQ ID NO:427 is the predicted amino acid sequence for SCC2-60

SEQ ID NO:428 is an extended cDNA sequence for the clone 20129, also referred to as 2LT-3, set forth in SEQ ID NO: 238

SEQ ID NO:429 is an extended cDNA sequence for the clone 20347, also referred to as 2LT-26, set forth in SEQ ID NO: 242

SEQ ID NO:430 is an extended cDNA sequence for the clone 21282, also referred to as 2LT-57, set forth in SEQ ID NO: 249

SEQ ID NO:431 is an extended cDNA sequence for the clone 21283, also referred to as 2LT-58, set forth in SEQ ID NO: 250

SEQ ID NO:432 is an extended cDNA sequence for the clone 21484, also referred to as 2LT-98, set forth in SEQ ID NO: 268

SEQ ID NO:433 is an extended cDNA sequence for the clone 21871, also referred to as 2LT-124, set forth in SEQ ID NO: 279

SEQ ID NO:434 is an amino acid sequence encoded by SEQ ID NO: 428

SEQ ID NO:435 is an amino acid sequence encoded by SEQ ID NO: 429

SEQ ID NO:436 is an amino acid sequence encoded by SEQ ID NO: 430

SEQ ID NO:437 is an amino acid sequence encoded by SEQ ID NO: 431

SEQ ID NO:438 is an amino acid sequence encoded by SEQ ID NO: 432

SEQ ID NO:439 is an amino acid sequence encoded by SEQ ID NO: 433

SEQ ID NO:440 is the determined cDNA sequence for clone 19A4

SEQ ID NO: 441 is the determined full-length cDNA sequence for clone 14F10.

SEQ ID NO: 442 is the determined 5′ cDNA sequence for clone 20E10.

SEQ ID NO: 443 is a first determined cDNA sequence for clone 55153.

SEQ ID NO: 444 is a second determined cDNA sequence for clone 55153.

SEQ ID NO: 445 is a first determined cDNA sequence for clone 55154.

SEQ ID NO: 446 is a second determined cDNA sequence for clone 55154.

SEQ ID NO: 447 is the determined cDNA sequence for clone 55155.

SEQ ID NO: 448 is a first determined cDNA sequence for clone 55156.

SEQ ID NO: 449 is a second determined cDNA sequence for clone 55156.

SEQ ID NO: 450 is a first determined cDNA sequence for clone 55157.

SEQ ID NO: 451 is a second determined cDNA sequence for clone 55157.

SEQ ID NO: 452 is the determined cDNA sequence for clone 55158.

SEQ ID NO: 453 is the determined cDNA sequence for clone 55159.

SEQ ID NO: 454 is a first determined cDNA sequence for clone 55161.

SEQ ID NO: 455 is a second determined cDNA sequence for clone 55161.

SEQ ID NO: 456 is a first determined cDNA sequence for clone 55162.

SEQ ID NO: 457 is a second determined cDNA sequence for clone 55162.

SEQ ID NO: 458 is a first determined cDNA sequence for clone 55163.

SEQ ID NO: 459 is a second determined cDNA sequence for clone 55163.

SEQ ID NO: 460 is a first determined cDNA sequence for clone 55164.

SEQ ID NO: 461 is a second determined cDNA sequence for clone 55164.

SEQ ID NO: 462 is a first determined cDNA sequence for clone 55165.

SEQ ID NO: 463 is a second determined cDNA sequence for clone 55165.

SEQ ID NO: 464 is a first determined cDNA sequence for clone 55166.

SEQ ID NO: 465 is a second determined cDNA sequence for clone 55166.

SEQ ID NO: 466 is a first determined cDNA sequence for clone 55167.

SEQ ID NO: 467 is a second determined cDNA sequence for clone 55167.

SEQ ID NO: 468 is a first determined cDNA sequence for clone 55168.

SEQ ID NO: 469 is a second determined cDNA sequence for clone 55168.

SEQ ID NO: 470 is a first determined cDNA sequence for clone 55169.

SEQ ID NO: 471 is a second determined cDNA sequence for clone 55169.

SEQ ID NO: 472 is a first determined cDNA sequence for clone 55170.

SEQ ID NO: 473 is a second determined cDNA sequence for clone 55170.

SEQ ID NO: 474 is the determined cDNA sequence for clone 55171.

SEQ ID NO: 475 is the determined cDNA sequence for clone 55172.

SEQ ID NO: 476 is the determined cDNA sequence for clone 55173.

SEQ ID NO: 477 is a first determined cDNA sequence for clone 55174.

SEQ ID NO: 478 is a second determined cDNA sequence for clone 55174.

SEQ ID NO: 479 is the determined cDNA sequence for clone 55175.

SEQ ID NO: 480 is the determined cDNA sequence for clone 55176.

SEQ ID NO: 481 is the determined cDNA sequence for contig 525.

SEQ ID NO: 482 is the determined cDNA sequence for contig 526.

SEQ ID NO: 483 is the determined cDNA sequence for contig 527.

SEQ ID NO: 484 is the determined cDNA sequence for contig 528.

SEQ ID NO: 485 is the determined cDNA sequence for contig 529.

SEQ ID NO: 486 is the determined cDNA sequence for contig 530.

SEQ ID NO: 487 is the determined cDNA sequence for contig 531.

SEQ ID NO: 488 is the determined cDNA sequence for contig 532.

SEQ ID NO: 489 is the determined cDNA sequence for contig 533.

SEQ ID NO: 490 is the determined cDNA sequence for contig 534.

SEQ ID NO: 491 is the determined cDNA sequence for contig 535.

SEQ ID NO: 492 is the determined cDNA sequence for contig 536.

SEQ ID NO: 493 is the determined cDNA sequence for contig 537.

SEQ ID NO: 494 is the determined cDNA sequence for contig 538.

SEQ ID NO: 495 is the determined cDNA sequence for contig 539.

SEQ ID NO: 496 is the determined cDNA sequence for contig 540.

SEQ ID NO: 497 is the determined cDNA sequence for contig 541.

SEQ ID NO: 498 is the determined cDNA sequence for contig 542.

SEQ ID NO: 499 is the determined cDNA sequence for contig 543.

SEQ ID NO: 500 is the determined cDNA sequence for contig 544.

SEQ ID NO: 501 is the determined cDNA sequence for contig 545.

SEQ ID NO: 502 is the determined cDNA sequence for contig 546.

SEQ ID NO: 503 is the determined cDNA sequence for contig 547.

SEQ ID NO: 504 is the determined cDNA sequence for contig 548.

SEQ ID NO: 505 is the determined cDNA sequence for contig 549.

SEQ ID NO: 506 is the determined cDNA sequence for contig 550.

SEQ ID NO: 507 is the determined cDNA sequence for contig 551.

SEQ ID NO: 508 is the determined cDNA sequence for contig 552.

SEQ ID NO: 509 is the determined cDNA sequence for contig 553.

SEQ ID NO: 510 is the determined cDNA sequence for contig 554.

SEQ ID NO: 511 is the determined cDNA sequence for contig 555.

SEQ ID NO: 512 is the determined cDNA sequence for clone 57207.

SEQ ID NO: 513 is the determined cDNA sequence for clone 57209.

SEQ ID NO: 514 is the determined cDNA sequence for clone 57210.

SEQ ID NO: 515 is the determined cDNA sequence for clone 57211.

SEQ ID NO: 516 is the determined cDNA sequence for clone 57212.

SEQ ID NO: 517 is the determined cDNA sequence for clone 57213.

SEQ ID NO: 518 is the determined cDNA sequence for clone 57215.

SEQ ID NO: 519 is the determined cDNA sequence for clone 57219.

SEQ ID NO: 520 is the determined cDNA sequence for clone 57221.

SEQ ID NO: 521 is the determined cDNA sequence for clone 57222.

SEQ ID NO: 522 is the determined cDNA sequence for clone 57223.

SEQ ID NO: 523 is the determined cDNA sequence for clone 57225.

SEQ ID NO: 524 is the determined cDNA sequence for clone 57227.

SEQ ID NO: 525 is the determined cDNA sequence for clone 57228.

SEQ ID NO: 526 is the determined cDNA sequence for clone 57229.

SEQ ID NO: 527 is the determined cDNA sequence for clone 57230.

SEQ ID NO: 528 is the determined cDNA sequence for clone 57231.

SEQ ID NO: 529 is the determined cDNA sequence for clone 57232.

SEQ ID NO: 530 is the determined cDNA sequence for clone 57233.

SEQ ID NO: 531 is the determined cDNA sequence for clone 57234.

SEQ ID NO: 532 is the determined cDNA sequence for clone 57235.

SEQ ID NO: 533 is the determined cDNA sequence for clone 57236.

SEQ ID NO: 534 is the determined cDNA sequence for clone 57237.

SEQ ID NO: 535 is the determined cDNA sequence for clone 57238.

SEQ ID NO: 536 is the determined cDNA sequence for clone 57239.

SEQ ID NO: 537 is the determined cDNA sequence for clone 57240.

SEQ ID NO: 538 is the determined cDNA sequence for clone 57242.

SEQ ID NO: 539 is the determined cDNA sequence for clone 57243.

SEQ ID NO: 540 is the determined cDNA sequence for clone 57245.

SEQ ID NO: 541 is the determined cDNA sequence for clone 57248.

SEQ ID NO: 542 is the determined cDNA sequence for clone 57249.

SEQ ID NO: 543 is the determined cDNA sequence for clone 57250.

SEQ ID NO: 544 is the determined cDNA sequence for clone 57251.

SEQ ID NO: 545 is the determined cDNA sequence for clone 57253.

SEQ ID NO: 546 is the determined cDNA sequence for clone 57254.

SEQ ID NO: 547 is the determined cDNA sequence for clone 57255.

SEQ ID NO: 548 is the determined cDNA sequence for clone 57257.

SEQ ID NO: 549 is the determined cDNA sequence for clone 57258.

SEQ ID NO: 550 is the determined cDNA sequence for clone 57259.

SEQ ID NO: 551 is the determined cDNA sequence for clone 57261.
SEQ ID NO: 552 is the determined cDNA sequence for clone 57262.
SEQ ID NO: 553 is the determined cDNA sequence for clone 57263.
SEQ ID NO: 554 is the determined cDNA sequence for clone 57264.
SEQ ID NO: 555 is the determined cDNA sequence for clone 57265.
SEQ ID NO: 556 is the determined cDNA sequence for clone 57266.
SEQ ID NO: 557 is the determined cDNA sequence for clone 57267.
SEQ ID NO: 558 is the determined cDNA sequence for clone 57268.
SEQ ID NO: 559 is the determined cDNA sequence for clone 57269.
SEQ ID NO: 560 is the determined cDNA sequence for clone 57270.
SEQ ID NO: 561 is the determined cDNA sequence for clone 57271.
SEQ ID NO: 562 is the determined cDNA sequence for clone 57272.
SEQ ID NO: 563 is the determined cDNA sequence for clone 57274.
SEQ ID NO: 564 is the determined cDNA sequence for clone 57275.
SEQ ID NO: 565 is the determined cDNA sequence for clone 57277.
SEQ ID NO: 566 is the determined cDNA sequence for clone 57280.
SEQ ID NO: 567 is the determined cDNA sequence for clone 57281.
SEQ ID NO: 568 is the determined cDNA sequence for clone 57282.
SEQ ID NO: 569 is the determined cDNA sequence for clone 57283.
SEQ ID NO: 570 is the determined cDNA sequence for clone 57285.
SEQ ID NO: 571 is the determined cDNA sequence for clone 57287.
SEQ ID NO: 572 is the determined cDNA sequence for clone 57288.
SEQ ID NO: 573 is the determined cDNA sequence for clone 57289.
SEQ ID NO: 574 is the determined cDNA sequence for clone 57290.
SEQ ID NO: 575 is the determined cDNA sequence for clone 57292.
SEQ ID NO: 576 is the determined cDNA sequence for clone 57295.
SEQ ID NO: 577 is the determined cDNA sequence for clone 57296.
SEQ ID NO: 578 is the determined cDNA sequence for clone 57297.
SEQ ID NO: 579 is the determined cDNA sequence for clone 57299.
SEQ ID NO: 580 is the determined cDNA sequence for clone 57301.

SEQ ID NO: 581 is the determined cDNA sequence for clone 57302.

SEQ ID NO: 582 is the determined cDNA sequence for the beta chain of a lung tumor specific T cell receptor.

SEQ ID NO: 583 is the determined cDNA sequence for the alpha chain of a lung tumor specific T cell receptor.

SEQ ID NO: 584 is the amino acid sequence encoded by SEQ ID NO: 583.

SEQ ID NO: 585 is the amino acid sequence encoded by SEQ ID NO: 582.

SEQ ID NO: 586 is the amino acid sequence encoded by the 5′ terminus of 14F10.

SEQ ID NO: 587 is the amino acid sequence of a T cell epitope contained within SEQ ID NO: 586.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed generally to compositions and their use in the therapy and diagnosis of cancer, particularly lung cancer. As described further below, illustrative compositions of the present invention include, but are not restricted to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such polypeptides, antibodies and other binding agents, antigen presenting cells (APCs) and immune system cells (*e.g.*, T cells).

The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook, et al. Molecular Cloning: A Laboratory Manual (2nd Edition, 1989); Maniatis et al. Molecular Cloning: A Laboratory Manual (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.); Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B.

Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal, A Practical Guide to Molecular Cloning (1984).

All publications, patents and patent applications cited herein, whether supra or infra, are hereby incorporated by reference in their entirety.

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates otherwise.

Polypeptide Compositions

As used herein, the term "polypeptide" is used in its conventional meaning, *i.e.*, as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide may be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising epitopes, *i.e.*, antigenic determinants substantially responsible for the immunogenic properties of a polypeptide and being capable of evoking an immune response.

Particularly illustrative polypeptides of the present invention comprise those encoded by a polynucleotide sequence set forth in any one of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly stringent conditions, to a polynucleotide sequence set forth in any one of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583. Certain other illustrative polypeptides of the invention comprise amino acid sequences as set forth in any one of SEQ ID NOs: 391, 393, 395, 397, 421, 425-427, 434-439 and 584-587.

The polypeptides of the present invention are sometimes herein referred to as lung tumor proteins or lung tumor polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in lung tumor samples. Thus, a "lung tumor polypeptide" or "lung tumor protein," refers generally to a polypeptide sequence of the present invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed in a substantial proportion of lung tumor samples, for example preferably greater than about 20%, more preferably greater than about 30%, and most preferably greater than about 50% or more of lung tumor samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in normal tissues, as determined using a representative assay provided herein. A lung tumor polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

In certain preferred embodiments, the polypeptides of the invention are immunogenic, *i.e.*, they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with lung cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual,* Cold Spring Harbor Laboratory, 1988. In one illustrative example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ^{125}I-labeled Protein A.

As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (*i.e.,* specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide. Immunogenic portions may generally be identified using well known techniques, such

as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well-known techniques.

In one preferred embodiment, an immunogenic portion of a polypeptide of the present invention is a portion that reacts with antisera and/or T-cells at a level that is not substantially less than the reactivity of the full-length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length polypeptide. In some instances, preferred immunogenic portions will be identified that have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, *e.g.*, having greater than about 100% or 150% or more immunogenic activity.

In certain other embodiments, illustrative immunogenic portions may include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other illustrative immunogenic portions will contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

In another embodiment, a polypeptide composition of the invention may also comprise one or more polypeptides that are immunologically reactive with T cells and/or antibodies generated against a polypeptide of the invention, particularly a polypeptide having an amino acid sequence disclosed herein, or to an immunogenic fragment or variant thereof.

In another embodiment of the invention, polypeptides are provided that comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies that are immunologically reactive with one or more polypeptides described herein, or

one or more polypeptides encoded by contiguous nucleic acid sequences contained in the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency.

The present invention, in another aspect, provides polypeptide fragments comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide compositions set forth herein, such as those set forth in SEQ ID NOs: 391, 393, 395, 397, 421, 425-427, 434-439 and 584-587, or those encoded by a polynucleotide sequence set forth in a sequence of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583.

In another aspect, the present invention provides variants of the polypeptide compositions described herein. Polypeptide variants generally encompassed by the present invention will typically exhibit at least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity (determined as described below), along its length, to a polypeptide sequences set forth herein.

In one preferred embodiment, the polypeptide fragments and variants provide by the present invention are immunologically reactive with an antibody and/or T-cell that reacts with a full-length polypeptide specifically set for the herein.

In another preferred embodiment, the polypeptide fragments and variants provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or more of that exhibited by a full-length polypeptide sequence specifically set forth herein.

A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants may be naturally occurring or may be synthetically generated, for example, by modifying one or more of the above polypeptide sequences of the invention and evaluating their immunogenic

activity as described herein and/or using any of a number of techniques well known in the art.

For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other illustrative variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

In many instances, a variant will contain conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide with desirable characteristics, *e.g.*, with immunogenic characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE 1

Amino Acids			Codons					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGA	GGC	GGG	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUA	AUC	AUU			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUA	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its

hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (–0.4); threonine (–0.7); serine (–0.8); tryptophan (–0.9); tyrosine (–1.3); proline (–1.6); histidine (–3.2); glutamate (–3.5); glutamine (–3.5); aspartate (–3.5); asparagine (–3.5); lysine (–3.9); and arginine (–4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (–0.4); proline (–0.5 ± 1); alanine (–0.5); histidine (–0.5); cysteine (–1.0); methionine (–1.3); valine (–1.5); leucine (–1.8); isoleucine (–1.8); tyrosine (–2.3); phenylalanine (–2.5); tryptophan (–3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that

take various of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5′ and/or 3′ ends; the use of phosphorothioate or 2′ O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the

polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

When comparing polypeptide sequences, two sequences are said to be "identical" if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS 5*:151-153; Myers, E.W. and Muller W. (1988) *CABIOS 4*:11-17; Robinson, E.D. (1971) *Comb. Theor 11*:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol. 4*:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA 80*:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these

algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

In one preferred approach, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Within other illustrative embodiments, a polypeptide may be a fusion polypeptide that comprises multiple polypeptides as described herein, or that comprises

at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

Fusion polypeptides may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3′ end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5′ end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion polypeptide using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as

linkers include those disclosed in Maratea et al., *Gene 40*:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA 83*:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5′ to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3′ to the DNA sequence encoding the second polypeptide.

The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, *336*:86-91, 1997).

In one preferred embodiment, the immunological fusion partner is derived from a Mycobacterium sp., such as a Mycobacterium tuberculosis-derived Ra12 fragment. Ra12 compositions and methods for their use in enhancing the expression and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; see also, Skeiky *et al.*, *Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference). C-terminal fragments of the MTB32A coding sequence express at high levels and remain as a soluble polypeptides throughout the

purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous immunogenic polypeptides with which it is fused. One preferred Ra12 fusion polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A. Other preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide. Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium Haemophilus influenza B (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemaglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is

derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the LytA gene; *Gene 43*:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology 10*:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion polypeptide. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as described in U.S. Patent No. 5,633,234. An immunogenic polypeptide of the invention, when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of $CD4^+$ T-cells specific for the polypeptide.

Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc. 85*:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

In general, polypeptide compositions (including fusion polypeptides) of the invention are isolated. An "isolated" polypeptide is one that is removed from its original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure.

Polynucleotide Compositions

The present invention, in other aspects, provides polynucleotide compositions. The terms "DNA" and "polynucleotide" are used essentially interchangeably herein to refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the

present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.,* an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or may comprise a sequence that encodes a variant or derivative, preferably and immunogenic variant or derivative, of such a sequence.

Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583, complements of a polynucleotide sequence set forth in any one of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583, and degenerate variants of a polynucleotide sequence set forth in any one of SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583. In certain preferred embodiments, the polynucleotide sequences set forth herein encode immunogenic polypeptides, as described above.

In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in SEQ ID NOs: 217-390, 392, 394, 396, 398-420 422-424, 428-433 and 440-583, for example those comprising at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide sequence of this invention using the methods described herein, (*e.g.*, BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the polypeptide encoded by the variant polynucleotide is not substantially diminished relative to a polypeptide encoded by a polynucleotide sequence specifically set forth

herein). The term "variants" should also be understood to encompasses homologous genes of xenogenic origin.

In additional embodiments, the present invention provides polynucleotide fragments comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-60°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. One skilled in the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable highly stringent hybridization conditions include those described above, with the exception that the temperature of hybridization is increased, *e.g.*, to 60-65°C or 65-70°C.

In certain preferred embodiments, the polynucleotides described above, *e.g.*, polynucleotide variants, fragments and hybridizing sequences, encode polypeptides

that are immunologically cross-reactive with a polypeptide sequence specifically set forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative polynucleotide segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

When comparing polynucleotide sequences, two sequences are said to be "identical" if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships.

In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS 5*:151-153; Myers, E.W. and Muller W. (1988) *CABIOS 4*:11-17; Robinson, E.D. (1971) *Comb. Theor 11*:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol. 4*:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy,* Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA 80*:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments;

or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.,* gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.,* the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of

immunogenic variants and/or derivatives of the polypeptides described herein. By this approach, specific modifications in a polypeptide sequence can be made through mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the polynucleotide.

Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25 nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson, 1987). Typically,

vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

In another approach for the production of polypeptide variants of the present invention, recursive sequence recombination, as described in U.S. Patent No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 nucleotide long contiguous sequence that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, *e.g.*, those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a sequence of interest will enable them to be of use in detecting the presence of complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in various bacterial cells. The total size of fragment, as well as the size of the

complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR™ technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, *e.g.*, one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

According to another embodiment of the present invention, polynucleotide compositions comprising antisense oligonucleotides are provided. Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein synthesis, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis is well established. For example, the synthesis of polygalactauronase and the muscarine

type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, striatal $GABA_A$ receptor and human EGF (Jaskulski *et al.*, Science. 1988 Jun 10;240(4858):1544-6; Vasanthakumar and Ahmed, Cancer Commun. 1989;1(4):225-32; Peris *et al.*, Brain Res Mol Brain Res. 1998 Jun 15;57(2):310-20; U. S. Patent 5,801,154; U.S. Patent 5,789,573; U. S. Patent 5,718,709 and U.S. Patent 5,610,288). Antisense constructs have also been described that inhibit and can be used to treat a variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683).

Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein, or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In each case, preferred compositions comprise a sequence region that is complementary, and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure, T_m, binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary to 5′ regions of the mRNA. These secondary structure analyses and target site selection

considerations can be performed, for example, using v.4 of the OLIGO primer analysis software and/or the BLASTN 2.0.5 algorithm software (Altschul *et al.,* Nucleic Acids Res. 1997, 25(17):3389-402).

The use of an antisense delivery method employing a short peptide vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, Nucleic Acids Res. 1997 Jul 15;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, Proc Natl Acad Sci U S A. 1987 Dec;84(24):8788-92; Forster and Symons, Cell. 1987 Apr 24;49(2):211-20). For example, a large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, Cell. 1981 Dec;27(3 Pt 2):487-96; Michel and Westhof, J Mol Biol. 1990 Dec 5;216(3):585-610; Reinhold-Hurek and Shub, Nature. 1992 May 14;357(6374):173-6). This specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs

through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action (Woolf *et al.*, Proc Natl Acad Sci U S A. 1992 Aug 15;89(16):7305-9). Thus, the specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead

1;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada *et al.*, Cell. 1983 Dec;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, Cell. 1990 May 18;61(4):685-96; Saville and Collins, Proc Natl Acad Sci U S A. 1991 Oct 1;88(19):8826-30; Collins and Olive, Biochemistry. 1993 Mar 23;32(11):2795-9); and an example of the Group I intron is described in (U. S. Patent 4,987,071). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO 92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by

incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells Ribozymes expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, Antisense Nucleic Acid Drug Dev. 1997 7(4) 431-37). PNA is able to be utilized in a number methods that traditionally have used RNA or DNA. Often PNA sequences perform better in

techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997 Jun;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, *Science* 1991 Dec 6;254(5037):1497-500; Hanvey *et al.*, Science. 1992 Nov 27;258(5087):1481-5; Hyrup and Nielsen, Bioorg Med Chem. 1996 Jan;4(1):5-23). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*, Bioorg Med Chem. 1995 Apr;3(4):437-45). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography,

providing yields and purity of product similar to those observed during the synthesis of peptides.

Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (for example, Norton *et al.*, Bioorg Med Chem. 1995 Apr;3(4):437-45; Petersen *et al.*, J Pept Sci. 1995 May-Jun;1(3):175-83; Orum *et al.*, Biotechniques. 1995 Sep;19(3):472-80; Footer *et al.*, Biochemistry. 1996 Aug 20;35(33):10673-9; Griffith *et al.*, Nucleic Acids Res. 1995 Aug 11;23(15):3003-8; Pardridge *et al.*, Proc Natl Acad Sci U S A. 1995 Jun 6;92(12):5592-6; Boffa *et al.*, Proc Natl Acad Sci U S A. 1995 Mar 14;92(6):1901-5; Gambacorti-Passerini *et al.*, Blood. 1996 Aug 15;88(4):1411-7; Armitage *et al.*, Proc Natl Acad Sci U S A. 1997 Nov 11;94(23):12320-5; Seeger *et al.*, Biotechniques. 1997 Sep;23(3):512-7). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (Anal Chem. 1993 Dec 15;65(24):3545-9) and Jensen *et al.* (Biochemistry. 1997 Apr 22;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, mutational analysis, enhancers of transcription, nucleic acid purification, isolation of

transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, *in situ* hybridization, and the like.

Polynucleotide Identification, Characterization and Expression

Polynucleotides compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques (see generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.,* expression that is at least two fold greater in a tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA 93*:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA 94*:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as tumor cells.

Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by reference in its entirety. Briefly, in PCR™, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse

transcription and PCR™ amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Any of a number of other template dependent processes, many of which are variations of the PCR ™ amplification technique, are readily known and available in the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Patent No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain Reaction (RCR). Still other amplification methods are described in Great Britain Pat. Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara, 1989) are also well-known to those of skill in the art.

An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (*e.g.*, a tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5′ and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5′ sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or

bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, amplification techniques, such as those described above, can be useful for obtaining a full length coding sequence from a partial cDNA sequence. One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res. 16*:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5′ and 3′ of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic. 1*:111-19, 1991) and walking PCR (Parker et al., *Nucl.*

Acids. Res. 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction

sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science 269*:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (*e.g.*, Creighton, T. (1983) Proteins, Structures and Molecular Principles, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate

expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York. N.Y.

A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (*e.g.*, baculovirus); plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5′ and 3′ untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains

multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem. 264*:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, Saccharomyces cerevisiae, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J. 6*:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J. 3*:1671-1680; Broglie, R. et al. (1984) *Science 224*:838-843; and Winter, J. et al. (1991)

Results Probl. Cell Differ. *17*:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in Spodoptera frugiperda cells or in Trichoplusia larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, S. frugiperda cells or Trichoplusia larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci. 91* :3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci. 81*:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion

thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ. 20*:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation. glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) *Cell 11*:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1990) *Cell 22*:817-23) genes which can be employed in tk.sup.- or

aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci. 77*:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol. 150*:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci. 85*:8047-51). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. et al. (1995) *Methods Mol. Biol. 55*:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells that contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies

specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul. Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med. 158*:1211-1216).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are

not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen. San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif. 3*:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; *DNA Cell Biol. 12*:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc. 85*:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

<u>Antibody Compositions, Fragments Thereof and Other Binding Agents</u>

According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunogically bind," and/or is "immunologically reactive" to a polypeptide of the invention if it reacts at a detectable level (within, for example, an

ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant (K_d) of the interaction, wherein a smaller K_d represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" (K_{on}) and the "off rate constant" (K_{off}) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of K_{off}/K_{on} enables cancellation of all parameters not related to affinity, and is thus equal to the dissociation constant K_d. See, generally, Davies et al. (1990) Annual Rev. Biochem. 59:439-473.

An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen,

and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

Binding agents may be further capable of differentiating between patients with and without a cancer, such as lung cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. Preferably, a statistically significant number of samples with and without the disease will be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a

superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol. 6*:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and

extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

A number of therapeutically useful molecules are known in the art which comprise antigen-binding sites that are capable of exhibiting immunological binding properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The enzyme pepsin is able to cleave IgG molecules to provide several fragments, including the "$F(ab')_2$ " fragment which comprises both antigen-binding sites. An "Fv" fragment can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a non-covalent V_H::V_L heterodimer including an antigen-binding site which retains much of the antigen recognition and binding capabilities of the native antibody molecule. Inbar et al. (1972) Proc. Nat. Acad. Sci. USA 69:2659-2662; Hochman et al. (1976) Biochem 15:2706-2710; and Ehrlich et al. (1980) Biochem 19:4091-4096.

A single chain Fv ("sFv") polypeptide is a covalently linked V_H::V_L heterodimer which is expressed from a gene fusion including V_H- and V_L-encoding genes linked by a peptide-encoding linker. Huston et al. (1988) Proc. Nat. Acad. Sci. USA 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated--but chemically separated--light and heavy polypeptide chains from an antibody V region into an sFv molecule which will fold into a three dimensional structure substantially similar to the structure of an antigen-binding site. See, *e.g.*, U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.; and U.S. Pat. No. 4,946,778, to Ladner et al.

Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRS and define the spatial relationship of the CDRs relative to each other. As used herein, the term "CDR set" refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-

terminus of a heavy or light chain, these regions are denoted as "CDR1," "CDR2," and "CDR3" respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (*e.g.*, a CDR1, CDR2 or CDR3) is referred to herein as a "molecular recognition unit." Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

As used herein, the term "FR set" refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues directly adjacent to the CDRS. Within FRs, certain amino residues and certain structural features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain "canonical" structures--regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

A number of "humanized" antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) Nature 349:293-299; Lobuglio et al. (1989) Proc. Nat. Acad. Sci. USA 86:4220-4224; Shaw et al. (1987) J Immunol. 138:4534-4538; and Brown et al. (1987) Cancer Res. 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant domain (Riechmann et al. (1988) Nature 332:323-327; Verhoeyen et al. (1988) Science

239:1534-1536; and Jones et al. (1986) Nature 321:522-525), and rodent CDRs supported by recombinantly veneered rodent FRs (European Patent Publication No. 519,596, published Dec. 23, 1992). These "humanized" molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

As used herein, the terms "veneered FRs" and "recombinantly veneered FRs" refer to the selective replacement of FR residues from, *e.g.*, a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the ligand binding characteristics of an antigen-binding site are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-binding surface. Davies et al. (1990) Ann. Rev. Biochem. 59:439-473. Thus, antigen binding specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other, and their interaction with the rest of the V region domains are carefully maintained. By using veneering techniques, exterior (*e.g.*, solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

The process of veneering makes use of the available sequence data for human antibody variable domains compiled by Kabat et al., in Sequences of Proteins of Immunological Interest, 4th ed., (U.S. Dept. of Health and Human Services, U.S. Government Printing Office, 1987), updates to the Kabat database, and other accessible U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V region amino acids can be deduced from the known three-dimensional structure for human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody molecule of interest are compared with corresponding FR sequences of human variable

domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the art. Residue switching is only carried out with moieties which are at least partially exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region domains, such as proline, glycine and charged amino acids.

In this manner, the resultant "veneered" murine antigen-binding sites are thus designed to retain the murine CDR residues, the residues substantially adjacent to the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (*e.g.*, electrostatic and hydrophobic) contacts between heavy and light chain domains, and the residues from conserved structural regions of the FRs which are believed to influence the "canonical" tertiary structures of the CDR loops. These design criteria are then used to prepare recombinant nucleotide sequences which combine the CDRs of both the heavy and light chain of a murine antigen-binding site into human-appearing FRs that can be used to transfect mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

In another embodiment of the invention, monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y, ^{123}I, ^{125}I, ^{131}I, ^{186}Re, ^{188}Re, ^{211}At, and ^{212}Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diptheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a

substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody.

Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

T Cell Compositions

The present invention, in another aspect, provides T cells specific for a tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide.

Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor polypeptide or polynucleotide of the invention is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a polypeptide of the present invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res. 54*:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.,* by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml - 100 μg/ml, preferably 200 ng/ml - 25 μg/ml) for 3 - 7 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.,* TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be $CD4^+$ and/or $CD8^+$. Tumor polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, $CD4^+$ or $CD8^+$ T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a

variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

Pharmaceutical Compositions

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

Therefore, in another aspect of the present invention, pharmaceutical compositions are provided comprising one or more of the polynucleotide, polypeptide, antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide and/or polypeptide compositions of the invention for use in prophylactic and theraputic vaccine applications. Vaccine preparation is generally described in, for example, M.F.

Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination with one or more immunostimulants.

It will be apparent that any of the pharmaceutical compositions described herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.*, salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.*, sodium, potassium, lithium, ammonium, calcium and magnesium salts).

In another embodiment, illustrative immunogenic compositions, *e.g.*, vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the polynucleotide may be administered within any of a variety of delivery systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems 15*:143-198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary regulatory DNA regulatory sequences for expression in a patient (such as a suitable promoter and terminating signal). Alternatively, bacterial delivery systems may involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

Therefore, in certain embodiments, polynucleotides encoding immunogenic polypeptides described herein are introduced into suitable mammalian host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to a subject. A number of illustrative retroviral systems have been described (*e.g.*, U.S.

Pat. No. 5,219,740; Miller and Rosman (1989) BioTechniques 7:980-990; Miller, A. D. (1990) Human Gene Therapy 1:5-14; Scarpa et al. (1991) Virology 180:849-852; Burns et al. (1993) Proc. Natl. Acad. Sci. USA 90:8033-8037; and Boris-Lawrie and Temin (1993) Cur. Opin. Genet. Develop. 3:102-109.

In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) J. Virol. 57:267-274; Bett et al. (1993) J. Virol. 67:5911-5921; Mittereder et al. (1994) Human Gene Therapy 5:717-729; Seth et al. (1994) J. Virol. 68:933-940; Barr et al. (1994) Gene Therapy 1:51-58; Berkner, K. L. (1988) BioTechniques 6:616-629; and Rich et al. (1993) Human Gene Therapy 4:461-476).

Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using techniques well known in the art. See, *e.g.*, U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) Molec. Cell. Biol. 8:3988-3996; Vincent et al. (1990) Vaccines 90 (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) Current Opinion in Biotechnology 3:533-539; Muzyczka, N. (1992) Current Topics in Microbiol. and Immunol. 158:97-129; Kotin, R. M. (1994) Human Gene Therapy 5:793-801; Shelling and Smith (1994) Gene Therapy 1:165-169; and Zhou et al. (1994) J. Exp. Med. 179:1867-1875.

Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene

encoding the polypeptide of interest into the viral genome. The resulting TK.sup.(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide or polynucleotides of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, *e.g.*, Elroy-Stein and Moss, Proc. Natl. Acad. Sci. USA (1990) 87:6743-6747; Fuerst et al. Proc. Natl. Acad. Sci. USA (1986) 83:8122-8126.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant Avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, *e.g.*, WO 91/12882; WO 89/03429; and WO 92/03545.

Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in U.S. Patent Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based

on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Patent Nos. 5,505,947 and 5,643,576.

Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. J. Biol. Chem. (1993) 268:6866-6869 and Wagner et al. Proc. Natl. Acad. Sci. USA (1992) 89:6099-6103, can also be used for gene delivery under the invention.

Additional illustrative information on these and other known viral-based delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA 86*:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci. 569*:86-103, 1989; Flexner et al., *Vaccine 8*:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques 6*:616-627, 1988; Rosenfeld et al., *Science 252*:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA 91*:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA 90*:11498-11502, 1993; Guzman et al., *Circulation 88*:2838-2848, 1993; and Guzman et al., *Cir. Res. 73*:1202-1207, 1993.

In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in the specific location and orientation *via* homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the polynucleotide may be stably maintained in the cell as a separate, episomal segment of DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. The manner in which the expression construct is delivered to a cell and where in the cell the polynucleotide remains is dependent on the type of expression construct employed.

In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al., *Science 259*:1745-1749, 1993 and reviewed by Cohen, *Science 259*:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described. In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK) and Powderject Vaccines Inc. (Madison, WI), some examples of which are described in U.S. Patent Nos. 5,846,796; 6,010,478; 5,865,796; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to high speed within a helium gas jet generated by a hand held device, propelling the particles into a target tissue of interest.

In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include those provided by Bioject, Inc. (Portland, OR), some examples of which are described in U.S. Patent Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639 and 5,993,412.

According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bortadella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Within certain embodiments of the invention, the adjuvant composition is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (*e.g.*, IFN-γ, TNFα, IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL® adjuvants are available from Corixa Corporation (Seattle, WA; *see*, for example, US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by Sato et al., *Science 273*:352, 1996. Another preferred adjuvant comprises a saponin, such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, MA); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins . Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example

combinations of at least two of the following group comprising QS21, QS7, Quil A, β-escin, or digitonin.

Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and polylactide-co-glycolide particles, poly-N-acetyl glucosamine-based polymer matrix, particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated together with a polyoxyethylene ether or ester, in either a non-particulate solution or suspension, or in a particulate structure such as a paucilamelar liposome or ISCOM. The saponins may also be formulated with excipients such as Carbopol[R] to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

In one preferred embodiment, the adjuvant system includes the combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL® adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-MPL® adjuvant and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Another enhanced adjuvant system involves the combination of a CpG-containing oligonucleotide and a saponin derivative particularly the combination of CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally comprises an oil in water emulsion and tocopherol.

Additional illustrative adjuvants for use in the pharmaceutical compositions of the invention include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart,

Belgium), Detox (Enhanzyn®) (Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties, and polyoxyethylene ether adjuvants such as those described in WO 99/52549A1.

Other preferred adjuvants include adjuvant molecules of the general formula

(I): $HO(CH_2CH_2O)_n$-A-R,

wherein, n is 1-50, A is a bond or –C(O)-, R is C_{1-50} alkyl or Phenyl C_{1-50} alkyl.

One embodiment of the present invention consists of a vaccine formulation comprising a polyoxyethylene ether of general formula (I), wherein *n* is between 1 and 50, preferably 4-24, most preferably 9; the *R* component is C_{1-50}, preferably C_4-C_{20} alkyl and most preferably C_{12} alkyl, and *A* is a bond. The concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether, polyoxyethylene-9-steoryl ether, polyoxyethylene-8-steoryl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether. Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck index (12th edition: entry 7717). These adjuvant molecules are described in WO 99/52549.

The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant combination is preferably with CpG as described in the pending UK patent application GB 9820956.2.

According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or

maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature 392*:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med. 50*:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med. 4*:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNFα to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNFα, CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fcγ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.,* CD54 and CD11) and costimulatory molecules (*e.g.,* CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide of the invention (or portion or other variant thereof) such that the encoded polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology 75*:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.,* vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.,* a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will typically vary depending on the mode of administration. Compositions of the

present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

Carriers for use within such pharmaceutical compositions are biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release. In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the level of ordinary skill in the art using known techniques. Illustrative carriers useful in this regard include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

In another illustrative embodiment, biodegradable microspheres (*e.g.*, polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763; 5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems. such as described in WO/99 40934, and references cited therein, will also be useful for many applications. Another illustrative carrier/delivery system employs a carrier comprising particulate-protein complexes, such as those described in U.S. Patent No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

The pharmaceutical compositions of the invention will often further comprise one or more buffers (*e.g.*, neutral buffered saline or phosphate buffered

saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate.

The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are typically sealed in such a way to preserve the sterility and stability of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art, some of which are briefly discussed below for general purposes of illustration.

In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (see, for example, Mathiowitz *et al.*, Nature 1997 Mar 27;386(6623):410-4; Hwang *et al.*, Crit Rev Ther Drug Carrier Syst 1998;15(3):243-84; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia,

cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds may be incorporated into sustained-release preparation and formulations.

Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared is such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

For oral administration the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363. In certain embodiments, solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain a preservative to prevent the growth of microorganisms.

Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U. S. Patent 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered

isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of course preferably meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

In another embodiment of the invention, the compositions disclosed herein may be formulated in a neutral or salt form. Illustrative pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

The carriers can further comprise any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. The phrase

"pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the lungs *via* nasal aerosol sprays has been described, *e.g.*, in U. S. Patent 5,756,353 and U. S. Patent 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, J Controlled Release 1998 Mar 2;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871) are also well-known in the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of a polytetrafluoroetheylene support matrix is described in U. S. Patent 5,780,045.

In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

The formation and use of liposome and liposome-like preparations as potential drug carriers is generally known to those of skill in the art (see for example, Lasic, Trends Biotechnol 1998 Jul;16(7):307-21; Takakura, Nippon Rinsho 1998 Mar;56(3):691-5; Chandran *et al.*, Indian J Exp Biol. 1997 Aug;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.,* J Biol Chem. 1990 Sep 25;265(27):16337-42; Muller *et al.*, DNA Cell Biol. 1990 Apr;9(3):221-9). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery

systems. Liposomes have been used effectively to introduce genes, various drugs, radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, he use of liposomes does not appear to be associated with autoimmune responses or unacceptable toxicity after systemic delivery.

In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs).

Alternatively, in other embodiments, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero *et al.*, Drug Dev Ind Pharm. 1998 Dec;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μm) may be designed using polymers able to be degraded *in vivo*. Such particles can be made as described, for example, by Couvreur *et al.,* Crit Rev Ther Drug Carrier Syst. 1988;5(1):1-20; zur Muhlen *et al.*, Eur J Pharm Biopharm. 1998 Mar;45(2):149-55; Zambaux *et al.* J Controlled Release. 1998 Jan 2;50(1-3):31-40; and U. S. Patent 5,145,684.

Cancer Therapeutic Methods

In further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for the immunotherapy of lung cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the

pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as $CD8^+$ cytotoxic T lymphocytes and $CD4^+$ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for

immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow in vivo and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews 157*:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or

partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 μg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

Cancer Detection and Diagnostic Compositions, Methods and Kits

In general, a cancer may be detected in a patient based on the presence of one or more lung tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as lung cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a lung tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual,* Cold Spring Harbor Laboratory,

1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length lung tumor proteins and polypeptide portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and

functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see*, *e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The

immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with lung cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as lung cancer, the signal detected from the reporter group that remains bound to the solid support is

generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site

generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within certain methods, a biological sample comprising $CD4^+$ and/or $CD8^+$ T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (*e.g.*, 5 - 25 μg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For $CD4^+$ T cells, activation is preferably detected by evaluating proliferation of the T cells. For $CD8^+$ T cells,

activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a tumor protein of the invention that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, *51*:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in

optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

PREPARATION OF LUNG TUMOR-SPECIFIC CDNA SEQUENCES USING DIFFERENTIAL DISPLAY RT-PCR

This example illustrates the preparation of cDNA molecules encoding lung tumor-specific polypeptides using a differential display screen.

Tissue samples were prepared from lung tumor and normal tissue of a patient with lung cancer that was confirmed by pathology after removal of samples from the patient. Normal RNA and tumor RNA was extracted from the samples and mRNA was isolated and converted into cDNA using a $(dT)_{12}AG$ (SEQ ID NO: 47)

anchored 3′ primer. Differential display PCR was then executed using a randomly chosen primer (SEQ ID NO: 48). Amplification conditions were standard buffer containing 1.5 mM $MgCl_2$, 20 pmol of primer, 500 pmol dNTP and 1 unit of Taq DNA polymerase (Perkin-Elmer, Branchburg, NJ). Forty cycles of amplification were performed using 94 °C denaturation for 30 seconds, 42 °C annealing for 1 minute and 72 °C extension for 30 seconds. Bands that were repeatedly observed to be specific to the RNA fingerprint pattern of the tumor were cut out of a silver stained gel, subcloned into the pGEM-T vector (Promega, Madison, WI) and sequenced. The isolated 3′ sequences are provided in SEQ ID NO: 1-16.

Comparison of these sequences to those in the public databases using the BLASTN program, revealed no significant homologies to the sequences provided in SEQ ID NO: 1-11. To the best of the inventors' knowledge, none of the isolated DNA sequences have previously been shown to be expressed at a greater level in human lung tumor tissue than in normal lung tissue.

EXAMPLE 2

USE OF PATIENT SERA TO IDENTIFY DNA SEQUENCES ENCODING LUNG TUMOR ANTIGENS

This example illustrates the isolation of cDNA sequences encoding lung tumor antigens by expression screening of lung tumor samples with autologous patient sera.

A human lung tumor directional cDNA expression library was constructed employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Total RNA for the library was taken from a late SCID mouse passaged human squamous epithelial lung carcinoma and poly A+ RNA was isolated using the Message Maker kit (Gibco BRL, Gaithersburg, MD). The resulting library was screened using *E. coli*-absorbed autologous patient serum, as described in Sambrook et al., (*Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989), with the secondary antibody being goat anti-human IgG-A-M (H + L) conjugated with alkaline phosphatase, developed with NBT/BCIP (Gibco

BRL). Positive plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the clones was determined.

Fifteen clones were isolated, referred to hereinafter as LT86-1 – LT86-15. The isolated cDNA sequences for LT86-1 – LT86-8 and LT86-10 - LT86-15 are provided in SEQ ID NO: 17-24 and 26-31, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 32-39 and 41-46, respectively. The determined cDNA sequence for LT86-9 is provided in SEQ ID NO: 25, with the corresponding predicted amino acid sequences from the 3′ and 5′ ends being provided in SEQ ID NO: 40 and 65, respectively. These sequences were compared to those in the gene bank as described above. Clones LT86-3, LT86-6 – LT86-9, LT86-11 – LT86-13 and LT86-15 (SEQ ID NO: 19, 22-25, 27-29 and 31, respectively) were found to show some homology to previously identified expressed sequence tags (ESTs), with clones LT86-6, LT86-8, LT86-11, LT86-12 and LT86-15 appearing to be similar or identical to each other. Clone LT86-3 was found to show some homology with a human transcription repressor. Clones LT86-6, 8, 9, 11, 12 and 15 were found to show some homology to a yeast RNA Pol II transcription regulation mediator. Clone LT86-13 was found to show some homology with a *C. elegans* leucine aminopeptidase. Clone LT86-9 appears to contain two inserts, with the 5′ sequence showing homology to the previously identified antisense sequence of interferon alpha-induced P27, and the 3′ sequence being similar to LT86-6. Clone LT86-14 (SEQ ID NO: 30) was found to show some homology to the trithorax gene and has an “RGD” cell attachment sequence and a beta-Lactamase A site which functions in hydrolysis of penicillin. Clones LT86-1, LT86-2, LT86-4, LT86-5 and LT86-10 (SEQ ID NOS: 17, 18, 20, 21 and 26, respectively) were found to show homology to previously identified genes. A subsequently determined extended cDNA sequence for LT86-4 is provided in SEQ ID NO: 66, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 67.

Subsequent studies led to the isolation of five additional clones, referred to as LT86-20, LT86-21, LT86-22, LT86-26 and LT86-27. The determined 5′ cDNA

sequences for LT86-20, LT86-22, LT86-26 and LT86-27 are provided in SEQ ID NO: 68 and 70-72, respectively, with the determined 3′ cDNA sequences for LT86-21 being provided in SEQ ID NO: 69. The corresponding predicted amino acid sequences for LT86-20, LT86-21, LT86-22, LT86-26 and LT86-27 are provided in SEQ ID NO: 73-77, respectively. LT86-22 and LT86-27 were found to be highly similar to each other. Comparison of these sequences to those in the gene bank as described above, revealed no significant homologies to LT86-22 and LT86-27. LT86-20, LT86-21 and LT86-26 were found to show homology to previously identified genes.

In further studies, a cDNA expression library was prepared using mRNA from a lung small cell carcinoma cell line in the lambda ZAP Express expression vector (Stratagene), and screened as described above, with a pool of two lung small cell carcinoma patient sera. The sera pool was adsorbed with *E. coli* lysate and human PBMC lysate was added to the serum to block antibody to proteins found in normal tissue. Seventy-three clones were isolated. The determined cDNA sequences of these clones are provided in SEQ ID NO: 290-362. The sequences of SEQ ID NO: 289-292, 294, 296-297, 300, 302, 303, 305, 307-315, 317-320, 322-325, 327-332, 334, 335, 338-341, 343-352, 354-358, 360 and 362 were found to show some homology to previously isolated genes. The sequences of SEQ ID NO: 293, 295, 298, 299, 301, 304, 306, 316, 321, 326, 333, 336, 337, 342, 353, 359 and 361 were found to show some homology to previously identified ESTs.

EXAMPLE 3

USE OF MOUSE ANTISERA TO IDENTIFY DNA SEQUENCES ENCODING LUNG TUMOR ANTIGENS

This example illustrates the isolation of cDNA sequences encoding lung tumor antigens by screening of lung tumor cDNA libraries with mouse anti-tumor sera.

A directional cDNA lung tumor expression library was prepared as described above in Example 2. Sera was obtained from SCID mice containing late passaged human squamous cell and adenocarcinoma tumors. These sera were pooled and injected into normal mice to produce anti-lung tumor serum. Approximately 200,000 PFUs were screened from the unamplified library using this antiserum. Using

a goat anti-mouse IgG-A-M (H+L) alkaline phosphatase second antibody developed with NBT/BCIP (BRL Labs.), approximately 40 positive plaques were identified. Phage was purified and phagemid excised for 9 clones with inserts in a pBK-CMV vector for expression in prokaryotic or eukaryotic cells.

The determined cDNA sequences for 7 of the isolated clones (hereinafter referred to as L86S-3, L86S-12, L86S-16, L86S-25, L86S-36, L86S-40 and L86S-46) are provided in SEQ ID NO: 49-55, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 56-62, respectively. The 5′ cDNA sequences for the remaining 2 clones (hereinafter referred to as L86S-30 and L86S-41) are provided in SEQ ID NO: 63 and 64. L86S-36 and L86S-46 were subsequently determined to represent the same gene. Comparison of these sequences with those in the public database as described above, revealed no significant homologies to clones L86S-30, L86S-36 and L86S-46 (SEQ ID NO: 63, 53 and 55, respectively). L86S-16 (SEQ ID NO: 51) was found to show some homology to an EST previously identified in fetal lung and germ cell tumor. The remaining clones were found to show at least some degree of homology to previously identified human genes. Subsequently determined extended cDNA sequences for L86S-12, L86S-36 and L86S-46 are provided in SEQ ID NO: 78-80, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 81-83.

Subsequent studies led to the determination of 5′ cDNA sequences for an additional nine clones, referred to as L86S-6, L86S-11, L86S-14, L86S-29, L86S-34, L86S-39, L86S-47, L86S-49 and L86S-51 (SEQ ID NO: 84-92, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NO: 93-101, respectively. L86S-30, L86S-39 and L86S-47 were found to be similar to each other. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to L86S-14. L86S-29 was found to show some homology to a previously identified EST. L86S-6, L86S-11, L86S-34, L86S-39, L86S-47, L86S-49 and L86S-51 were found to show some homology to previously identified genes.

In further studies, a directional cDNA library was constructed using a Stratagene kit with a Lambda Zap Express vector. Total RNA for the library was isolated from two primary squamous lung tumors and poly A+ RNA was isolated using an oligo dT column. Antiserum was developed in normal mice using a pool of sera from three SCID mice implanted with human squamous lung carcinomas. Approximately 700,000 PFUs were screened from the unamplified library with *E. coli* absorbed mouse anti-SCID tumor serum. Positive plaques were identified as described above. Phage was purified and phagemid excised for 180 clones with inserts in a pBK-CMV vector for expression in prokaryotic or eukaryotic cells.

The determined cDNA sequences for 23 of the isolated clones are provided in SEQ ID NO: 126-148. Comparison of these sequences with those in the public database as described above revealed no significant homologies to the sequences of SEQ ID NO: 139 and 143-148. The sequences of SEQ ID NO: 126-138 and 140-142 were found to show homology to previously identified human polynucleotide sequences.

EXAMPLE 4

USE OF MOUSE ANTISERA TO SCREEN LUNG TUMOR LIBRARIES PREPARED FROM SCID MICE

This example illustrates the isolation of cDNA sequences encoding lung tumor antigens by screening of lung tumor cDNA libraries prepared from SCID mice with mouse anti-tumor sera.

A directional cDNA lung tumor expression library was prepared using a Stratagene kit with a Lambda Zap Express vector. Total RNA for the library was taken from a late passaged lung adenocarcinoma grown in SCID mice. Poly A+ RNA was isolated using a Message Maker Kit (Gibco BRL). Sera was obtained from two SCID mice implanted with lung adenocarcinomas. These sera were pooled and injected into normal mice to produce anti-lung tumor serum. Approximately 700,000 PFUs were screened from the unamplified library with *E. coli*-absorbed mouse anti-SCID tumor serum. Positive plaques were identified with a goat anti-mouse IgG-A-M (H+L) alkaline phosphatase second antibody developed with NBT/BCIP (Gibco BRL). Phage

was purified and phagemid excised for 100 clones with insert in a pBK-CMV vector for expression in prokaryotic or eukaryotic cells.

The determined 5′ cDNA sequences for 33 of the isolated clones are provided in SEQ ID NO: 149-181. The corresponding predicted amino acid sequences for SEQ ID NO: 149, 150, 152-154, 156-158 and 160-181 are provided in SEQ ID NO: 182, 183, 186, 188-193 and 194-215, respectively. The clone of SEQ ID NO: 151 (referred to as SAL-25) was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 184 and 185. The clone of SEQ ID NO: 153 (referred to as SAL-50) was found to contain two open reading frames encoding the predicted amino acid sequences of SEQ ID NO: 187 and 216. Similarly, the clone of SEQ ID NO: 155 (referred to as SAL-66) was found to contain two open reading frames encoding the predicted amino acid sequences of SEQ ID NO: 189 and 190. Comparison of the isolated sequences with those in the public database revealed no significant homologies to the sequences of SEQ ID NO: 151, 153 and 154. The sequences of SEQ ID NO: 149, 152, 156, 157 and 158 were found to show some homology to previously isolated expressed sequence tags (ESTs). The sequences of SEQ ID NO: 150, 155 and 159-181 were found to show homology to sequences previously identified in humans.

Using the procedures described above, two directional cDNA libraries (referred to as LT46-90 and LT86-21) were prepared from two late passaged lung squamous carcinomas grown in SCID mice and screened with sera obtained from SCID mice implanted with human squamous lung carcinomas. The determined cDNA sequences for the isolated clones are provided in SEQ ID NO: 217-237 and 286-289. SEQ ID NO: 286 was found to be a longer sequence of LT4690-71 (SEQ ID NO: 237). Comparison of these sequences with those in the public databases revealed no known homologies to the sequences of SEQ ID NO: 219, 220, 225, 226, 287 and 288. The sequences of SEQ ID NO: 218, 221, 222 and 224 were found to show some homology to previously identified sequences of unknown function. The sequence of SEQ ID NO: 236 was found to show homology to a known mouse mRNA sequence. The sequences

of SEQ ID NO: 217, 223, 227-237, 286 and 289 showed some homology to known human DNA and/or RNA sequences.

In further studies using the techniques described above, one of the cDNA libraries described above (LT86-21) was screened with *E. coli*-absorbed mouse anti-SCID tumor serum. This serum was obtained from normal mice immunized with a pool of 3 sera taken from SCID mice implanted with human squamous lung carcinomas. The determined cDNA sequences for the isolated clones are provided in SEQ ID NO: 238-285. Comparison of these sequences with those in the public databases revealed no significant homologies to the sequences of SEQ ID NO: 253, 260, 277 and 285. The sequences of SEQ ID NO: 249, 250, 256, 266, 276 and 282 were found to show some homology to previously isolated expressed sequence tags (ESTs). The sequences of SEQ ID NO: 238-248, 251, 252, 254, 255, 257-259, 261-263, 265, 267-275, 278-281, 283 and 284 were found to show some homology to previously identified DNA or RNA sequences.

The expression levels of certain of the isolated antigens in lung tumor tissues compared to expression levels in normal tissues was determined by microarray technology. The results of these studies are shown below in Table 2, together with the databank analyses for these sequences.

TABLE 2

Clone	SEQ ID NO:	Description	LT+F/N	SCC+M/N	Squa/ N	Adeno/N
2LT-3	238	Unknown (KIAA0712)	2.2	3.8	3.3	-
2LT-6	239	Lactate DH B	2.3	3.8	4.1	-
2LT-22	240	Fumarate hydratase	-	3.0	-	-
2LT-26	242	CG1-39	-	-	12.8	-
2LT-31	243	ADH7	-	-	8.4	2.2
2LT-36	244	ADH7	-	2.4	2.0	-
2LT-42	245	HMG-CoA synthase	2.2	2.6	2.2	-
2LT-54	247	(Mus) ninein	-	2.1	-	-
2LT-55	248	Ubiquitin	2.2	-	2.5	2.0
2LT-57	249	Novel	2.1	2.9	2.4	-

2LT-58	250	Novel	2.3	4.0	2.9	-
2LT-59	251	Unknown KIAA0784	2.4	3.0	2.3	2.0
2LT_62	252	Nuc Pore Cmplx-ass pro TPR	-	-	-	2.1
2LT-70	256	Unknown KIAA0871	-	2.5	2.2	2.1
2LT-73	257	Mus polyadenylate-binding	-	2.0	-	-
2LT-76	259	Trans-Golgi p230	2.1	-	2.6	-
2LT-85	263	Ribosomal protein (LS29)	-	-	-	2.1
2LT-89	265	Unknown PAC212G6	-	2.0	-	-
2LT-98	268	Melanoma diff assoc pro 9	-	-	-	2.2
2LT-100	269	Mus Collagen alpha VI	-	-	-	2.1
2LT-105	271	NY-CO-7 antigen	-	3.2	-	-
2LT-108	273	Unknown RG363M04	-	3.1	-	-
2LT-124	279	Galectin-9 (secreted)	2.3	2.7	2.0	-
2LT-126	280	L1 element L1.33 p40	2.5	-	3.1	-
2LT-128	282	Novel (kappa B-ras 2)	2.3+	-	20.4	2.5
2LT-133	284	alpha II spectrin	-	2.3	-	-

LT+F/N = Lung Tumor plus Fetal tissue over Normal tissues
SC+M/N = Lung Small Cell carcinoma plus Metastatic over Normal tissues
Squa/N = Squamous lung tumor over Normal tissues
Aden/N = Adenocarcinoma over Normal tissues

Full-length sequencing studies on antigen 2LT-128 (SEQ ID NO: 282) resulted in the isolation of the full-length cDNA sequence provided in SEQ ID NO: 392. This amino acid sequence encoded by this full-length cDNA sequence is provided in SEQ ID NO: 393. This antigen shows 20-fold over-expression in squamous cell carcinoma and 2.5-fold over-expression in lung adenocarcinoma. This gene has been described as a potential ras oncogene (Fenwick et al. *Science, 287*:869-873, 2000).

Extended sequence information was obtained for clones 2LT-3 (SEQ ID NO:238), 2LT-26 (SEQ ID NO:242), 2LT-57 (SEQ ID NO: 249), 2LT-58 (SEQ ID NO:250), 2LT-98 (SEQ ID NO:268) and 2LT-124 (SEQ ID NO:279). The extended cDNA sequences for these clones are set forth in SEQ ID NOs:428-433, respectively, encoding the polypeptide sequences set forth in SEQ ID NOs: 434-439, respectively.

EXAMPLE 5

DETERMINATION OF TISSUE SPECIFICITY OF LUNG TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for representative lung tumor polypeptides were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent. First strand synthesis was carried out using 2 μg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42°C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. 1 μl of 1:30 dilution of cDNA was employed to enable the linear range amplification of the β-actin template and was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in five different types of tumor tissue (lung squamous tumor from 3 patients, lung adenocarcinoma, prostate tumor, colon tumor and lung tumor), and different normal tissues, including lung from four patients, prostate, brain, kidney, liver, ovary, skeletal muscle, skin, small intestine, myocardium, retina and testes. L86S-46 was found to be expressed at high levels in lung squamous tumor, colon tumor and prostate tumor, and was undetectable in the other tissues examined. L86S-5 was found to be expressed in the lung tumor samples and in 2 out of 4 normal lung samples, but not in the other normal or tumor tissues

tested. L86S-16 was found to be expressed in all tissues except normal liver and normal stomach. Using real-time PCR, L86S-46 was found to be over-expressed in lung squamous tissue and normal tonsil, with expression being low or undetectable in all other tissues examined.

EXAMPLE 6

ISOLATION OF DNA SEQUENCES ENCODING LUNG TUMOR ANTIGENS

DNA sequences encoding antigens potentially involved in squamous cell lung tumor formation were isolated as follows.

A lung tumor directional cDNA expression library was constructed employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Total RNA for the library was taken from a pool of two human squamous epithelial lung carcinomas and poly A+ RNA was isolated using oligo-dT cellulose (Gibco BRL, Gaithersburg, MD). Phagemid were rescued at random and the cDNA sequences of isolated clones were determined.

The determined cDNA sequence for the clone SLT-T1 is provided in SEQ ID NO: 102, with the determined 5′ cDNA sequences for the clones SLT-T2, SLT-T3, SLT-T5, SLT-T7, SLT-T9, SLT-T10, SLT-T11 and SLT-T12 being provided in SEQ ID NO: 103-110, respectively. The corresponding predicted amino acid sequence for SLT-T1, SLT-T2, SLT-T3, SLT-T10 and SLT-T12 are provided in SEQ ID NO: 111-115, respectively. Comparison of the sequences for SLT-T2, SLT-T3, SLT-T5, SLT-T7, SLT-T9 and SLT-T11 with those in the public databases as described above, revealed no significant homologies. The sequences for SLT-T10 and SLT-T12 were found to show some homology to sequences previously identified in humans.

The sequence of SLT-T1 was determined to show some homology to a PAC clone of unknown protein function. The cDNA sequence of SLT-T1 (SEQ ID NO: 102) was found to contain a mutator (MUTT) domain. Such domains are known to function in removal of damaged guanine from DNA that can cause A to G transversions (see, for example, el-Deiry, W.S., 1997 *Curr. Opin. Oncol. 9*:79-87; Okamoto, K. et al. 1996 *Int. J. Cancer 65*:437-41; Wu, C. et al. 1995 *Biochem. Biophys. Res. Commun. 214*:1239-45; Porter, D.W. et al. 1996 *Chem. Res. Toxicol. 9*:1375-81). SLT-T1 may

thus be of use in the treatment, by gene therapy, of lung cancers caused by, or associated with, a disruption in DNA repair.

In further studies, DNA sequences encoding antigens potentially involved in adenocarcinoma lung tumor formation were isolated as follows. A human lung tumor directional cDNA expression library was constructed employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Total RNA for the library was taken from a late SCID mouse passaged human adenocarcinoma and poly A+ RNA was isolated using the Message Maker kit (Gibco BRL, Gaithersburg, MD). Phagemid were rescued at random and the cDNA sequences of isolated clones were determined.

The determined 5′ cDNA sequences for five isolated clones (referred to as SALT-T3, SALT-T4, SALT-T7, SALT-T8, and SALT-T9) are provided in SEQ ID NO: 116-120, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 121-125. SALT-T3 was found to show 98% identity to the previously identified human transducin-like enhancer protein TLE2. SALT-T4 appears to be the human homologue of the mouse H beta 58 gene. SALT-T7 was found to have 97% identity to human 3-mercaptopyruvate sulfurtransferase and SALT-T8 was found to show homology to human interferon-inducible protein 1-8U. SALT-T9 shows approximately 90% identity to human mucin MUC 5B.

cDNA sequences encoding antigens potentially involved in small cell lung carcinoma development were isolated as follows. cDNA expression libraries were constructed with mRNA from the small cell lung carcinoma cell lines NCIH69, NCIH128 and DMS79 (all available from the American Type Culture Collection, Manassas, VA) employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Phagemid were rescued at random and the cDNA sequences of 27 isolated clones were determined. Comparison of the determined cDNA sequences revealed no significant homologies to the sequences of SEQ ID NO: 372 and 373. The sequences of SEQ ID NO: 364, 369, 377, 379 and 386 showed some homology to previously isolated ESTs. The sequences of the remaining 20 clones showed some homology to previously identified genes. The cDNA sequences of these clones are provided in SEQ ID NO:

363, 365-368, 370, 371, 374-376, 378, 380-385 and 387-389, wherein SEQ ID NO: 363, 366-368, 370, 375, 376, 378, 380-382, 384 and 385 are full-length sequences.

Comparison of the cDNA sequence of SEQ ID NO: 372 indicated that this clone (referred to as 128T1) is a novel member of a family of putative seven pass transmembrane proteins. Specifically, using the computer algorithm PSORT, the protein was predicted to be a type IIIA plasma membrane seven pass transmembrane protein. A genomic clone was identified in the Genbank database which contained the predicted N-terminal 58 amino acids missing from the amino acid sequence encoded by SEQ ID NO: 372. The determined full-length cDNA sequence for the 128T1 clone is provided in SEQ ID NO: 390, with the corresponding amino acid sequence being provided in SEQ ID NO: 391.

The expression levels of certain of the isolated antigens in lung tumor tissues compared to expression levels in normal tissues was determined by microarray technology. The results of these studies are shown below in Table 3, together with the databank analyses for these sequences.

TABLE 3

Clone	SEQ ID NO:	Description	LT+F/N	SCC+M/N	Squa/N	Adeno/N
DMS79-T1	363	STAT-ind inhib of cytokine	-	2.0	-	-
DMS79-T6	367	Neuronal cell death related	-	2.2	-	-
DMS79-T9	369	Novel	-	2.2	-	-
DMS79-T10	370	Ubiquitin carrier protein	-	3.9	2.2	-
DMS79-T11	371	HPV16E1 pro binding protein	-	2.1	-	-
128-T9	378	Elongation factor 1 alpha	-	2.7	-	-
128T11	380	Malate dehyrogenase	-	2.3	2.0	-
128-T12	381	Apurinic/apyrim endonuclease	-	5.4	-	-
NCIH69-	382	Sm-like protein	-	-	2.4	-

T3		CaSm				
NCIH69-T6	384	Transcription factor BTF3a	-	2.5	-	-

LT+F/N = Lung Tumor plus Fetal tissue over Normal tissues
SC+M/N = Lung Small Cell carcinoma plus Metastatic over Normal tissues
Squa/N = Squamous lung tumor over Normal tissues
Aden/N = Adenocarcinoma over Normal tissues

EXAMPLE 7

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N′,N′-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 8

ISOLATION AND CHARACTERIZATION OF DNA SEQUENCES ENCODING LUNG TUMOR ANTIGENS BY T-CELL EXPRESSION CLONING

Lung tumor antigens may also be identified by T cell expression cloning. One source of tumor specific T cells is from surgically excised tumors from human patients.

A non-small cell lung carcinoma was minced and enzymatically digested for several hours to release tumor cells and infiltrating lymphocytes (tumor infiltrating T cells, or TILs). The cells were washed in HBSS buffer and passed over a Ficoll (100%/75%/HBSS) discontinuous gradient to separate tumor cells and lymphocytes from non-viable cells. Two bands were harvested from the interfaces; the upper band at the 75%/HBSS interface contained predominantly tumor cells, while the lower band at the 100%/75%/HBSS interface contained a majority of lymphocytes. The TILs were expanded in culture, either in 24-well plates with culture media supplemented with 10 ng/ml IL-7 and 100 U/ml IL-2, or alternatively, 24-well plates that have been pre-coated with the anti-CD3 monoclonal antibody OKT3. The resulting TIL cultures were analyzed by FACS to confirm that a high percentage were CD8+ T cells (>90% of gated population) with only a small percentage of CD4+ cells.

In addition, non-small cell lung carcinoma cells were expanded in culture using standard techniques to establish a tumor cell line (referred to as LT391-06), which was later confirmed to be a lung carcinoma cell line by immunohistochemical analysis. This tumor cell line was transduced with a retroviral vector to express human CD80, and characterized by FACS analysis to confirm high expression levels of CD80, class I MHC and class II MHC molecules.

The ability of the TIL lines to specifically recognize autologous lung tumor was demonstrated by cytokine release assays (IFN-γ and TNF-α) as well as ^{51}Cr release assays. Briefly, TIL cells from day 21 cultures were co-cultured with either autologous or allogeneic tumor cells, EBV-immortalized LCL, or control cell lines Daudi and K562, and the culture supernatant monitored by ELISA for the presence of cytokines. The TIL specifically recognized autologous tumor but not allogeneic tumor. In addition, there was no recognition of EBV-immortalized LCL or the control cell lines, indicating that the TIL lines are tumor specific and are potentially recognizing a tumor antigen presented by autologous MHC molecules.

The characterized tumor-specific TIL lines were expanded to suitable numbers for T cell expression cloning using soluble anti-CD3 antibody in culture with irradiated EBV transformed LCLs and PBL feeder cells in the presence of 20 U/ml IL-

2. Clones from the expanded TIL lines were generated by standard limiting dilution techniques. Specifically, TIL cells were seeded at 0.5 cells/well in a 96-well U bottom plate and stimulated with CD-80-transduced autologous tumor cells, EBV transformed LCL, and PBL feeder cells in the presence of 50 U/ml IL-2. The specificity of these clones for autologous tumor was confirmed by ^{51}Cr microcytotoxicity and IFN-γ bioassays.

These CTL clones were demonstrated to be HLA-B/C restricted by antibody blocking experiments. A representative CTL clone was tested on a panel of allogeneic lung carcinomas and it recognized both autologous tumor and a lung squamous cell carcinoma (936T). As the only class I MHC molecule shared among these tumors was HLA-Cw1203, this indicated that this was the restriction element used by the CTL. This finding was confirmed by the recognition of a number of allogeneic lung carcinomas transduced with a retroviral vector encoding HLA-Cw1203 by the CTL.

PolyA mRNA was prepared from a lung tumor cell line referred to as LT391-06 using Message Maker (Life Technologies; Rockville, MD). The subsequent steps involving cDNA synthesis were performed according to Life Technologies cloning manual (SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning). Modifications to the protocol were made as follows. At the adapter addition step, EcoRI-XmnI adapters (New England Biolabs; Beverly, MA) were substituted. Size fractionated cDNAs were ligated into the expression vector system HisMax A, B, C (Invitrogen; Carlsbad, CA) to optimize for protein expression in all three coding frames. Library plasmids were then aliquotted at approximately 100 CFU/well into a 96-well block for overnight liquid amplification. From these cultures, glycerol stocks were made and pooled plasmid was prepared by automated robot (Qiagen; Valencia, CA). The concentration of the plasmid DNA in each well of the library plates was determined to be approximately 150 ng/ul. Initial characterization of the cDNA expression library was performed by randomly sequencing 24 primary transformants and subjecting the resulting sequences to BLAST searches against available databases.

The determined cDNA sequences are provided in SEQ ID NO: 443-480, with the results of the BLAST searches being provided in Table 4.

TABLE 4

Clone	SEQ ID NO:	GenBank Accession	Description
55163	458, 459		*Novel in Genbank*
55158	452		*Novel in Genbank*
Homology to known sequences with unknown function			
55153	443, 444	7018516	H. sapiens mRNA; cDNA DKFZp434M035
55154	445, 446	6437562	H. sapiens Chr 22q11 PAC Clone p393
55157	450, 451	2887408	H. sapiens KIAA0417 mRNA
55165	462, 463	3970871	H. sapiens HRIHFB2122 mRNA
Homology to known sequences with known function			
55155	447	7677405	H. sapiens F-box protein FBS (FBS)
55156	448, 449	3929584	H. sapiens EEN pseudogene
55161	454, 455	4503350	H. sapiens DNA (cytosine-5-)-methyltransferase 1 (DNMT1)
55162	456, 457	31220	ERK1 mRNA for protein serine/threonine kinase
55164	460, 461	6677666	H. sapiens RNA-binding protein (autoantigenic) (RALY)
55166	464, 465	3249540	H. sapiens ribonuclease P protein subunit p40 (RPP40)
55167	466, 467	7657497	H. sapiens renal tumor antigen (RAGE)
55168	468, 469	2873376	H. sapiens exportin t mRNA
55169	470, 471	3135472	H. sapiens Cre binding protein-like 2 mRNA
55171	474	4759151	H. sapiens spermine synthase (SMS)
55173	476	6688148	H. sapiens partial mRNA for NICE-3 protein
55174	477, 478	531394	Human transcriptional coactivator PC4
55175	479	6563201	H. sapiens translation initiation factor eIF-2b delta subunit
55176	480	29860	hCENP-Bgene, for centromere autoantigen B (CENP-B)
Homology to Ribosomal Protein			
55159	453	337494	Ribosomal protein L7a (surf 3) large subunit mRNA
55170	472, 473	4506648	H.sapiens mRNA for ribosomal protein L3

Clone	SEQ ID NO:	GenBank Accession	Description
55172	475	388031	H. sapiens ribosomal protein L11

For T cell screening, approximately 80 ng of the library plasmid DNA and 80 ng of HLA-Cw1203 plasmid DNA was mixed with the lipid Fugene according to the manufacturers' instructions and transfected in duplicate into COS-7 cells. After incubation at 37 °C for 48 hours, the transfection mixture was removed and 10,000 LT391-06 CTL were added to each well in fresh media containing human serum.

The ability of T cells to recognize an antigen in the library was assessed by cytokine release after 6 hours (TNF-alpha, WEHI bio-assay) or after 24 hours (IFN-gamma, ELISA). Approximately 2.0 x 10^5 clones (in plasmid pools of 100) were screened using this system in COS-7 cells. Three plasmid pools were identified (referred to as 14F10, 19A4, and 20E10) that were recognized by LT391-06 CTL. Transfection of these plasmid pools into COS-7 cells led to production of both IFN-gamma and TNF-alpha from the LT391-06 CTL at levels significantly above background. Pools 14F10, 19A4 and 20E10 were "broken down" into several hundred individual plasmid DNAs and retested. The sequences of 24 novel clones isolated from pool 14F10 are provided in SEQ ID NO: 481-511.

One plasmid (3D9) from pool 14F10, one plasmid from pool 20E10 and 5 plasmids (2A6, 2E11, 2F12, 3F4, 3H8) from pool 19A4 were capable of reconstituting T cell recognition. Sequencing of these plasmids led to the identification of a 7.8 kB cDNA insert (referred to as clone 14F10), a 2.2 kB cDNA insert (referred to as clone 19A4; SEQ ID NO:440), and a clone referred to as 20E10. The full-length cDNA sequence for 14F10 is provided in SEQ ID NO: 441. Clone 14F10 does not contain the first two "G" nucleotides found at the 5′ end of 19A4, and the 3′-proximal 24 bp of 19A4 differ from the corresponding region of 14F10 (nucleotides 2145-2165). Furthermore, 3837 bp of 3′ additional sequence was isolated for clone 14F10. The 5′ terminal cDNA sequence (337 bp) of clone 20E10 is provided in SEQ ID NO: 442. 20E10 contains an additional 3 nucleotides (as compared to 19A4) at the 5′-most end. The additional sequence from the 5′ end of clone 20E10 contains an "ATG" and

therefore appears to contain the translational start site of a novel open reading frame. BLAST search analysis against the GenBank database identified these sequences as having significant homology with a truncated human cystine/glutamate transporter gene. Unlike the published sequence, however, clones 14F10 and 19A4 contain a unique 5′ terminus consisting of 181 nucleotides. This novel sequence replaces the published 5′ region and results in the removal of the reported initiating methionine (start codon) and an additional two amino acids of the reported transporter protein. Therefore, the translated product of clones 14F10 and 19A4 is different than the cystine/glutamate transporter protein. Furthermore, T cell recognition of other lung tumors demonstrates that this antigen is expressed by other tumors as well.

The epitope and amino acid sequence encoded within clones 19A4 and 14F10 which reconstitutes T cell recognition of anti-LT391-06 cells were mapped as follows. Cos-7 cells were transfected with 80 ng/well HLA-Cw1203 along with titrated amounts of cDNA encoding clone 19A4, a potential open reading frame located in the unique 5′ terminus of 19A4, or the open reading frame from the cystine/glutamate (Cys-Glu) transporter gene, cloned into a eukaryotic expression vector and tested for stimulation of anti-LT391-06 T cells in a TNF assay. As a positive control Cos-7 cells were co-transfected with HLA-Cw1203 and the positive plasmid clone 19A4 described above. The Cys-Glu transporter expression construct was isolated by PCR using 5′ and 3′ primers specific for the known ORF of the transporter with 19A4 as template. In addition, each 5′ primer contained a Kozak translation initiation site and starting methionine to drive translation of the polypeptide. CTL against LT391-06 did not recognize transfectants expressing the Cys-Glu transporter construct, but did recognize transfectants expressing 19A4 and the 5′ ORF from 19A4.

In subsequent experiments, Cos-7 cells were co-transfected with 80 ng/well HLA-Cw1203 along with titrated amounts of DNA of transposition mutants F10 and C12, respectively, and tested for simulation of anti-LT391-06 T cells in a TNF assay. As a positive control, Cos-7 cells were co-transfected with HLA-Cw1203 and clones of the 5′ ORF of 19A4. Transposition mutants F10 and C12 were obtained by transposon-mediated mutation of the 14F10 clone and screening for insertion site by

sequence analyses. The transposon of mutant F10 is inserted approximately 304 bp from the 5′ EcoRI cloning site of the 14F10 cDNA. This mutation did not disrupt translation of the T cell epitope. By contrast, the transposon of mutant C12, which is inserted approximately 116 bp from the 5′ EcoRI cloning site of the 14F10 cDNA, was found to interrupt translation of the T cell eptiope. Thus the epitope in 14F10 maps between these two transposon insertion sites. The amino acid sequence of the region between the C12 and F10 transposon insertion sites is provided in SEQ ID NO: 586.

A series of 11 overlapping 16-mer and 15-mer peptides for the region shown in SEQ ID NO: 586 were prepared and tested for stimulation of anti-LT391-06 cells, as determined by cytokine release in TNF and IFN-γ assays. Only the peptide provided in SEQ ID NO: 587 (corresponding to residues 5-20 of SEQ ID NO: 586) stimulated cytokine release. These studies demonstrate that the HLA-Cw1203 restricted epitope of the LT391-06 antigen is contained within SEQ ID NO: 587.

EXAMPLE 9

ISOLATION AND CHARACTERIZATION OF DNA SEQUENCES ENCODING LUNG TUMOR ANTIGENS BY PCR SUBTRACTION

This example describes the isolation and characterization of cDNA clones from a PCR subtracted expression library prepared from the human lung tumor cell line LT391-06 described above.

Tester poly A mRNA was prepared from the cell line LT391-06 as described above. Driver poly A mRNA was isolated from a human acute T cell leukemia/T lymphocyte cell line (Jurkat) which is derived from non-lung cells and is not recognized by LT391-06 reactive T cells. The subtraction was performed according to the method of Clontech (Palo Alto, CA) with the following changes: 1) a second restriction digestion reaction of cDNA was completed using a pool of enzymes (MscI, PvuII, StuI and DraI). This was in addition to, and separate from, the Clontech recommended single restriction enzyme digestion with RsaI. Each restriction digest set was treated as a separate library to ensure that the final mixed library contained overlapping fragments. Thus, the epitope recognized by the T cells should be represented on a fragment within the library and not destroyed by the presence of a

single restriction site within it. 2) The ratio of driver to tester cDNA was increased in the hybridization steps to increase subtraction stringency. To analyze the efficiency of the subtraction, actin was PCR amplified from dilutions of subtracted, as well as unsubtracted, PCR samples. The second amplification step utilized primers that were modified from those normally used. Three nested PCR primers were engineered to contain a cleavable EcoRI site (not utilized during cloning) that was in one of three frames. Thus, secondary amplification with these primers resulted in products that could be ligated directly into the eukaryotic expression plasmid pcDNA4His/Max-Topo (Invitrogen). This resulted in the PCR subtracted and amplified fragments being represented in-frame somewhere within the library. Due to the mechanics of the subtraction only 50% of fragments will be in the correct orientation. The complexity and redundancy of the library was characterized by sequencing 96 randomly picked clones from the final pooled PCR subtraction expression library, referred to as LT391-06PCR. These sequences (SEQ ID NO: 512-581) were analyzed by comparison to sequences in publicly available databases (Table 5).

TABLE 5

Clone	SEQ ID NO:	GenBank Accession	Description
57235	532		*Novel in Genbank*
57255	547		*Novel in Genbank*
57264	554		*Novel in Genbank*
Homology to known sequences with unknown function			
57215	518	5689540	H. sapiens mRNA for KIAA1102 protein
57223	522	2341006	Human Xq13 3′ end of PAC 92E23
57227	524	7022540	H. sapiens cDNA FLJ10480 fis, clone NT2RP2000126
57238	535	6807795	H. sapiens mRNA; cDNA DKFZp761G02121
57239	536	5757546	H. sapiens clone DJ0823F17
57243	539	7023805	H. sapiens cDNA FLJ11259 fis, clone PLACE1009045
57245	540	4884472	H. sapiens mRNA; cDNA DKFZp586O2223
57267	557	6808218	H. sapiens mRNA; cDNA DKFZp434O1519
57268	558	10040400	Sequence 12 from Patent WO9954460

Clone	SEQ ID NO:	GenBank Accession	Description
57270	560	7959775	H. sapiens PRO1489 mRNA
57271	561	4500158	H. sapiens mRNA; cDNA DKFZp586B0918
57281	567	6560920	H. sapiens clone RP11- 501O7
57283	569	285962	Human mRNA for KIAA0108 gene
57285	570	7019813	H. sapiens cDNA FLJ20002 fis, clone ADKA01577
Homology to known sequences with known function			
57207	512	517176	H. sapiens YAP65 mRNA
57210	514	6841233	H. sapiens HSPC292 mRNA
57211	515	2606093	H. sapiens Cyr61 protein (CYR61) mRNA
57212	516	339648	Human thioredoxin (TXN) mRNA
57219	519	4504616	H. sapiens insulin- like growth factor binding protein 3 (IGFBP3)
57221	520	7274241	H. sapiens novel retinal pigment epithelial cell protein (NORPEG)
57222	521	189564	Human, plasminogen activator inhibitor- 1 gene
57228	525	4757755	H. sapiens annexin A2 (ANXA2)
57230	527	180800	Human alpha- 1 collagen type IV gene, exon 52
57232	529	6729061	H. sapiens clone RPC11- 98D12 from 7q31
57233	530	338391	Spermidine/ spermine N1- acetyltransferase
57234	531	7305302	H. sapiens NCK- associated protein 1 (NCKAP1)
57236	533	4929722	H. sapiens CGI- 127 protein
57242	538	4503558	H. sapiens epithelial membrane protein 1 (EMP1)
57248	541	183585	Human pregnancy- specific beta-glycoprotein c
57250	543	4759283	H. sapiens ubiquitin carboxyl- terminal esterase L1 (UCHL1)
57251	544	1236321	Human laminin gamma2 chain gene (LAMC2)
57253	545	213831	H. sapiens lysyl hydroxylase isoform 2 (PLOD2)
57254	546	536897	Human follistatin- related protein precursor mRNA
57257	548	339656	Human endothelial cell thrombomodulin
57258	549	190467	Human prion protein (PrP) mRNA
57261	551	338031	Human serglycin gene
57262	552	178430	Human alphoid DNA (alphoid repetitive

Clone	SEQ ID NO:	GenBank Accession	Description
			sequence)
57265	555	4502562	H. sapiens calpain, large polypeptide L2 (CAPN2)
57266	556	398163	H. sapiens mRNA for insulin- like growth factor binding protein- 3
57269	559	7262375	H. carboxylesterase 2 (intestine, liver) (CES2)
57272	562	467560	H. sapiens mRNA for cysteine dioxygenase type 1
57274	563	482664	H. sapiens annexin A3 (ANXA3)
57275	564	2281904	H. sapiens Bruton's tyr. kinase (BTK), alpha- D- galactosidase A (GLA)
57277	565	4557498	H. sapiens C- terminal binding protein 2 (CTBP2)
57282	568	189245	Human, NAD(P) H: menadione oxidoreductase mRNA
57287	571	28525	Human mRNA for amyloid A4 precursor of Alzheimer's disease
57288	572	4757755	H. sapiens annexin A2 (ANXA2)
57289	573	5729841	H. sapiens glyoxalase I (GLO1) mRNA
57290	574	6103642	H. sapiens F- box protein FBX3 mRNA
57295	576	182513	Human ferritin L chain mRNA
57299	579	37137	Human mRNA for thrombospondin
57301	580	179682	Human (clone A12) C4b- binding protein beta- chain
57302	581	6042205	H. sapiens membrane metallo- endopeptidase (neutral endopeptidase,enkephalinase, CALLA, CD10) (MME)
57213	517	2665791	H. sapiens caveolin- 2 mRNA
57259	550	2665791	H. sapiens caveolin- 2 mRNA
57225	523	179765	Human calcyclin gene
57229	526	179765	Human calcyclin gene
57237	534	186962	Human laminin B2 chain gene
57249	542	186962	Human laminin B2 chain gene
57231	528	4972626	H. sapiens caveolin 1 (CAV1) gene
57296	577	4972626	H. sapiens caveolin 1 (CAV1) gene
57297	578	4972626	H. sapiens caveolin 1 (CAV1) gene
57240	537	266237	insulin- like growth factor binding protein 3
57292	575	184522	Human insulin- like growth factor- binding protein- 3 gene
57263	553	4504618	H. sapiens insulin- like growth factor

Clone	SEQ ID NO:	GenBank Accession	Description
			binding protein 7 (IGFBP7)
57280	566	4504618	H. sapiens insulin- like growth factor binding protein 7 (IGFBP7)
Homology to Ribosomal Protein			
57209	513	337504	Human ribosomal protein S24 mRNA

EXAMPLE 10

ISOLATION AND CHARACTERIZATION OF T CELL RECEPTORS FROM T CELL CLONES SPECIFIC FOR LUNG TUMOR ANTIGENS

This example describes the cloning and sequencing of T cell receptor (TCR) alpha and beta chains from a CD8 T cell clone specific for an antigen expressed by the lung tumor cell line LT391-06. T cells have a limited lifespan. Cloning of TCR chains and subsequent transfer would essentially enable infinite propagation of the T cell specificity. Cloning of tumor antigen TCR chains allows the transfer of the specificity into T cells isolated from patients that share TCR MHC-restricting alleles. Such T cells can then be expanded and used in adoptive transfer techniques to introduce the tumor antigen specificity into patients carrying tumors that express the antigen (see, for example, Clay et al. *J. Immunol. 163*:507 (1999)).

Cytotoxic T lymphocyte (CTL) clones specific for the lung tumor cell line LT391-06 were generated. Total mRNA from 2 x 10^6 cells from 15 such clones was isolated using Trizol reagent and cDNA was synthesized using Ready-to-Go kits (Pharmacia). To determine Va and Vb sequences in these clones, a panel of Va and Vb subtype-specific primers was synthesized and used in RT-PCR reactions with cDNA generated from each of the clones. The RT-PCR reactions demonstrated that each of the clones expressed a common Vb sequence that corresponded to the Vb13 subfamily. Using cDNA generated from one of the clones (referred to as 1105), the Va sequence expressed was determined to be Va22. To clone the full TCR alpha and beta chains from clone 1105, primers were designed that spanned the initiator and terminator-coding TCR nucleotides. Standard 35-cycle RT-PCR reactions were established using cDNA synthesized from the CTL clone and the primers, with PWO (BMB) as the

thermostable polymerase. The resultant specific bands (approximately 850 bp for the alpha chain and approximately 950 bp for the beta chain) were ligated into the PCR blunt vector (Invitrogen) and transformed into *E. coli*. *E. coli* transformed with plasmids containing the full-length alpha and beta chains were identified, and large scale preparations of the corresponding plasmids were generated. Plasmids containing full-length TCR alpha and beta chains were sequenced. The determined cDNA sequences for the alpha and beta chains are provided in SEQ ID NO: 583 and 582, respectively, with the corresponding amino acid sequences being provided in SEQ ID NO: 584 and 585, respectively.

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

CLAIMS

What is Claimed:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583;

(b) complements of the sequences provided in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583;

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583, under moderately stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583; and

(g) degenerate variants of a sequence provided in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583.

2. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) SEQ ID NO: 584-587;

(b) sequences encoded by a polynucleotide of claim 1; and

(c) sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 1; and

(d) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 1.

3. An expression vector comprising a polynucleotide of claim 1 operably linked to an expression control sequence.

4. A host cell transformed or transfected with an expression vector according to claim 3.

5. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 2.

6. A method for detecting the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 2;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

7. A fusion protein comprising at least one polypeptide according to claim 2.

8. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 390, 392, 394, 396, 398-420, 422-424, 428-433 and 440-583 under moderately stringent conditions.

9. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) polypeptides according to claim 2;

(b) polynucleotides according to claim 1; and

(c) antigen-presenting cells that express a polypeptide according to claim 1,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

10. An isolated T cell population, comprising T cells prepared according to the method of claim 9.

11. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

(a) polypeptides according to claim 2;

(b) polynucleotides according to claim 1;

(c) antibodies according to claim 5;

(d) fusion proteins according to claim 7;

(e) T cell populations according to claim 10; and

(f) antigen presenting cells that express a polypeptide according to claim 2.

12. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 11.

13. A method for the treatment of a cancer in a patient, comprising administering to the patient a composition of claim 11.

14. A method for determining the presence of a cancer in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with an oligonucleotide according to claim 8;

(c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(d) compare the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

15. A diagnostic kit comprising at least one oligonucleotide according to claim 8.

16. A diagnostic kit comprising at least one antibody according to claim 5 and a detection reagent, wherein the detection reagent comprises a reporter group.

17. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of: (i) polypeptides according to claim 2; (ii) polynucleotides according to claim 1; and (iii) antigen presenting cells that express a polypeptide of claim 2, such that T cell proliferate;

(b) administering to the patient an effective amount of the proliferated T cells,

and thereby inhibiting the development of a cancer in the patient.

SEQUENCE LISTING

```
<110> Corixa Corporation
      Reed, Steven G.
      Henderson, Robert A.
      Lodes, Michael J.
      Fling, Steven P.
      Mohamath, Raodoh
      Algate, Paul A.
      Secrist, Heather
      Indirias, Carol Yoseph
      Benson, Darin R.
      Elliot, Mark
      Mannion, Jane
      Kalos, Michael D.


<120> COMPOSITIONS AND METHODS FOR
THE THERAPY AND DIAGNOSIS OF LUNG CANCER


<130> 210121.47501PC

<140> PCT
<141> 2001-03-38

<160> 587

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 339
<212> DNA
<213> Homo sapien

<400> 1
gtactcagac aggatagtca tcatgtagca caaagcamat cctgtttcta tacttgtagt      60
ttgctctcac tcagtggcat ratcattact atacagtgta gaatgttrtt atgtagcata     120
gatgtggggt ctctagccca cagctctsta cctttgtcta gcactcctgt cctcatacct     180
ragtggcctg tccatcagca tgtttctcat ctactttgct tgtccagtcc actgtggtcc     240
tcccttgccc tctcccttat gtggcagagt ggaaccagct gtcctgagac ttgagttcaa     300
catctggttc gcccatytgc atgtttgtgg tctgagtac                             339

<210> 2
<211> 698
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(698)
<223> n = A,T,C or G

<400> 2
gtactcagac cacgactgca ttttctccac tgctgacggg tctaatacca gctgcttccc      60
tttcttggag gcagagctng tgaccttgag aaagtgacct gtgaccatca tgtgggtagt     120
gagctgctgc aaggtgtcat gggagctccc acactccatg cactttwaga tctgggactt     180
```

gcaggcctca ractgccagg tgtagctcgc tccattttgg tagccatagc gsttgttgga 240
ggacaactgc aagttggcgt tcttctgaga agaaaaagaa tctgcaaaag atcctgtggt 300
tgaatcgggg gaacacggcc gattgacatc aaaaacgcgt ttcttagccc gggtgaccat 360
tttcgaggaa atggttgggg actggctcct tcaaaggcac tttttggtta tgttttgttt 420
yaatcatgtk gacgctccaa tcttggragg gaatcgaang rantcnccnc caaaacatrc 480
stttcagraa ccttttgarc atcctctttt ttccgtrtcc cggmaargcc cytttccckg 540
ggctttgaaa wyagcctsgt tgggttctta aattaccart ccacnwgttg gaattccccg 600
ggccccctgc ccggktccaa ccaattttgg graaaacccc cncansccgt tkggantgcn 660
acaacntggn ntttttcntt tcgtgntccc ctngaacc 698

<210> 3
<211> 697
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(697)
<223> n = A,T,C or G

<400> 3
gtactcagac ccccaacctc gaacagccag aagacaggtt gtctcctggg ccttggacac 60
agccngccag gccattgaag ganaagcaaa gacgaagcga accatctctc tccattgtgg 120
gggccaagta gctgcantan ccttcagtcc cagttgcatt gggttaaaga gctcatacat 180
actatgtgtn aggggtacag aagcttttcc tcatagggca tgagctctcc nagagttgac 240
cttttgcctn aacttggggt ttctgtggtt cataaagttn ggatatgtat ttttttttcaa 300
atggaanaaa atccgtattt ggcaaaaaga ctccaggggg atgatactgt ccttgccact 360
tacagtccaa angatnttcc ccaaagaata gacatttttt cctctcatca cttctggatg 420
caaaatcttt tattttttttc ctttctcgca ccnccccaga ccccttnnag gttnaaccgc 480
ttcccatctc cccattcca cacgatnttg aattngcann ncgttgntgg tcgggtcccn 540
nccgaaaggg tntttttatt cggggtnctg anttnnnaac cnctnagttg aatccgcggg 600
gcggccnngn gggttnnacc atgntgggga naactncccn ccgcgnttgg aatgccanag 660
ccttgaaant tttcttttgg tcgccccccn gagattc 697

<210> 4
<211> 712
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(712)
<223> n = A,T,C or G

<400> 4
gtactcagac aaccaatagg tgtgttyctc anatctgaaa cacaaaaaga ttctagctna 60
taatgttsaa tggttgaggg tttaagtgat cttggtatgt tngatttagc agcgatnggc 120
cgggtgcggt ggctcacgca tgtatcccag cactttggga ggccgaggca ggaggatcac 180
ctgaggtcag gagtttgaga ccagcctggc cgacatggtn aaaccccgtc tctactanga 240
atacanaaat tagcccgggc atagtggcgc gtgcctrtga cctcsgctac tttggggatt 300
ctcctgagga agaattgctt gaactcaggg aagtggargt ttgcagtgag cttaaatcaa 360
gccactggca ctcccagcct gggktaacag agccamgact ctkgccgaaa aaaaaraama 420
cgacggagaa nmagntctgt tattccatgg gaaattkgaa tttccttcyt tkaaatatct 480
taaaatnggt cctcctwaaa aaagttcggc tggggcccgk tggctcacat tttkttaycc 540
cyccccccttt tggggarggc caarggccgg kttgawtnnc ccttgagggg ccanaactcc 600
agnaaccrgn cccgggccar smgwkgkstr armccctttc cyyccmaraa aawwcsmaaa 660
wwttycccsc cygsykggct ggkasckgtt myyyyygmtm csyagcttgc tt 712

<210> 5
<211> 679
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(679)
<223> n = A,T,C or G

<400> 5
gtactcagac cacctcacat gcagggtnag aaacatggag tgtgcggcag catcctcctc 60
acatcccttt gtgagcacgg ctgctccgga atactgacca tctgggctag cacgacctaa 120
cagagggttc tgcaggatgt gctattttaa agcagctggg tgcaacttgt gaaaacggga 180
atctngaagc agaacatgtn atcagcgatg gctgggattg gtggacagga ttgacaggag 240
tatttgaggc tctaccaggc ctgtctacag gacagcttca tcgaagggac attttttaac 300
ctgttatttt anatnccaca tatnttttt aatgctnaag catacaggtt gaatttctgg 360
atcgtaacta ctagtgactt ctgaggttta cagttngaat atgttctcnn aggtttatca 420
agttntgtta ttgatgatng gtaatctaca cctctggaag ctgtngaatg tgaaaaagat 480
ncntncanct gaccagtttg nagggcactc tcttctggna agnaatccgn ccaaaaaaat 540
tgtttcnagg gggcntgggg ggtttaaaaa aatgtttctn ttnccntaaa aatgtttacc 600
cnnctattga aaaaatgggg gtcgnggggg gcttnaaatc cccnanttnt gaatnttnta 660
tccggaanct tggtttccc 679

<210> 6
<211> 369
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(369)
<223> n = A,T,C or G

<400> 6
tcagtccagt catgggtcct ataagagaag tcactctgtg agtttccatg gaggaagaaa 60
aagcttcatt tctttaccct gcagcaacag cggagggagg gagagcctat cttctttgca 120
aattcattaa ctttgtggtt gaagggagca gcgtcngaaa ctgctttagc acagtgggag 180
gaaaacaaac agattcatct ccggaaacca aaggaaaggg tragtgggtt tttattagcc 240
agctgtatcc tagatggtca atttccagtg gatgaataca ccttacgtac gtttctcttg 300
cttcctacct nggcctgatc agctnggcac ttraatcatt ccgtnggggt wgctgtnaca 360
ctggactga 369

<210> 7
<211> 264
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(264)
<223> n = A,T,C or G

<400> 7
tgctggatra gggatggggc acgggagcac agatmgactt taactgcccc cacgttntcm 60
aggaaaggat tacaggcgtg agccactgcg cccggcctct tctccacttt cataggttcc 120
agtctctggt tcttctttct cagtttgttg tttttgcttc ttaaatmatg gagatnagaa 180
tgaacactac actcggaatc aggaagccct gcctggcgcc tctgtcacct gtctaggggc 240

ttcttctcac tgagtcatcc agca 264

<210> 8
<211> 280
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(280)
<223> n = A,T,C or G

<400> 8
acctcaactg cccanaacan aactgttgta caagatttga ggatttaaca atatttcaca 60
tgaaatattt cagacctacg ngagggctta aagacnaatt aaatgagcac cngtgtgccc 120
accgccccna ttaagaatta gagcaagcag tgaggtgaag ccttgtcctt gcttttaaca 180
tagaaagtga tccaaattca ccaaacttga cttnnggttt tgcagtgtgg cctcctgatt 240
ctagacnctg gcgaaacatt tgatgggcaa aaaaaaaaaa 280

<210> 9
<211> 449
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(449)
<223> n = A,T,C or G

<400> 9
tcgtcaactc caggatggct ttgaaaatna atggacacag atctctcctg ttttgatrat 60
ntgcagtgct natgactggc tttgcagttn attttgattc aggcaacaga tgttcctttt 120
ggttccctgt ctcccatggg cgtcatttca tgttgtcctc tgccttcccc cagatattct 180
aagttcagga cacaagcttc tggcccatgc agagcagagg ccatgagggg tcacagcatg 240
ggtacgggag gaaacactgg gctnacccag atnctggact tgagtcttgc ctctgctgct 300
tgctgcacag cttctgtcat ggtgctaaac ctgtgacctg cctcacaggc ttagagcatg 360
cccgtagaag tactctnaac taaratgctt tccacaaatg agatggtttc atgaaaactt 420
caaatagagg gcctgggcaa aaaaaaaaa 449

<210> 10
<211> 538
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(538)
<223> n = A,T,C or G

<400> 10
tttttttttt ttcccaaagg cctcaraaca ctagtcttct aattccaagc agaaagttac 60
atccgccggg atacatgcca cttggtttga taaatcaaaa tacagcatcc ttcagatccc 120
tttgctgagc aatacaatta tttgtatatg ttactttttt ttctgtttgg ctnaaagatt 180
tgatatgagc tgaggaaaat gaagccntta ctgctatnag atctnatccc tttccaccac 240
ctttcaggga tnttggcact gcayatattc agaattcccc nnagtcgctn gtgataaaaa 300
tgtcttcaga gatggcagaa tatgtttcct ttggtacatg ttcattaaaa atatacacgt 360
gctcactact gtggatatgt atgtnttgac cgatnacaca ggctgattta gggaagagat 420
aaaagcacac ttngaattta ttagcctttc accnagacta anattctgaa attaagaatg 480

tattccttgg tcaacaattt tcctcttctc ttagccctct tacattgtan tggactga 538

<210> 11
<211> 543
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(543)
<223> n = A,T,C or G

<400> 11
tttttttttt ttgcccacag ctgccatctt tgtgtgataa ggccaacctt ctatgggaat 60
caaccctcgc catcccagca aatcccctct ctcccttctc atgggagtgc cttgtattca 120
tcaggcatct gggacttgat gtgggtntgg gatttgaaat cagagcacct nggtctctst 180
caccattctn tcacttatta gctctnacct tgggtnaata cctgccttag tgtcntaggt 240
acaatatgaa tattgtctat ttctcaggga ttgcaatgac nagtnnatna gtgcatgaga 300
gggtaaaacc acagggtact ccgctcctcc naagaatgga gaatttttc tagaagccca 360
natntgcttg gaaggttggc caccnagagc cnnaatcttc ttttatttnc cactgaangc 420
ctaagaggna attctgaact catccccnna tgacctctcc cgaatmagaa tatctctggc 480
acttaccata ttttcttgcc ctcttccact tacnaaactc ctttattcct taacnggacg 540
aaa 543

<210> 12
<211> 329
<212> DNA
<213> Homo sapien

<400> 12
cgatgacttg ggcagtgagt gggcctcctg ccaggtggca gggcacagct tagaccaaac 60
ccttggcctc ccccctctgc agstacctct gaccaagaag gaaactagca agcctatgct 120
ggcaagacca taggtggggt gctgggaatc ctcggggccg gctggcaccc actcctggtg 180
ctcaagggag agacccactt gttcagatgc atrggcctca ggcggttcaa ggcrgtctta 240
gagccacaga gtcaaataaa aatcaatttt gagagaccac agcacctgct gctttgatcg 300
tgatgttcaa ggcaagttgc aagtcatcg 329

<210> 13
<211> 314
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(314)
<223> n = A,T,C or G

<400> 13
cgatgacttg cacccgggag ctgtgacagt ggcctggaag cagatggcag ccccgtcaag 60
gcgggagtgg agaccaccaa accctccaaa cagagcaaca actagtacgc ggccagcagc 120
tacctgagcc tgacgcccga gcagtggaag tcccacagaa gctacagctg ccaggtcacg 180
catgaaggga gcaccgtgga gaagacagtg gcccctacag aatgttcata ggttcccnac 240
tctnacccca cccacgggag cctgganctg cangatcccg ggggaagggt ctctctcccc 300
atcccaagtc atcg 314

<210> 14
<211> 691
<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(691)
<223> n = A,T,C or G

<400> 14
cgattacttg cacaatgcan attagaaccc aaatgaaggg tacaacccag atcttctggc 60
ttccagttca gtgctgctgg gtttttctta ctaaaccaaa acaatkaaga gcatagaagg 120
gaagagaaga ataaagtcta ttttggtctt tggtagcchg ggtaangaga atgctstcac 180
tctacnagaa aacccnaagt gaacccggct aatcaggacc gtgcttggga agggagcagg 240
ggcattacct ttcaacacca gaggttcttt gccttctctc tgcagggact cgargactat 300
gtgaagtggc tgggarggca tcactcggct tggttcattg gtrttctcat cataaactat 360
natttctttg gaaaaagatc ctcttgaaag artccttgcc ttccctacag gaaatcaagt 420
ctaggacagt gatcttgccc ctgcttgcas tctccgccgg ctgatcttat csgscccagt 480
tkatgtgsam cgctccttgg atrtkactct tgttttwctc cvaggaaggg gcytgcmagt 540
ccnwtnaatg amssgggccc ttaactccgg scrggtnamy ncttgsctsc rattttgggt 600
ycytcttcyt ttgsccmggt tcktcnaaac cacttngttr aattccccgg sccgcctkgc 660
nggtycaacc wttttgggaa mamcyccccc c 691

<210> 15
<211> 355
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(355)
<223> n = A,T,C or G

<400> 15
acctgaactg tgtgttgaag agtgatgtcc tgctgcctgg agctcaagtc actactgatg 60
accgtgccta tgtccgacag ctagttncct ccatggatgt gactgagacc aatgtcttct 120
tcyaccctcg gctcttacct ttgacnaagt ctcccgttga gagtactacc gaaccaccag 180
cagttcgagc ctctnaagag cgtctaagcg atggggatat atatttactg gagaatgggc 240
tcaacctctt cctctgggtg ggagcaagcg tccagcaggg tgttgtccag agccttttca 300
gcgtctcctc cttcagtcag atcaccagtg gtntgagtgt tctgccagtt caggt 355

<210> 16
<211> 522
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(522)
<223> n = A,T,C or G

<400> 16
tcagtccagt gaggtggaag acttcgaggc tcgtgggagc cgcttctcca agtctgctga 60
tgagagacag cgcatgctgg tgcagcgtan ggacgaactc ctccagcaag ctcgcagacg 120
tttcttgaac aaaagttctg aagatgatgc ggcctcagag agcttcctcc cctcggaagg 180
tgcgtcctct gaccccgtga ccctncgtcg aangatgctg gctgccgccg cggaacggan 240
gcttcagaag cagcagacct cctngcgctc ccttgccttc ctcagctgcc tcctgcgccc 300
tgtgcccggc tgactggagg aggcctgtcc aattctgccc gccccatgga aaagcgggct 360
tgactgcatt gccgctgtat naaagcatgt ggtcttacag tgttnggacn gctnatnaat 420
ttnatcctnc tntgtaatac ttcctatgtg acatttctct tccccttgga aacactgcan 480

attttaactg tgagtttgat ctcttctngt gttactggac tg 522

<210> 17
<211> 317
<212> DNA
<213> Homo sapien

<400> 17
gtgtcgcgaa ttcgcggtgg tgctaagaaa aggaagaaga agtcttacac cactcccaag 60
aaggataagc accagagaaa gaaggttcag ccggccgtcc tgaaatatta taaggtggat 120
gagaatggca aaattagttg ccttcgtcga gagtgcccct ctgatgaatg tggtgctggg 180
gtgtttatgg caagtcactt tgacagacat tattgtggca aatgttgtct gacccactgt 240
ttcaactaac cagaagacaa gtaactgtat gagttaatta aagacatgaa ctaaaaaaaa 300
aaaaaaaaaa actcgag 317

<210> 18
<211> 392
<212> DNA
<213> Homo sapien

<400> 18
tggagatttc taatgaggtg aggaagttcc gtacattgac agaattgatc ctcgatgctc 60
aggaacatgt taaaaatcct tacaaaggca aaaaactcaa gaaacaccca gacttcccca 120
agaagcccct gaccccttat ttccgcttct tcatggagaa gcgggccaag tatgcgaaac 180
tccaccctca gatgagcaac ctggacctga ccaagattct gtccaagaaa tacaaggagc 240
ttccggagaa gaagaagatg aaatatgttc cggacttcca gagaagagaa acaggagttc 300
gagcgaaacc tggcccgatt cagggaggat cacccccacc ttatccagaa tgccaagaat 360
cggacatccc agagaagccc caagaccccc cg 392

<210> 19
<211> 2624
<212> DNA
<213> Homo sapien

<400> 19
gaaacagtga gaaggagatt cctgtgctca atgagctgcc agtccccatg gtggcccgct 60
acattcgcat aaaccctcag tcctggtttg ataacgggag catctgcatg aggatggaga 120
tcttgggctg cccactgccg gatcctaata actattatca ccgacgtaat gagatgacca 180
ccacggatga cctggatttt aagcaccaca actattagga aatgcgccag ttgatgaagg 240
ttgtcaatga aatgtgcccc aatattacca ggatttacaa cattggcaaa agccaccagg 300
gcctgaaatt gtatgcggta gagatctctg accatcctgg ggaacatgaa gttggtgagc 360
ccgagttcca ctacatcgca ggggcccacg gcaatgaggt tctgggacga gaactgctgc 420
tgctgctgct gcacttcctc tgccaggaat actcggcgca gaacgcacgc atcgtccgct 480
tggtggagga gactcgaatc cacattctac cctccctcaa tcctgatggc tatgagaagg 540
cctatgaagg aggttccgag ttgggaggct ggtccctggg acgttggacc catgatggca 600
tcgatatcaa caacaacttt ccggatttaa actcgctgct ctgggaggca gaggaccagc 660
agaatgcccc aaggaaggtc cccaaccact acattgccat ccctgagtgg tttctgtctg 720
agaatgccac agtggccaca gagaccagag ccgtcatcgc ctggatggag aagatcccgt 780
ttgtgctggg aggcaaccta caggggggtg agctggtcgt ggcatacccc tatgacatgg 840
tgcggtccct gtggaagacc caggagcaca ccccaacacc tgatgatcat gtgttccgct 900
ggctggcgta ttcctacgcc tccactcacc gcctcatgac agatgccagg aggcgagtgt 960
gccacacgga agattttcag aaggaggagg gcaccgtcaa tggggcttcc tggcacacag 1020
tggctggaag tctaaacgat ttcagctacc tccatacaaa ctgctttgag ctgtccatct 1080
acgtgggctg tgataaatac ccacacgaga gcgagctgcc ggaggaatgg gagaataacc 1140
gggagtctct gattgtgttc atggagcagg ttcatcgagg catcaaaggc atagtgagag 1200
atttacaagg gaaagggatt tcaaatgctg tcatctctgt ggaaggtgtt aaccatgaca 1260
tccggacagc cagcgatggg gattactggc gtctactgaa ccctggcgaa tatgtggtca 1320
cagccaaggc ggaaggcttt atcacttcca ccaagaactg catggttggc tatgatatgg 1380

gagctactcg gtgtgacttc accctcacaa agaccaacct ggctaggata agagaaatta 1440
tggagacatt tgggaagcag cctgtcagcc taccctccag gcgcctgaag ctgcggggac 1500
ggaaaaggcg gcagcgtggg tgaccctgtc ggacacttga gacatacccc agaccgtgca 1560
aataaaaatc cactccagta gtaactctgt agcaggcttt ccctgttgtt ttgactgtaa 1620
ttcaagagac actcaggagc atacctgcat ggcttggctg accccaaagg ggagggctgg 1680
tggctcaggg tgttttgttt tttgtttttt gtttttttcct ttgttctcat ttatccaaat 1740
accttgaaca gagcagcaga gaaaggccgg tggcagtgag ggaattaatt cagtgagtca 1800
gtctgagatt ctaaaaaggg tgcttgacca ctggccagga agggaaatca ggccttcccc 1860
catttgcgtg acattcaagc ttcccagtgc atttgcaagt ggcacagttg acattgcagc 1920
acccagggaa tcctttgccc cagatgttat catttgagat gctcttatgc agcctaagaa 1980
aatccatcct ctctggcccc aggggacaag ccaagctgct atgtacacac tcggtgttct 2040
attgacaata gaggcattta ttaccaagtg tgcatcgctg agtcctaaat cagctctgtt 2100
ccttttttcca acaaagcttg tcttcctaag agcagacaga agtggagagc acccaagaat 2160
gagtgctggg cagcagaccc tgggggaggg ggcttgctat cccagaaagc ccctaaaccc 2220
tttgctgctc cattagccct ggggtgagga gagccagaca tgttaggagg ccagagcagt 2280
cagtcagggc atcttggaaa agaccttgaa ggaagcaaac cctgggttcc ttttgctcca 2340
gaatgtgaga gctccaagtt ggccccaatc aggaggggag taatgatgaa catacagacg 2400
gccacatctt gccaatcaag catcatctga tgaaaaagaa agcaatctta ggattacctg 2460
ggacacgtca gtctgggaga ggtggttgaa tcattgtgta agggaatagt gtatctaatc 2520
tgtgttgatc ctgctgcctt gttgacctgg agagaatgaa acaaacaaac acataaacaa 2580
ataaagcaaa tggtaagatt aaaaaaaaaa aaaaaaaact cgag 2624

<210> 20
<211> 488
<212> DNA
<213> Homo sapien

<400> 20
ctttcaaccc gcgctcgccg gctccagccc cgcgcgcccc caccccttgc cctcccggcg 60
gctccgcagg gtgaggtggc tttgaccccg ggttgcccgg ccagcacgac cgaggaggtg 120
gctggacagc tggaggatga acggagaagc cgactgcccc acagacctgg aaatggccgc 180
ccccagaggc caagaccgtt ggtcccagga agacatgctg actttgctgg aatgcatgaa 240
gaacaacctt ccatccaatg acagctccca gttcaaaacc acccaaacac acatggaccg 300
ggaaaaagtt gcattgaaag acttttctgg agacatgtgc aagctcaaat gggtcgagat 360
ctctaatgag gtgaggaagt tccgtacatt gacagaattg atcctcgata ctcaggaaca 420
tgtttaaaat ccttacaaag gcaaaaaatc aagaaacacc ccgacttccc cgagaaagcc 480
cctaaccc 488

<210> 21
<211> 391
<212> DNA
<213> Homo sapien

<400> 21
atggaattgt ggttttctct ttgggatcaa tggtctcaga aattccagag aagaaagctg 60
tggcgattgc tgatgctttg ggcaaaatcc ctcagacagt cctgtggcgg tacactggaa 120
cccgaccatc gaatcttgcg aacaacacga tacttgttca gtggctaccc caaaacgatc 180
tgcttggtca cccaatgacc cgtgccttta tcacccatgc tagttcccat ggtgttaatg 240
aaagcatatg caatggcgtt cccatggtga tgataccctt atttggtgat cagatggaca 300
atgcaaagcg cagggagact aagggagctg gagtgaccct gaatgttctg gagatgactt 360
ctgaagatct agaagatgct ctgaagagca g 391

<210> 22
<211> 1320
<212> DNA
<213> Homo sapien

<400> 22

```
aatctgctgg gaatttcttg ggttgacagc tcttggatcc ctattttgaa cagtggtagt     60
gtcctggatt acttttcaga aagaagtaat cctttttatg acagaacatg taataatgaa    120
gtggtcaaaa tgcagaggct aacattagaa cacttgaatc agatggttgg aatcgagtac    180
atcctttgc atgctcaaga gcccattctt ttcatcattc ggaagcaaca gcggcagtcc    240
cctgcccaag ttatcccact agctgattac tatatcattg ctggagtgat ctatcaggca    300
ccagacttgg gatcagttat aaactctaga gtgcttactg cagtgcatgg tattcagtca    360
gcttttgatg aagctatgtc atactgtcga tatcatcctt ccaaagggta ttggtggcac    420
ttcaaagatc atgaagagca agataaagtc agacctaaag ccaaaaggaa agaagaacca    480
agctctattt ttcagagaca acgtgtggat gctttacttt tagacctcag acaaaaattt    540
ccacccaaat ttgtgcagct aaagcctgga gaaaagcctg ttccagtgga tcaaacaaag    600
aaagaggcag aacctatacc agaaactgta aaacctgagg agaaggagac cacaaagaat    660
gtacaacaga cagtgagtgc taaaggcccc cctgaaaaac ggatgagact tcagtgagta    720
ctggacaaaa gagaagcctg gaagactcct catgctagtt atcatacctc agtactgtgg    780
ctcttgagct ttgaagtact ttattgtaac cttcttattt gtatggaatg cgcttatttt    840
ttgaaaggat attaggccgg atgtggtggc tcacgcctgt aatcccagca ctttgggagg    900
ccatggcggg tggatcactt gaggtcagaa gttcaagacc agcctgacca atatggtgaa    960
accccgtctc tactaaaaat acaaaaatta gccgggcgtg gtggcgggcg cccatagtcc   1020
cagctactcg ggaggctgag acaggagact tgcttgaacc cgggaggtgg aggttgccct   1080
gagctgatca tcctgctgtt gcactccagc ttgggcgaaa gagcgagact ttgtctctat   1140
aaagaaggaa agatattatt cccatcatga tttcttgtga atatttgtaa tatgtttttt   1200
gtaacctttc ctttcccgga cttgagcaac ctacacactc acatgtttaa tggtagatat   1260
gttttaaagc aagataaagg tattggtttt aaaaaaaaaa aaaaaaaaaa aaaactcgag   1320
```

<210> 23
<211> 633
<212> DNA
<213> Homo sapien

<400> 23

```
ctaagggcag tgaaggtgaa aaccctctca cggtcccagg gagggagaag gaaggcatgc     60
tgatgggggt taagccgggg gaggacgcat cggggcctgc tgaagacctt gtgagaagat    120
ctgagaaaga tactgcagct gttgtctcca gacagggcag ctccctgaac ctctttgaag    180
atgtgcagat cacagaacca gaagctgagc cagagtccaa gtctgaaccg agacctccaa    240
tttcctctcc gagggctccc cagaccagag ctgtcaagcc ccgacttcat cctgtgaagc    300
caatgaatgc cacggccacc aaggttgcta actgcagctt gggaactgcc accatcatcg    360
gtgagaactt gaacaatgag gtcatgatga agaaatacag cccctcggac cctgcatttg    420
catatgcgca gctgacccac gatgagctga ttcagctggt cctcaaacag aaggaaacga    480
taagcaagaa ggagttccag gtccgcgagc tggaagacta cattgacaac ctgctcgtca    540
gggtcatgga agaaaccccc aatatcctcc gcatcccgac tcaggttggc aaaaaagcag    600
gaaagatgta aattagcaga aaaaaaactc gag                                 633
```

<210> 24
<211> 1328
<212> DNA
<213> Homo sapien

<400> 24

```
gtaaacgctc tcggaattat ggcggcggtg gatatccgag acaatctgct gggaatttct     60
tgggttgaca gctcttggat ccctattttg aacagtggta gtgtcctgga ttacttttca    120
gaaagaagta atccttttta tgacagaaca tgtaataatg aagtggtcaa aatgcagagg    180
ctaacattag aacacttgaa tcagatggtt ggaatcgagt acatcctttt gcatgctcaa    240
gagcccattc ttttcatcat tcggaagcaa cagcggcagt cccctgccca agttatccca    300
ctagctgatt actatatcat tgctggagtg atctatcagg caccagactt gggatcagtt    360
ataaactcta gagtgcttac tgcagtgcat ggtattcagt cagcttttga tgaagctatg    420
tcatactgtc gatatcatcc ttccaaaggg tattggtggc acttcaaaga tcatgaagag    480
caagataaag tcagacctaa agccaaaagg aaagaagaac caagctctat ttttcagaga    540
caacgtgtgg atgctttact tttagacctc agacaaaaaa tttccaccca aatttgtgca    600
gtggatcaaa caaagaaaga ggcagaacct ataccagaaa ctgtaaaacc tgaggagaag    660
```

gagaccacaa agaatgtaca acagacagtg agtgctaaag gcccccctga aaaacggatg 720
agacttcagt gagtactgga caaaagagaa gcctggaaga ctcctcatgc tagttatcat 780
acctcagtac tgtggctctt gagctttgaa gtactttatt gtaaccttct tatttgtatg 840
gaatgcgctt atttttttga aaggatatta ggccggatgt ggtggctcac gcctgtaatc 900
ccagcacttt gggaggccat ggcgggtgga tcacttgagg tcagaagttc aagaccagcc 960
tgaccaatat ggtgaaaccc cgtctctact aaaaatacaa aaattagccg ggcgtggtgg 1020
cgggcgccca tagtcccagc tactcgggag gctgagacag gagacttgct tgaacccggg 1080
aggtggaggt tgccctgagc tgattatcat gctgttgcac tccagcttgg gcgacagagc 1140
gagactttgt ctcaaaaaag aagaaaagat attattccca tcatgatttc ttgtgaatat 1200
ttgtgatatg tcttctgtaa cctttcctct cccggacttg agcaacctac acactcacat 1260
gtttactggt agatatgttt aaaagcaaaa taaaggtatt tgtataaaaa aaaaaaaaaa 1320
aaactcga 1328

<210> 25
<211> 1758
<212> DNA
<213> Homo sapien

<400> 25
gttttttttt tttttttttt aaagagttgc aacaattcat ctttatttct tattttcctc 60
tggagatgca gaatttggta tatttcaccc caagtatatt tgggatagtt ggctcctcgc 120
tgggtcagga tggctgggtg ccttctcccc tggcatggtt ctcttctctg cagggcgagg 180
ggcagggagc tagtaaaacc tcgcaatgac agccgcaatg gcagacccaa tggagcccag 240
gatgaacttg gtcaatccgg agagtccagt tgctcccagt gactgcagag tagccacaag 300
gctgccccgag gcaactccac ccccattggc aatggccgcc gcggacatca tcttggctgc 360
tatggaggac gaggcgattc ccgccgcagt gaagcccatg gcactgagtg gcggcggtgg 420
atatccgaga caatctgctg ggaatttctt gggttgacag ctcttggatc cctattttga 480
acagtggtag tgtcctggat tacttttcag aaagaagtaa tcctttttat gacagaacat 540
gtaataatga agtggtcaaa atgcagaggc taacattaga acacttgaat cagatggttg 600
gaatcgagta catccttttg catgctcaag agcccattct tttcatcatt cggaagcaac 660
agcggcagtc ccctgcccaa gttatcccac tagctgatta ctatatcatt gctggagtga 720
tctatcaggc accagacttg ggatcagtta taaactctag agtgcttact gcagtgcatg 780
gtattcagtc agcttttgat gaagctatgt catactgtcg atatcatcct tccaaagggt 840
attggtggca cttcaaagat catgaagagc aagataaagt cagacctaaa gccaaaagga 900
aagaagaacc aagctctatt tttcagagac aacgtgtgga tgctttactt ttagacctca 960
gacaaaaatt tccacccaaa tttgtgcagc taaagcctgg agaaaagcct gttccagtgg 1020
atcaaacaaa gaaagaggca gaacctatac cagaaactgt aaaacctgag gagaaggaga 1080
ccacaaagaa tgtacaacag acagtgagtg ctaaaggccc ccctgaaaaa cggatgagac 1140
ttcagtgagt actggacaaa agagaagcct ggaagactcc tcatgctagt tatcatacct 1200
cagtactgtg gctcttgagc tttgaagtac tttattgtaa ccttcttatt tgtatggaat 1260
gcgcttattt tttgaaagga tattaggccg gatgtggtgg ctcacgcctg taatcccagc 1320
actttgggag gccatggcgg gtggatcact tgaggtcaga agttcaagac cagcctgacc 1380
aatatggtga aaccccgtct ctactaaaaa tacaaaaatt agccgggcgt ggtggcgggc 1440
gcccatagtc ccagctactc gggaggctga gacaggagac ttgcttgaac ccgggaggtg 1500
gaggttgccc tgagctgatt atcatgctgt tgcactccag cttgggcgac agagcgagac 1560
tttgtctcaa aaaagaagaa aagatattat tcccatcatg atttcttgtg aatatttgtt 1620
atatgtcttc tgttaccttt cctctcccgg aattgagcaa cctacacact cacatgttta 1680
ctggtagata tgtttaaaag caaataaagg tattggtata tattgcttca aaaaaaaaaa 1740
aaaaaaaaaa aactcgag 1758

<210> 26
<211> 493
<212> DNA
<213> Homo sapien

<400> 26
gaggcgagcg gcagggcctg gtggcgagag cgcggctgtc actgcgcccg agcatcccag 60
agctttccga gcggacgagc cggccgtgcc gggcatcccc agcctcgcta ccctcgcagc 120

```
acacgtcgag ccccgcacag gcaagggtcc ggaacttagc ccaaagcacg tttcccctgg     180
cagcgcagga gacgcccggc cgcgcgccgg cgcacgcccc cctctcctcc tttgttccgg     240
gggtcggcgg ccgctctcct gccagcgtcg ggatctcggc cccgggaggc gggccgtcgg     300
gcgcagccgc gaagattccg ttggaactga cgcagagccg agtgcagaag atctgggtgc     360
ccgtggacca caggccctcg ttgcccagat cctgtgggcc aaagctgacc aactccccgg     420
ccgtcttcgt catggtgggc ctcccccgcc cggggcaaga cctacttctc cacgaaagct     480
tactcgctgc ctc                                                        493
```

<210> 27
<211> 1331
<212> DNA
<213> Homo sapien

<400> 27

```
ggtggatatc cgagacaatc tgctgggaat ttcttgggtt gacagctctt ggatccctat      60
tttgaacagt ggtagtgtcc tggattactt ttcagaaaga agtaatcctt tttatgacag     120
aacatgtaat aatgaagtgg tcaaaatgca gaggctaaca ttagaacact tgaatcagat     180
ggttggaatc gagtacatcc ttttgcatgc tcaagagccc attcttttca tcattcggaa     240
gcaacagcgg cagtcccctg cccaagttat cccactagct gattactata tcattgctgg     300
agtgatctat caggcaccag acttgggatc agttataaac tctagagtgc ttactgcagt     360
gcatggtatt cagtcagctt ttgatgaagc tatgtcatac tgtcgatatc atccttccaa     420
agggtattgg tggcacttca aagatcatga agagcaagat aaagtcagac ctaaagccaa     480
aaggaaagaa gaaccaagct ctatttttca gagacaacgt gtggatgctt tacttttaga     540
cctcagacaa aaatttccac ccaaatttgt gcagctaaag cctggagaaa agcctgttcc     600
agtggatcaa acaaagaaag aggcagaacc tataccagaa actgtaaaac ctgaggagaa     660
ggagaccaca aagaatgtac aacagacagt gagtgctaaa ggcccccctg aaaaacggat     720
gagacttcag tgagtactgg acaaaagaga agcctggaag actcctcatg ctagttatca     780
tacctcagta ctgtggctct tgagctttga agtactttat tgtaaccttc ttatttgtat     840
ggaatgcgct tatttttttga aaggatatta ggccggatgt ggtggctcac gcctgtaatc    900
ccagcacttt gggaggccat ggcgggtgga tcacttgagg tcagaagttc aagaccagcc     960
tgaccaatat ggtgaaaccc cgtctctact aaaaatacaa aaattagccg ggcgtggtgg    1020
cgggcgccca tagtcccagc tactcgggag gctgagacag gagacttgct tgaacccggg    1080
aggtggaggt tgccctgagc tgattatcat gctgttgcac tccagcttgg gcgacagagc    1140
gagactttgt ctcaaaaaaa gaagaaaaga tattattccc atcatgattt cttgtgaata    1200
tttgttatat gtcttctgta acctttcctc tcccggactt gagcaaccta cacactcaca    1260
tgtttactgg tagatatgtt taaaagcaaa ataaaggtat tggtataaaa aaaaaaaaaa    1320
aaaaactcga g                                                         1331
```

<210> 28
<211> 1333
<212> DNA
<213> Homo sapien

<400> 28

```
cggcggtgga tatccgagac aatctgctgg gaatttcttg ggttgacagc tcttggatcc      60
ctattttgaa cagtggtagt gtcctggatt acttttcaga aagaagtaat cctttttatg     120
acagaacatg taataatgaa gtggtcaaaa tgcagaggct aacattagaa cacttgaatc     180
agatggttgg aatcgagtac atccttttgc atgctcaaga gcccattctt ttcatcattc     240
ggaagcaaca gcggcagtcc cctgcccaag ttatcccact agctgattac tatatcattg     300
ctggagtgat ctatcaggca ccagacttgg gatcagttat aaactctaga gtgcttactg     360
cagtgcatgg tattcagtca gcttttgatg aagctatgtc atactgtcga tatcatcctt     420
ccaaagggta ttggtggcac ttcaaagatc atgaagagca agataaagtc agacctaaag     480
ccaaaaggaa agaagaacca agctctattt ttcagagaca acgtgtggat gctttacttt     540
tagacctcag acaaaaattt ccacccaaat ttgtgcagct aaagcctgga gaaaagcctg     600
ttccagtgga tcaaacaaag aaagaggcag aacctatacc agaaactgta aaacctgagg     660
agaaggagac cacaaagaat gtacaacaga cagtgagtgc taaaggcccc cctgaaaaac     720
ggatgagact tcagtgagta ctggacaaaa gagaagcctg gaagactcct catgctagtt     780
atcatacctc agtactgtgg ctcttgagct ttgaagtact ttattgtaac cttcttattt     840
```

gtatggaatg cgcttatttt ttgaaaggat attaggccgg atgtggtggc tcacgcctgt 900
aatcccagca ctttgggagg ccatggcggg tggatcactt gaggtcagaa gttcaagacc 960
agcctgacca atatggtgaa accccgtctc tactaaaaat acaaaaatta gccgggcgtg 1020
gtggcgggcg cccatagtcc cagctactcg ggaggctgag acaggagact tgcttgaacc 1080
cgggaggtgg aggttgccct gagctgatta tcatgctgtt gcactccagc ttgggcgaca 1140
gagcgagact ttgtctcaaa aaagaagaaa agatattatt cccatcatga tttcttgtga 1200
atatttgtga tatgtcttct gtaacctttc ctctcccgga cttgagcaac ctacacactc 1260
acatgtttac tggtagatat gtttaaaagc aaaataaagg tatttgtata aaaaaaaaaa 1320
aaaaaaactc gag 1333

<210> 29
<211> 813
<212> DNA
<213> Homo sapien

<400> 29
ctgagctgca cttcagcgaa ttcacctcgg ctgtggctga catgaagaac tccgtggcgg 60
accgagacaa cagccccagc tcctgtgctg gcctcttcat tgcttcacac atcgggtttg 120
actggcccgg ggtctgggtc cacctggaca tcgctgctcc agtgcatgct ggcgagcgag 180
ccacaggctt tggggtggct ctcctactgg ctctttttgg ccgtgcctcc gaggacccgc 240
tgctgaacct ggtatccccg ctggactgtg aggtggatgc ccaggaaggc gacaacatgg 300
ggcgtgactc caagagacgg aggctcgtgt gagggctact tcccagctgg tgacacaggg 360
ttccttacct cattttgcac tgactgattt taagcaattg aaagattaac taactcttaa 420
gatgagtttg gcttctcctt ctgtgcccag tggtgacagg agtgagccat tcttctctta 480
gaagcagctt aggggcttgg tggggtctgg agaaaattgt cacagacccc ataggtctcc 540
atctgtaagc tctgtccctt gtcctccacc ctggtcttta gagccacctc aggtcaccct 600
ctgtagtgag tgtacttcct gacccaggcc cttgctcaag ctggggctcc ctggggtgtc 660
taaccagccc tgggtagatg tgactggctg ttagggaccc cattctgtga agcaggagac 720
cctcacagct cccaccaacc cccagttcac ttgaagttga attaaatatg gccacaacat 780
aaaaaaaaaa aaaaaaaaaa aaaaaaactc gag 813

<210> 30
<211> 1316
<212> DNA
<213> Homo sapien

<400> 30
caggcgccca gtcatggccc aagagacagc accaccgtgt ggcccagtct caaggggtga 60
cagtccaatc atagaaaaga tggaaaaaag gacatgtgcc ctgtgccctg aaggccacga 120
gtggagtcaa atatactttt caccatcagg aaatatagtt gctcatgaaa actgtttgct 180
gtattcatca ggactggtgg agtgtgagac tcttgatcta cgtaatacaa ttagaaactt 240
tgatgtcaaa tctgtaaaga aagagatctg gagaggaaga agattgaaat gctcattctg 300
taacaaagga ggcgccaccg tggggtgtga tttatggttc tgtaagaaga gttaccacta 360
tgtctgtgcc aaaaaggacc aagcaattct tcaagttgat ggaaaccatg gaacttacaa 420
attattttgc ccagaacatt ctccagaaca agaagaggcc actgaaagtg ctgatgaccc 480
aagcatgaag aagaagagag gaaaaaacaa acgcctctca tcaggccctc ctgcacagcc 540
aaaaacgatg aaatgtagta acgccaaaag acatatgaca gaagagcctc atggtcacac 600
agatgcagct gtcaaatctc cttttcttaa gaaatgccag gaagcaggac ttcttactga 660
actatttgaa cacatactag aaaatatgga ttcagttcat ggaagacttg tggatgagac 720
tgcctcagag tcggactatg aagggatcga gaccttactg tttgactgtg gattatttaa 780
agacacacta agaaaattcc aagaagtaat caagagtaaa gcttgtgaat gggaagaaag 840
gcaaaggcag atgaagcagc agcttgaggc acttgcagac ttacaacaaa gcttgtgctc 900
atttcaagaa aatggggacc tggactgctc aagttctaca tcaggatcct tgctacctcc 960
tgaggaccac cagtaaaagc tgttcctcag gaaaactgga tggggcctcc atgttctcca 1020
aggatcgagg aagtcttcct gcctaccctg cccaccccag tcaagggcag caacaccaga 1080
gctttgctca gccttaaatg gaatcttaga gctttctctt gcttctgcta ctcctacaga 1140
tggcctcatc atggtctcca ctcagtatta ataactccat cagcatagag caaactcaac 1200
actgtgcatt gcacactgtt accatgggtt tatgctcact atcatatcac attgccaata 1260

tttagcacac ttaataaatg cttgtcaaaa cccaaaaaaa aaaaaaaaaa ctcgag 1316

<210> 31
<211> 1355
<212> DNA
<213> Homo sapien

<400> 31
cggcggtgga tatccgagac aatctgctgg gaatttcttg ggttgacagc tcttggatcc 60
ctattttgaa cagtggtagt gtcctggatt acttttcaga aagaagtaat cctttttatg 120
acagaacatg taataatgaa gtggtcaaaa tgcagaggct aacattagaa cacttgaatc 180
agatggttgg aatcgagtac atccttttgc atgctcaaga gcccattctt ttcatcattc 240
ggaagcaaca gcggcagtcc cctgcccaag ttatcccact agctgattac tatatcattg 300
ctggagtgat ctatcaggca ccagacttgg gatcagttat aaactctaga gtgcttactg 360
cagtgcatgg tattcagtca gcttttgatg aagctatgtc atactgtcga tatcatcctt 420
ccaaagggta ttggtggcac ttcaaagatc atgaagagca agataaagtc agacctaaag 480
ccaaaaggaa agaagaacca agctctattt ttcagagaca acgtgtggat gctttacttt 540
tagacctcag acaaaaattt ccacccaaat ttgtgcagct aaagcctgga gaaaagcctg 600
ttccagtgga tcaaacaaag aaagaggcag aacctatacc agaaactgta aaacctgagg 660
agaaggagac cacaaagaat gtacaacaga cagtgagtgc taaaggcccc cctgaaaaac 720
ggatgagact tcagtgagta ctggacaaaa gagaagcctg gaagactcct catgctagtt 780
atcatacctc agtactgtgg ctcttgagct ttgaagtact ttattgtaac cttcttattt 840
gtatggaatg cgcttatttt ttgaaaggat attaggccgg atgtggtggc tcacgcctgt 900
aatcccagca ctttgggagg ccatggcggg tggatcactt gaggtcagaa gttcaagacc 960
agcctgacca atatggtgaa accccgtctc tactaaaaat acaaaaatta gccgggcgtg 1020
gtggcgggcg cccatagtcc cagctactcg ggaggctgag acaggagact tgcttgaacc 1080
cgggaggtgg aggttgccct gagctgatta tcatgctgtt gcactccagc ttgggcgaca 1140
gaacgagact ttgtctcaaa aaaagaagaa aagatattat tcccatcatg atttcttgtg 1200
aatatttgtt atatgtcttc tggtaacctt tcctctcccg gacttgaagc aacctcacac 1260
actcacatgt ttactggtag atatgtttta aaagcaaaat aaaggtattt gtttttccaa 1320
aaaaaaaaaa aaaaaaaaaa aaaaaaaaac tcgag 1355

<210> 32
<211> 80
<212> PRT
<213> Homo sapien

<400> 32
Val Ser Arg Ile Arg Gly Gly Ala Lys Lys Arg Lys Lys Lys Ser Tyr
1 5 10 15
Thr Thr Pro Lys Lys Asp Lys His Gln Arg Lys Lys Val Gln Pro Ala
20 25 30
Val Leu Lys Tyr Tyr Lys Val Asp Glu Asn Gly Lys Ile Ser Cys Leu
35 40 45
Arg Arg Glu Cys Pro Ser Asp Glu Cys Gly Ala Gly Val Phe Met Ala
50 55 60
Ser His Phe Asp Arg His Tyr Cys Gly Lys Cys Cys Leu Thr His Cys
65 70 75 80

<210> 33
<211> 130
<212> PRT
<213> Homo sapien

<400> 33
Glu Ile Ser Asn Glu Val Arg Lys Phe Arg Thr Leu Thr Glu Leu Ile
1 5 10 15
Leu Asp Ala Gln Glu His Val Lys Asn Pro Tyr Lys Gly Lys Lys Leu

```
        20                  25                  30
Lys Lys His Pro Asp Phe Pro Lys Lys Pro Leu Thr Pro Tyr Phe Arg
    35                  40                  45
Phe Phe Met Glu Lys Arg Ala Lys Tyr Ala Lys Leu His Pro Gln Met
    50                  55                  60
Ser Asn Leu Asp Leu Thr Lys Ile Leu Ser Lys Lys Tyr Lys Glu Leu
65                  70                  75                  80
Pro Glu Lys Lys Lys Met Lys Tyr Val Pro Asp Phe Gln Arg Arg Glu
                85                  90                  95
Thr Gly Val Arg Ala Lys Pro Gly Pro Ile Gln Gly Gly Ser Pro Pro
            100                 105                 110
Pro Tyr Pro Glu Cys Gln Glu Ser Asp Ile Pro Glu Lys Pro Gln Asp
        115                 120                 125
Pro Pro
    130

      <210> 34
      <211> 506
      <212> PRT
      <213> Homo sapien

      <400> 34
Asn Ser Glu Lys Glu Ile Pro Val Leu Asn Glu Leu Pro Val Pro Met
 1               5                  10                  15
Val Ala Arg Tyr Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp Asn Gly
            20                  25                  30
Ser Ile Cys Met Arg Met Glu Ile Leu Gly Cys Pro Leu Pro Asp Pro
        35                  40                  45
Asn Asn Tyr Tyr His Arg Arg Asn Glu Met Thr Thr Thr Asp Asp Leu
    50                  55                  60
Asp Phe Lys His His Asn Tyr Lys Glu Met Arg Gln Leu Met Lys Val
65                  70                  75                  80
Val Asn Glu Met Cys Pro Asn Ile Thr Arg Ile Tyr Asn Ile Gly Lys
                85                  90                  95
Ser His Gln Gly Leu Lys Leu Tyr Ala Val Glu Ile Ser Asp His Pro
            100                 105                 110
Gly Glu His Glu Val Gly Glu Pro Glu Phe His Tyr Ile Ala Gly Ala
        115                 120                 125
His Gly Asn Glu Val Leu Gly Arg Glu Leu Leu Leu Leu Leu Leu His
    130                 135                 140
Phe Leu Cys Gln Glu Tyr Ser Ala Gln Asn Ala Arg Ile Val Arg Leu
145                 150                 155                 160
Val Glu Glu Thr Arg Ile His Ile Leu Pro Ser Leu Asn Pro Asp Gly
                165                 170                 175
Tyr Glu Lys Ala Tyr Glu Gly Gly Ser Glu Leu Gly Gly Trp Ser Leu
            180                 185                 190
Gly Arg Trp Thr His Asp Gly Ile Asp Ile Asn Asn Asn Phe Pro Asp
        195                 200                 205
Leu Asn Ser Leu Leu Trp Glu Ala Glu Asp Gln Gln Asn Ala Pro Arg
    210                 215                 220
Lys Val Pro Asn His Tyr Ile Ala Ile Pro Glu Trp Phe Leu Ser Glu
225                 230                 235                 240
Asn Ala Thr Val Ala Thr Glu Thr Arg Ala Val Ile Ala Trp Met Glu
                245                 250                 255
Lys Ile Pro Phe Val Leu Gly Gly Asn Leu Gln Gly Gly Glu Leu Val
            260                 265                 270
Val Ala Tyr Pro Tyr Asp Met Val Arg Ser Leu Trp Lys Thr Gln Glu
        275                 280                 285
```

His Thr Pro Thr Pro Asp Asp His Val Phe Arg Trp Leu Ala Tyr Ser
290 295 300
Tyr Ala Ser Thr His Arg Leu Met Thr Asp Ala Arg Arg Arg Val Cys
305 310 315 320
His Thr Glu Asp Phe Gln Lys Glu Glu Gly Thr Val Asn Gly Ala Ser
325 330 335
Trp His Thr Val Ala Gly Ser Leu Asn Asp Phe Ser Tyr Leu His Thr
340 345 350
Asn Cys Phe Glu Leu Ser Ile Tyr Val Gly Cys Asp Lys Tyr Pro His
355 360 365
Glu Ser Glu Leu Pro Glu Glu Trp Glu Asn Asn Arg Glu Ser Leu Ile
370 375 380
Val Phe Met Glu Gln Val His Arg Gly Ile Lys Gly Ile Val Arg Asp
385 390 395 400
Leu Gln Gly Lys Gly Ile Ser Asn Ala Val Ile Ser Val Glu Gly Val
405 410 415
Asn His Asp Ile Arg Thr Ala Ser Asp Gly Asp Tyr Trp Arg Leu Leu
420 425 430
Asn Pro Gly Glu Tyr Val Val Thr Ala Lys Ala Glu Gly Phe Ile Thr
435 440 445
Ser Thr Lys Asn Cys Met Val Gly Tyr Asp Met Gly Ala Thr Arg Cys
450 455 460
Asp Phe Thr Leu Thr Lys Thr Asn Leu Ala Arg Ile Arg Glu Ile Met
465 470 475 480
Glu Thr Phe Gly Lys Gln Pro Val Ser Leu Pro Ser Arg Arg Leu Lys
485 490 495
Leu Arg Gly Arg Lys Arg Arg Gln Arg Gly
500 505

<210> 35
<211> 96
<212> PRT
<213> Homo sapien

<400> 35
Met Asn Gly Glu Ala Asp Cys Pro Thr Asp Leu Glu Met Ala Ala Pro
1 5 10 15
Arg Gly Gln Asp Arg Trp Ser Gln Glu Asp Met Leu Thr Leu Leu Glu
20 25 30
Cys Met Lys Asn Asn Leu Pro Ser Asn Asp Ser Ser Gln Phe Lys Thr
35 40 45
Thr Gln Thr His Met Asp Arg Glu Lys Val Ala Leu Lys Asp Phe Ser
50 55 60
Gly Asp Met Cys Lys Leu Lys Trp Val Glu Ile Ser Asn Glu Val Arg
65 70 75 80
Lys Phe Arg Thr Leu Thr Glu Leu Ile Leu Asp Thr Gln Glu His Val
85 90 95

<210> 36
<211> 129
<212> PRT
<213> Homo sapien

<400> 36
Gly Ile Val Val Phe Ser Leu Gly Ser Met Val Ser Glu Ile Pro Glu
1 5 10 15
Lys Lys Ala Val Ala Ile Ala Asp Ala Leu Gly Lys Ile Pro Gln Thr
20 25 30

Val Leu Trp Arg Tyr Thr Gly Thr Arg Pro Ser Asn Leu Ala Asn Asn
35 40 45
Thr Ile Leu Val Gln Trp Leu Pro Gln Asn Asp Leu Leu Gly His Pro
50 55 60
Met Thr Arg Ala Phe Ile Thr His Ala Ser Ser His Gly Val Asn Glu
65 70 75 80
Ser Ile Cys Asn Gly Val Pro Met Val Met Ile Pro Leu Phe Gly Asp
85 90 95
Gln Met Asp Asn Ala Lys Arg Arg Glu Thr Lys Gly Ala Gly Val Thr
100 105 110
Leu Asn Val Leu Glu Met Thr Ser Glu Asp Leu Glu Asp Ala Leu Lys
115 120 125
Ser

<210> 37
<211> 238
<212> PRT
<213> Homo sapien

<400> 37
Asn Leu Leu Gly Ile Ser Trp Val Asp Ser Ser Trp Ile Pro Ile Leu
1 5 10 15
Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser Glu Arg Ser Asn Pro Phe
20 25 30
Tyr Asp Arg Thr Cys Asn Asn Glu Val Val Lys Met Gln Arg Leu Thr
35 40 45
Leu Glu His Leu Asn Gln Met Val Gly Ile Glu Tyr Ile Leu Leu His
50 55 60
Ala Gln Glu Pro Ile Leu Phe Ile Ile Arg Lys Gln Gln Arg Gln Ser
65 70 75 80
Pro Ala Gln Val Ile Pro Leu Ala Asp Tyr Tyr Ile Ile Ala Gly Val
85 90 95
Ile Tyr Gln Ala Pro Asp Leu Gly Ser Val Ile Asn Ser Arg Val Leu
100 105 110
Thr Ala Val His Gly Ile Gln Ser Ala Phe Asp Glu Ala Met Ser Tyr
115 120 125
Cys Arg Tyr His Pro Ser Lys Gly Tyr Trp Trp His Phe Lys Asp His
130 135 140
Glu Glu Gln Asp Lys Val Arg Pro Lys Ala Lys Arg Lys Glu Glu Pro
145 150 155 160
Ser Ser Ile Phe Gln Arg Gln Arg Val Asp Ala Leu Leu Leu Asp Leu
165 170 175
Arg Gln Lys Phe Pro Pro Lys Phe Val Gln Leu Lys Pro Gly Glu Lys
180 185 190
Pro Val Pro Val Asp Gln Thr Lys Lys Glu Ala Glu Pro Ile Pro Glu
195 200 205
Thr Val Lys Pro Glu Glu Lys Glu Thr Thr Lys Asn Val Gln Gln Thr
210 215 220
Val Ser Ala Lys Gly Pro Pro Glu Lys Arg Met Arg Leu Gln
225 230 235

<210> 38
<211> 202
<212> PRT
<213> Homo sapien

<400> 38

Lys Gly Ser Glu Gly Glu Asn Pro Leu Thr Val Pro Gly Arg Glu Lys
 1   5   10   15
Glu Gly Met Leu Met Gly Val Lys Pro Gly Glu Asp Ala Ser Gly Pro
            20   25   30
Ala Glu Asp Leu Val Arg Arg Ser Glu Lys Asp Thr Ala Ala Val Val
        35   40   45
Ser Arg Gln Gly Ser Ser Leu Asn Leu Phe Glu Asp Val Gln Ile Thr
    50   55   60
Glu Pro Glu Ala Glu Pro Glu Ser Lys Ser Glu Pro Arg Pro Pro Ile
65   70   75   80
Ser Ser Pro Arg Ala Pro Gln Thr Arg Ala Val Lys Pro Arg Leu His
                85   90   95
Pro Val Lys Pro Met Asn Ala Thr Ala Thr Lys Val Ala Asn Cys Ser
            100   105   110
Leu Gly Thr Ala Thr Ile Ile Gly Glu Asn Leu Asn Asn Glu Val Met
        115   120   125
Met Lys Lys Tyr Ser Pro Ser Asp Pro Ala Phe Ala Tyr Ala Gln Leu
    130   135   140
Thr His Asp Glu Leu Ile Gln Leu Val Leu Lys Gln Lys Glu Thr Ile
145   150   155   160
Ser Lys Lys Glu Phe Gln Val Arg Glu Leu Glu Asp Tyr Ile Asp Asn
                165   170   175
Leu Leu Val Arg Val Met Glu Glu Thr Pro Asn Ile Leu Arg Ile Pro
            180   185   190
Thr Gln Val Gly Lys Lys Ala Gly Lys Met
        195   200

<210> 39
<211> 243
<212> PRT
<213> Homo sapien

<400> 39
Val Asn Ala Leu Gly Ile Met Ala Ala Val Asp Ile Arg Asp Asn Leu
 1   5   10   15
Leu Gly Ile Ser Trp Val Asp Ser Ser Trp Ile Pro Ile Leu Asn Ser
            20   25   30
Gly Ser Val Leu Asp Tyr Phe Ser Glu Arg Ser Asn Pro Phe Tyr Asp
        35   40   45
Arg Thr Cys Asn Asn Glu Val Val Lys Met Gln Arg Leu Thr Leu Glu
    50   55   60
His Leu Asn Gln Met Val Gly Ile Glu Tyr Ile Leu Leu His Ala Gln
65   70   75   80
Glu Pro Ile Leu Phe Ile Ile Arg Lys Gln Gln Arg Gln Ser Pro Ala
                85   90   95
Gln Val Ile Pro Leu Ala Asp Tyr Tyr Ile Ile Ala Gly Val Ile Tyr
            100   105   110
Gln Ala Pro Asp Leu Gly Ser Val Ile Asn Ser Arg Val Leu Thr Ala
        115   120   125
Val His Gly Ile Gln Ser Ala Phe Asp Glu Ala Met Ser Tyr Cys Arg
    130   135   140
Tyr His Pro Ser Lys Gly Tyr Trp Trp His Phe Lys Asp His Glu Glu
145   150   155   160
Gln Asp Lys Val Arg Pro Lys Ala Lys Arg Lys Glu Glu Pro Ser Ser
                165   170   175
Ile Phe Gln Arg Gln Arg Val Asp Ala Leu Leu Leu Asp Leu Arg Gln
            180   185   190
Lys Ile Ser Thr Gln Ile Cys Ala Val Asp Gln Thr Lys Lys Glu Ala

195 200 205
Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr Lys
210 215 220
Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg Met
225 230 235 240
Arg Leu Gln

<210> 40
<211> 245
<212> PRT
<213> Homo sapien

<400> 40
Ala Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp
1 5 10 15
Ser Ser Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr Phe
20 25 30
Ser Glu Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu Val
35 40 45
Val Lys Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val Gly
50 55 60
Ile Glu Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile Ile
65 70 75 80
Arg Lys Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala Asp
85 90 95
Tyr Tyr Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly Ser
100 105 110
Val Ile Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser Ala
115 120 125
Phe Asp Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly Tyr
130 135 140
Trp Trp His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro Lys
145 150 155 160
Ala Lys Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg Val
165 170 175
Asp Ala Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe Val
180 185 190
Gln Leu Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys Lys
195 200 205
Glu Ala Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr
210 215 220
Thr Lys Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys
225 230 235 240
Arg Met Arg Leu Gln
245

<210> 41
<211> 163
<212> PRT
<213> Homo sapien

<400> 41
Gly Glu Arg Gln Gly Leu Val Ala Arg Ala Arg Leu Ser Leu Arg Pro
1 5 10 15
Ser Ile Pro Glu Leu Ser Glu Arg Thr Ser Arg Pro Cys Arg Ala Ser
20 25 30
Pro Ala Ser Leu Pro Ser Gln His Thr Ser Ser Pro Ala Gln Ala Arg

```
        35                  40                  45
Val Arg Asn Leu Ala Gln Ser Thr Phe Pro Leu Ala Ala Gln Glu Thr
    50                  55                  60
Pro Gly Arg Ala Pro Ala His Ala Pro Leu Ser Ser Phe Val Pro Gly
65                  70                  75                  80
Val Gly Gly Arg Ser Pro Ala Ser Val Gly Ile Ser Ala Pro Gly Gly
                85                  90                  95
Gly Pro Ser Gly Ala Ala Ala Lys Ile Pro Leu Glu Leu Thr Gln Ser
            100                 105                 110
Arg Val Gln Lys Ile Trp Val Pro Val Asp His Arg Pro Ser Leu Pro
        115                 120                 125
Arg Ser Cys Gly Pro Lys Leu Thr Asn Ser Pro Ala Val Phe Val Met
    130                 135                 140
Val Gly Leu Pro Arg Pro Gly Gln Asp Leu Leu Leu His Glu Ser Leu
145                 150                 155                 160
Leu Ala Ala


      <210> 42
      <211> 243
      <212> PRT
      <213> Homo sapien

      <400> 42
Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp Ser Ser
 1               5                  10                  15
Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser Glu
            20                  25                  30
Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu Val Val Lys
        35                  40                  45
Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val Gly Ile Glu
    50                  55                  60
Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile Ile Arg Lys
65                  70                  75                  80
Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala Asp Tyr Tyr
                85                  90                  95
Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly Ser Val Ile
            100                 105                 110
Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser Ala Phe Asp
        115                 120                 125
Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly Tyr Trp Trp
    130                 135                 140
His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro Lys Ala Lys
145                 150                 155                 160
Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg Val Asp Ala
                165                 170                 175
Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe Val Gln Leu
            180                 185                 190
Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys Lys Glu Ala
        195                 200                 205
Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr Lys
    210                 215                 220
Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg Met
225                 230                 235                 240
Arg Leu Gln


      <210> 43
```

<211> 244
<212> PRT
<213> Homo sapien

<400> 43
Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp Ser
1 5 10 15
Ser Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser
20 25 30
Glu Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu Val Val
35 40 45
Lys Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val Gly Ile
50 55 60
Glu Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile Ile Arg
65 70 75 80
Lys Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala Asp Tyr
85 90 95
Tyr Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly Ser Val
100 105 110
Ile Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser Ala Phe
115 120 125
Asp Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly Tyr Trp
130 135 140
Trp His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro Lys Ala
145 150 155 160
Lys Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg Val Asp
165 170 175
Ala Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe Val Gln
180 185 190
Leu Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys Lys Glu
195 200 205
Ala Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr
210 215 220
Lys Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg
225 230 235 240
Met Arg Leu Gln

<210> 44
<211> 109
<212> PRT
<213> Homo sapien

<400> 44
Glu Leu His Phe Ser Glu Phe Thr Ser Ala Val Ala Asp Met Lys Asn
1 5 10 15
Ser Val Ala Asp Arg Asp Asn Ser Pro Ser Ser Cys Ala Gly Leu Phe
20 25 30
Ile Ala Ser His Ile Gly Phe Asp Trp Pro Gly Val Trp Val His Leu
35 40 45
Asp Ile Ala Ala Pro Val His Ala Gly Glu Arg Ala Thr Gly Phe Gly
50 55 60
Val Ala Leu Leu Leu Ala Leu Phe Gly Arg Ala Ser Glu Asp Pro Leu
65 70 75 80
Leu Asn Leu Val Ser Pro Leu Asp Cys Glu Val Asp Ala Gln Glu Gly
85 90 95
Asp Asn Met Gly Arg Asp Ser Lys Arg Arg Arg Leu Val
100 105

```
      <210> 45
      <211> 324
      <212> PRT
      <213> Homo sapien

      <400> 45
Arg Arg Pro Val Met Ala Gln Glu Thr Ala Pro Pro Cys Gly Pro Val
 1               5                  10                  15
Ser Arg Gly Asp Ser Pro Ile Ile Glu Lys Met Glu Lys Arg Thr Cys
            20                  25                  30
Ala Leu Cys Pro Glu Gly His Glu Trp Ser Gln Ile Tyr Phe Ser Pro
        35                  40                  45
Ser Gly Asn Ile Val Ala His Glu Asn Cys Leu Leu Tyr Ser Ser Gly
    50                  55                  60
Leu Val Glu Cys Glu Thr Leu Asp Leu Arg Asn Thr Ile Arg Asn Phe
65                  70                  75                  80
Asp Val Lys Ser Val Lys Lys Glu Ile Trp Arg Gly Arg Arg Leu Lys
                85                  90                  95
Cys Ser Phe Cys Asn Lys Gly Gly Ala Thr Val Gly Cys Asp Leu Trp
            100                 105                 110
Phe Cys Lys Lys Ser Tyr His Tyr Val Cys Ala Lys Lys Asp Gln Ala
        115                 120                 125
Ile Leu Gln Val Asp Gly Asn His Gly Thr Tyr Lys Leu Phe Cys Pro
    130                 135                 140
Glu His Ser Pro Glu Gln Glu Glu Ala Thr Glu Ser Ala Asp Asp Pro
145                 150                 155                 160
Ser Met Lys Lys Lys Arg Gly Lys Asn Lys Arg Leu Ser Ser Gly Pro
                165                 170                 175
Pro Ala Gln Pro Lys Thr Met Lys Cys Ser Asn Ala Lys Arg His Met
            180                 185                 190
Thr Glu Glu Pro His Gly His Thr Asp Ala Ala Val Lys Ser Pro Phe
        195                 200                 205
Leu Lys Lys Cys Gln Glu Ala Gly Leu Leu Thr Glu Leu Phe Glu His
    210                 215                 220
Ile Leu Glu Asn Met Asp Ser Val His Gly Arg Leu Val Asp Glu Thr
225                 230                 235                 240
Ala Ser Glu Ser Asp Tyr Glu Gly Ile Glu Thr Leu Leu Phe Asp Cys
                245                 250                 255
Gly Leu Phe Lys Asp Thr Leu Arg Lys Phe Gln Glu Val Ile Lys Ser
            260                 265                 270
Lys Ala Cys Glu Trp Glu Glu Arg Gln Arg Gln Met Lys Gln Gln Leu
        275                 280                 285
Glu Ala Leu Ala Asp Leu Gln Gln Ser Leu Cys Ser Phe Gln Glu Asn
    290                 295                 300
Gly Asp Leu Asp Cys Ser Ser Ser Thr Ser Gly Ser Leu Leu Pro Pro
305                 310                 315                 320
Glu Asp His Gln


      <210> 46
      <211> 244
      <212> PRT
      <213> Homo sapien

      <400> 46
Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val Asp Ser
 1               5                  10                  15
```

Ser Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr Phe Ser
20 25 30
Glu Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu Val Val
35 40 45
Lys Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val Gly Ile
50 55 60
Glu Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile Ile Arg
65 70 75 80
Lys Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala Asp Tyr
85 90 95
Tyr Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly Ser Val
100 105 110
Ile Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser Ala Phe
115 120 125
Asp Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly Tyr Trp
130 135 140
Trp His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro Lys Ala
145 150 155 160
Lys Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg Val Asp
165 170 175
Ala Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe Val Gln
180 185 190
Leu Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys Lys Glu
195 200 205
Ala Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu Thr Thr
210 215 220
Lys Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu Lys Arg
225 230 235 240
Met Arg Leu Gln

<210> 47
<211> 14
<212> DNA
<213> Homo sapien

<400> 47
tttttttttt ttag 14

<210> 48
<211> 10
<212> DNA
<213> Homo sapien

<400> 48
cttcaacctc 10

<210> 49
<211> 496
<212> DNA
<213> Homo sapien

<400> 49
gcaccatgta ccgagcactt cggctcctcg cgcgctcgcg tcccctcgtg cgggctccag 60
ccgcagcctt agcttcggct cccggcttgg gtggcgcggc cgtgccctcg ttttggcctc 120
cgaacgcggc tcgaatggca agccaaaatt ccttccggat agaatatgat acctttggtg 180
aactaaaggt gccaaatgat aagtattatg gcgcccagac cgtgagatct acgatgaact 240
ttaagattgg aggtgtgaca gaacgcatgc caaccccagt tattaaagct tttggcatct 300

tgaagcgagc ggccgctgaa gtaaaccagg attatggtct tgatccaaag attgctaatg 360
caataatgaa ggcagcagat gaggtagctg aaggtaaatt aaatgatcat tttcctctcg 420
tggtatggca gactggatca ggaactcaga caaatatgaa tgtaaatgaa gtcattagcc 480
aatagagcaa ttgaaa 496

<210> 50
<211> 499
<212> DNA
<213> Homo sapien

<400> 50
agaaaaagtc tatgtttgca gaaatacaga tccaagacaa agacaggatg ggcactgctg 60
gaaaagttat taaatgcaaa gcagctgtgc tttgggagca gaagcaaccc ttctccattg 120
aggaaataga agttgcccca ccaaagacta aagaagttcg cattaagatt ttggccacag 180
gaatctgtcg cacagatgac catgtgataa aaggaacaat ggtgtccaag tttccagtga 240
ttgtgggaca tgaggcaact gggattgtag agagcattgg agaaggagtg actacagtga 300
aaccaggtga caaagtcatc cctctctttc tgccacaatg tagagaatgc aatgcttgtc 360
gcaacccaga tggcaacctt tgcattagga gcgatattac tggtcgtgga gtactggctg 420
atggcaccac cagatttaca tgcaagggcg aaccagtcca ccacttcatg aacaccagta 480
catttaccga gtacacagt 499

<210> 51
<211> 887
<212> DNA
<213> Homo sapien

<400> 51
gagtctgagc agaaaggaaa agcagccttg gcagccacgt tagaggaata caaagccaca 60
gtggccagtg accagataga gatgaatcgc ctgaaggctc agctggagaa tgaaaagcag 120
aaagtggcag agctgtattc tatccataac tctggagaca aatctgatat tcaggacctc 180
ctggagagtg tcaggctgga caaagaaaaa gcagagactt tggctagtag cttgcaggaa 240
gatctggctc atacccgaaa tgatgccaat cgattacagg atgccattgc taaggtagag 300
gatgaatacc gagccttcca agaagaagct aagaaacaaa ttgaagattt gaatatgacg 360
ttagaaaaat taagatcaga cctggatgaa aaagaaacag aaaggagtga catgaaagaa 420
accatctttg aacttgaaga tgaagtagaa caacatcgtg ctgtgaaact tcatgacaac 480
ctcattattt ctgatctaga gaatacagtt aaaaaactcc aggaccaaaa gcacgacatg 540
gaaagagaaa taaagacact ccacagaaga cttcgggaag aatctgcgga atggcggcag 600
tttcaggctg atctccagac tgcagtagtc attgcaaatg acattaaatc tgaagcccaa 660
gaggagattg gtgatctaaa gcgccggtta catgaggctc aagaaaaaaa tgagaaactc 720
acaaaagaat tggaggaaat aaagtcacgc aagcaagagg aggagcgagg cgggtataca 780
attacatgaa tgccgttgag agagatttgg cagccttaag gcagggaatg ggactgagta 840
gaaggtcctc gacttcctca gagccaactc ctacagtaaa aaccctc 887

<210> 52
<211> 491
<212> DNA
<213> Homo sapien

<400> 52
ggcacgagct tttccaaaaa tcatgctgct cctttctcta aagttcttac attttataga 60
aaggaacctt tcactcttga ggcctactac agctctcctc aggatttgcc ctatccagat 120
cctgctatag ctcagttttc agttcagaaa gtcactcctc agtctgatgg ctccagttca 180
aaagtgaaag tcaaagttcg agtaaatgtc catggcattt tcagtgtgtc cagtgcatct 240
ttagtggagg ttcacaagtc tgaggaaaat gaggagccaa tggaaacaga tcagaatgca 300
aaggaggaag agaagatgca agtggaccag gaggaaccac atgttgaaga gcaacagcag 360
cagacaccag gcagaaaata aggcagagtc tgaagaaatg gagacctctc aagctggatc 420
caaggataaa aagatggacc aaccacccca agccaagaag gcaaaagtga agaccagtac 480
tgtggacctg g 491

<210> 53
<211> 787
<212> DNA
<213> *Homo sapien*

<400> 53
aagcagttga gtaggcagaa aaaagaacct cttcattaag gattaaaatg tataggccag 60
cacgtgtaac ttcgacttca agatttctga atccatatgt agtatgtttc attgtcgtcg 120
caggggtagt gatcctggca gtcaccatag ctctacttgt ttacttttta gcttttgatc 180
aaaaatctta cttttatagg agcagttttc aactcctaaa tgttgaatat aatagtcagt 240
taaattcacc agctacacag gaatacagga ctttgagtgg aagaattgaa tctctgatta 300
ctaaaacatt caaagaatca aatttaagaa atcagttcat cagagctcat gttgccaaac 360
tgaggcaaga tggtagtggt gtgagagcgg atgttgtcat gaaatttcaa ttcactagaa 420
ataacaatgg agcatcaatg aaaagcagaa ttgagtctgt tttacgacaa atgctgaata 480
actctggaaa cctggaaata aacccttcaa ctgagataac atcacttact gaccaggctg 540
cagcaaattg gcttattaat gaatgtgggg ccggtccaga cctaataaca ttgtctgagc 600
agagaatcct tggaggcact gaggctgagg agggaagctg gccgtggcaa gtcagtctgc 660
ggctcaataa tgcccaccac tgtggaggca gcctgatcaa taacatgtgg atcctgacag 720
cagctcactg cttcagaagc aactctaatc ctcgtgactg gattgccacg tctggtattt 780
ccacaac 787

<210> 54
<211> 386
<212> DNA
<213> Homo sapien

<400> 54
ggcattttca gtgtgtccag tgcatcttta gtggaggttc acaagtctga ggaaaatgag 60
gagccaatgg aaacagatca gaatgcaaag gaggaagaga agatgcaagt ggaccaggag 120
gaaccacatg ttgaagagca acagcagcag acaccagcag aaaataaggc agagtctgaa 180
gaaatggaga cctctcaagc tggatccaag gataaaaaga tggaccaacc accccaagcc 240
aagaaggcaa aagtgaagac cagtactgtg gacctgccaa tcgagaatca gctattatgg 300
cagatagaca gagagatgct caacttgtac attgaaaatg agggtaagat gatcatgcag 360
gataaactgg agaaggagcg gaatga 386

<210> 55
<211> 1462
<212> DNA
<213> Homo sapien

<400> 55
aagcagttga gtaggcagaa aaaagaacct cttcattaag gattaaaatg tataggccag 60
cacgtgtaac ttcgacttca agatttctga atccatatgt agtatgtttc attgtcgtcg 120
caggggtagt gatcctggca gtcaccatag ctctacttgt ttacttttta gcttttgatc 180
aaaaatctta cttttatagg agcagttttc aactcctaaa tgttgaatat aatagtcagt 240
taaattcacc agctacacag gaatacagga ctttgagtgg aagaattgaa tctctgatta 300
ctaaaacatt caaagaatca aatttaagaa atcagttcat cagagctcat gttgccaaac 360
tgaggcaaga tggtagtggt gtgagagcgg atgttgtcat gaaatttcaa ttcactagaa 420
ataacaatgg agcatcaatg aaaagcagaa ttgagtctgt tttacgacaa atgctgaata 480
actctggaaa cctggaaata aacccttcaa ctgagataac atcacttact gaccaggctg 540
cagcaaattg gcttattaat gaatgtgggg ccggtccaga cctaataaca ttgtctgagc 600
agagaatcct tggaggcact gaggctgagg agggaagctg gccgtggcaa gtcagtctgc 660
ggctcaataa tgcccaccac tgtggaggca gcctgatcaa taacatgtgg atcctgacag 720
cagctcactg cttcagaagc aactctaatc ctcgtgactg gattgccacg tctggtattt 780
ccacaacatt tcctaaacta agaatgagag taagaaatat tttaattcat aacaattata 840
aatctgcaac tcatgaaaat gacattgcac ttgtgagact tgagaacagt gtcaccttta 900
ccaaagatat ccatagtgtg tgtctcccag ctgctaccca gaatattcca cctggctcta 960

```
ctgcttatgt aacaggatgg ggcgctcaag aatatgctgg ccacacagtt ccagagctaa    1020
ggcaaggaca ggtcagaata ataagtaatg atgtatgtaa tgcaccacat agttataatg    1080
gagccatctt gtctggaatg ctgtgtgctg gagtacctca aggtggagtg gacgcatgtc    1140
agggtgactc tggtggccca ctagtacaag aagactcacg gcggctttgg tttattgtgg    1200
ggatagtaag ctggggagat cagtgtggcc tgccggataa gccaggagtg tatactcgag    1260
tgacagcata cattgactgg attaggcaac aaactgggat ctagtgcaac aagtgcatcc    1320
ctgttgcaaa gtctgtatgc aggtgtgcct gtcttaaatt ccaaagcttt acatttcaac    1380
tgaaaaagaa actagaaatg tcctaattta acatcttgtt acataaatat ggtttaacaa    1440
aaaaaaaaaa aaaaaactcg ag                                             1462
```

```
      <210> 56
      <211> 159
      <212> PRT
      <213> Homo sapien

      <400> 56
Thr Met Tyr Arg Ala Leu Arg Leu Leu Ala Arg Ser Arg Pro Leu Val
 1               5                  10                  15
Arg Ala Pro Ala Ala Ala Leu Ala Ser Ala Pro Gly Leu Gly Gly Ala
            20                  25                  30
Ala Val Pro Ser Phe Trp Pro Pro Asn Ala Ala Arg Met Ala Ser Gln
        35                  40                  45
Asn Ser Phe Arg Ile Glu Tyr Asp Thr Phe Gly Glu Leu Lys Val Pro
    50                  55                  60
Asn Asp Lys Tyr Tyr Gly Ala Gln Thr Val Arg Ser Thr Met Asn Phe
65                  70                  75                  80
Lys Ile Gly Gly Val Thr Glu Arg Met Pro Thr Pro Val Ile Lys Ala
                85                  90                  95
Phe Gly Ile Leu Lys Arg Ala Ala Ala Glu Val Asn Gln Asp Tyr Gly
            100                 105                 110
Leu Asp Pro Lys Ile Ala Asn Ala Ile Met Lys Ala Ala Asp Glu Val
        115                 120                 125
Ala Glu Gly Lys Leu Asn Asp His Phe Pro Leu Val Val Trp Gln Thr
    130                 135                 140
Gly Ser Gly Thr Gln Thr Asn Met Asn Val Asn Glu Val Ile Ser
145                 150                 155

      <210> 57
      <211> 165
      <212> PRT
      <213> Homo sapien

      <400> 57
Lys Lys Ser Met Phe Ala Glu Ile Gln Ile Gln Asp Lys Asp Arg Met
 1               5                  10                  15
Gly Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp Glu
            20                  25                  30
Gln Lys Gln Pro Phe Ser Ile Glu Glu Ile Glu Val Ala Pro Pro Lys
        35                  40                  45
Thr Lys Glu Val Arg Ile Lys Ile Leu Ala Thr Gly Ile Cys Arg Thr
    50                  55                  60
Asp Asp His Val Ile Lys Gly Thr Met Val Ser Lys Phe Pro Val Ile
65                  70                  75                  80
Val Gly His Glu Ala Thr Gly Ile Val Glu Ser Ile Gly Glu Gly Val
                85                  90                  95
Thr Thr Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Leu Pro Gln
            100                 105                 110
Cys Arg Glu Cys Asn Ala Cys Arg Asn Pro Asp Gly Asn Leu Cys Ile
```

```
        115                 120                 125
Arg Ser Asp Ile Thr Gly Arg Gly Val Leu Ala Asp Gly Thr Thr Arg
    130                 135                 140
Phe Thr Cys Lys Gly Glu Pro Val His His Phe Met Asn Thr Ser Thr
145                 150                 155                 160
Phe Thr Glu Tyr Thr
                165
```

<210> 58
<211> 259
<212> PRT
<213> Homo sapien

<400> 58

```
Glu Ser Glu Gln Lys Gly Lys Ala Ala Leu Ala Ala Thr Leu Glu Glu
 1               5                  10                  15
Tyr Lys Ala Thr Val Ala Ser Asp Gln Ile Glu Met Asn Arg Leu Lys
            20                  25                  30
Ala Gln Leu Glu Asn Glu Lys Gln Lys Val Ala Glu Leu Tyr Ser Ile
        35                  40                  45
His Asn Ser Gly Asp Lys Ser Asp Ile Gln Asp Leu Leu Glu Ser Val
    50                  55                  60
Arg Leu Asp Lys Glu Lys Ala Glu Thr Leu Ala Ser Ser Leu Gln Glu
65                  70                  75                  80
Asp Leu Ala His Thr Arg Asn Asp Ala Asn Arg Leu Gln Asp Ala Ile
                85                  90                  95
Ala Lys Val Glu Asp Glu Tyr Arg Ala Phe Gln Glu Glu Ala Lys Lys
            100                 105                 110
Gln Ile Glu Asp Leu Asn Met Thr Leu Glu Lys Leu Arg Ser Asp Leu
        115                 120                 125
Asp Glu Lys Glu Thr Glu Arg Ser Asp Met Lys Glu Thr Ile Phe Glu
    130                 135                 140
Leu Glu Asp Glu Val Glu Gln His Arg Ala Val Lys Leu His Asp Asn
145                 150                 155                 160
Leu Ile Ile Ser Asp Leu Glu Asn Thr Val Lys Lys Leu Gln Asp Gln
                165                 170                 175
Lys His Asp Met Glu Arg Glu Ile Lys Thr Leu His Arg Arg Leu Arg
            180                 185                 190
Glu Glu Ser Ala Glu Trp Arg Gln Phe Gln Ala Asp Leu Gln Thr Ala
        195                 200                 205
Val Val Ile Ala Asn Asp Ile Lys Ser Glu Ala Gln Glu Glu Ile Gly
    210                 215                 220
Asp Leu Lys Arg Arg Leu His Glu Ala Gln Glu Lys Asn Glu Lys Leu
225                 230                 235                 240
Thr Lys Glu Leu Glu Glu Ile Lys Ser Arg Lys Gln Glu Glu Glu Arg
                245                 250                 255
Gly Gly Tyr
```

<210> 59
<211> 125
<212> PRT
<213> Homo sapien

<400> 59

```
Gly Thr Ser Phe Ser Lys Asn His Ala Ala Pro Phe Ser Lys Val Leu
 1               5                  10                  15
Thr Phe Tyr Arg Lys Glu Pro Phe Thr Leu Glu Ala Tyr Tyr Ser Ser
```

```
                20                  25                  30
Pro Gln Asp Leu Pro Tyr Pro Asp Pro Ala Ile Ala Gln Phe Ser Val
        35                  40                  45
Gln Lys Val Thr Pro Gln Ser Asp Gly Ser Ser Ser Lys Val Lys Val
    50                  55                  60
Lys Val Arg Val Asn Val His Gly Ile Phe Ser Val Ser Ser Ala Ser
65                  70                  75                  80
Leu Val Glu Val His Lys Ser Glu Glu Asn Glu Glu Pro Met Glu Thr
                85                  90                  95
Asp Gln Asn Ala Lys Glu Glu Glu Lys Met Gln Val Asp Gln Glu Glu
            100                 105                 110
Pro His Val Glu Glu Gln Gln Gln Gln Thr Pro Gly Arg
        115                 120                 125

      <210> 60
      <211> 246
      <212> PRT
      <213> Homo sapien

      <400> 60
Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro
 1               5                  10                  15
Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val
            20                  25                  30
Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr
        35                  40                  45
Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln
    50                  55                  60
Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile
65                  70                  75                  80
Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln
                85                  90                  95
Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val
            100                 105                 110
Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly
        115                 120                 125
Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn
    130                 135                 140
Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu
145                 150                 155                 160
Thr Asp Gln Ala Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly
                165                 170                 175
Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu
            180                 185                 190
Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn
        195                 200                 205
Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr
    210                 215                 220
Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala
225                 230                 235                 240
Thr Ser Gly Ile Ser Thr
                245

      <210> 61
      <211> 128
      <212> PRT
      <213> Homo sapien
```

<400> 61
Gly Ile Phe Ser Val Ser Ser Ala Ser Leu Val Glu Val His Lys Ser
1 5 10 15
Glu Glu Asn Glu Glu Pro Met Glu Thr Asp Gln Asn Ala Lys Glu Glu
20 25 30
Glu Lys Met Gln Val Asp Gln Glu Glu Pro His Val Glu Glu Gln Gln
35 40 45
Gln Gln Thr Pro Ala Glu Asn Lys Ala Glu Ser Glu Glu Met Glu Thr
50 55 60
Ser Gln Ala Gly Ser Lys Asp Lys Lys Met Asp Gln Pro Pro Gln Ala
65 70 75 80
Lys Lys Ala Lys Val Lys Thr Ser Thr Val Asp Leu Pro Ile Glu Asn
85 90 95
Gln Leu Leu Trp Gln Ile Asp Arg Glu Met Leu Asn Leu Tyr Ile Glu
100 105 110
Asn Glu Gly Lys Met Ile Met Gln Asp Lys Leu Glu Lys Glu Arg Asn
115 120 125

<210> 62
<211> 418
<212> PRT
<213> Homo sapien

<400> 62
Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro
1 5 10 15
Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val
20 25 30
Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr
35 40 45
Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln
50 55 60
Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile
65 70 75 80
Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln
85 90 95
Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val
100 105 110
Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly
115 120 125
Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn
130 135 140
Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu
145 150 155 160
Thr Asp Gln Ala Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly
165 170 175
Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu
180 185 190
Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn
195 200 205
Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr
210 215 220
Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala
225 230 235 240
Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg
245 250 255
Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp
260 265 270

```
Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile
        275                 280                 285
His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser
    290                 295                 300
Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr
305                 310                 315                 320
Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val
                325                 330                 335
Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu
            340                 345                 350
Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser
        355                 360                 365
Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val
    370                 375                 380
Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly
385                 390                 395                 400
Val Tyr Thr Arg Val Thr Ala Tyr Ile Asp Trp Ile Arg Gln Gln Thr
                405                 410                 415
Gly Ile
```

```
<210> 63
<211> 776
<212> DNA
<213> Homo sapien

<400> 63
cacagatggt gatagaggaa tccatcttgc agtcagataa agccctcact gatagagaga      60
aggcagtagc agtggatcgg gccaagaagg aggcagctga gaaggaacag gaacttttaa     120
aacagaaatt acaggagcag ccagcaacag atggaggctc aagataagag tcgcaaggaa     180
aactagccaa ctgaaggaga agctgcagat ggagagagaa cacctactga gagagcagat     240
tatgatgttg gagcacacgc agaaggtcca aaatgattgg cttcatgaag gatttaagaa     300
gaagtatgag gagatgaatg cagagataag tcaatttaaa cgtatgattg atactacaaa     360
aaatgatgat actccctgga ttgcacgaac cttggacaac cttgccgatg agctaactgc     420
aatattgtct gctcctgcta aattaattgg tcatggtgtc aaaggtgtga gctcactctt     480
taaaaagcat aagctcccct tttaaggata ttatagattg tacatatatg ctttggacta     540
tttttgatct gtatgttttt cattttcatt cagcaagttt tttttttttt tcagagtctt     600
actctgttgc ccaggctgga gtacagtggt gcaatctcag ctcactgcaa cctctgcctc     660
ctgggttcaa gagattcacc tgcctcagcc ccctagtagc tgggattata ggtgtacacc     720
accacaccca gctaattttt gtatttttag tagagatggg gtttcactat gttggc         776

<210> 64
<211> 160
<212> DNA
<213> Homo sapien

<400> 64
gcagcgctct cggttgcagt acccactgga aggacttagg cgctcgcgtg gacaccgcaa      60
gcccctcagt agcctcggcc caagaggcct gctttccact cgctagcccc gccgggggtc     120
cgtgtcctgt ctcggtggcc ggacccgggc ccgagcccga                           160

<210> 65
<211> 72
<212> PRT
<213> Homo sapien

<400> 65
Leu Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser Ser Ile
```

```
 1               5                   10                  15
Ala Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val
            20                  25                  30
Ala Ser Gly Ser Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Thr Gly
        35                  40                  45
Leu Ser Gly Leu Thr Lys Phe Ile Leu Gly Ser Ile Gly Ser Ala Ile
    50                  55                  60
Ala Ala Val Ile Ala Arg Phe Tyr
65                  70
```

```
      <210> 66
      <211> 2581
      <212> DNA
      <213> Homo sapien

      <400> 66
ctttcaaccc gcgctcgccg gctccagccc cgcgcgcccc caccccttgc cctcccggcg      60
gctccgcagg gtgaggtggc tttgaccccg ggttgcccgg ccagcacgac cgaggaggtg     120
gctggacagc tggaggatga acggagaagc cgactgcccc acagacctgg aaatggccgc     180
ccccaaaggc caagaccgtt ggtcccagga agacatgctg actttgctgg aatgcatgaa     240
gaacaacctt ccatccaatg acagctccaa gttcaaaacc accgaatcac acatggactg     300
ggaaaaagta gcatttaaag acttttctgg agacatgtgc aagctcaaat gggtggagat     360
ttctaatgag gtgaggaagt tccgtacatt gacagaattg atcctcgatg ctcaggaaca     420
tgttaaaaat ccttacaaag gcaaaaaact caagaaacac ccagacttcc caaagaagcc     480
cctgacccct tatttccgct tcttcatgga gaagcgggcc aagtatgcga aactccaccc     540
tgagatgagc aacctggacc taaccaagat tctgtccaag aaatacaagg agcttccgga     600
gaagaagaag atgaaatata ttcaggactt ccagagagag aaacaggagt tcgagcgaaa     660
cctggcccga ttcagggagg atcaccccga cctaatccag aatgccaaga aatcggacat     720
cccagagaag cccaaaaccc cccagcagct gtggtacacc cacgagaaga aggtgtatct     780
caaagtgcgg ccagatgcca ctacgaagga ggtgaaggac tccctgggga agcagtggtc     840
tcagctctcg gacaaaaaga ggctgaaatg gattcataag gccctggagc agcggaagga     900
gtacgaggag atcatgagag actatatcca gaagcaccca gagctgaaca tcagtgagga     960
gggtatcacc aagtccaccc tcaccaaggc cgaacgccag ctcaaggaca agtttgacgg    1020
gcgacccacc aagccacctc cgaacagcta ctcgctgtac tgcgcagagc tcatggccaa    1080
catgaaggac gtgcccagca cagagcgcat ggtgctgtgc agccagcagt ggaagctgct    1140
gtcccagaag gagaaggacg cctatcacaa gaagtgtgat cagaaaaaga aagattacga    1200
ggtggagctg ctccgtttcc tcgagagcct gcctgaggag gagcagcagc gggtcttggg    1260
ggaagagaag atgctgaaca tcaacaagaa gcaggccacc agccccgcct ccaagaagcc    1320
agcccaggaa gggggcaagg gcggctccga gaagcccaag cggcccgtgt cggccatgtt    1380
catcttctcg gaggagaaac ggcggcagct gcaggaggag cggcctgagc tctccgagag    1440
cgagctgacc cgcctgctgg cccgaatgtg gaacgacctg tctgagaaga agaaggccaa    1500
gtacaaggcc cgagaggcgg cgctcaaggc tcagtcggag aggaagcccg gcggggagcg    1560
cgaggaacgg ggcaagctgc ccgagtcccc caaaagagct gaggagatct ggcaacagag    1620
cgttatcggc gactacctgg cccgcttcaa gaatgaccgg gtgaaggcct tgaaagccat    1680
ggaaatgacc tggaataaca tggaaaagaa ggagaaactg atgtggatta agaaggcagc    1740
cgaagaccaa aagcgatatg agagagagct gagtgagatg cgggcacctc cagctgctac    1800
aaattcttcc aagaagatga aattccaggg agaacccaag aagcctccca tgaacggtta    1860
ccagaagttc tcccaggagc tgctgtccaa tggggagctg aaccacctgc cgctgaagga    1920
gcgcatggtg gagatcggca gtcgctggca gcgcatctcc cagagccaga aggagcacta    1980
caaaaagctg gccgaggagc agcaaaagca gtacaaggtg cacctggacc tctgggttaa    2040
gagcctgtct ccccaggacc gtgcagcata taaagagtac atctccaata aacgtaagag    2100
catgaccaag ctgcgaggcc caaaccccaa atccagccgg actactctgc agtccaagtc    2160
ggagtccgag gaggatgatg aagaggatga ggatgacgag gacgaggatg aagaagagga    2220
agatgatgag aatggggact cctctgaaga tggcggcgac tcctctgagt ccagcagcga    2280
ggacgagagc gaggatgggg atgagaatga agaggatgac gaggacgaag acgacgacga    2340
ggatgacgat gaggatgaag ataatgagtc cgagggcagc agctccagct cctcctcctt    2400
aggggactcc tcagactttg actccaactg aggcttagcc ccaccccagg ggagccaggg    2460
agagcccagg agctcccctc cccaactgac cacctttgtt tcttccccat gttctgtccc    2520
```

ttgcccccct ggcctccccc actttctttc tttctttaaa aaaaaaaaaa aaaaactcga 2580
g 2581

<210> 67
<211> 764
<212> PRT
<213> Homo sapien

<400> 67
Met Asn Gly Glu Ala Asp Cys Pro Thr Asp Leu Glu Met Ala Ala Pro
1 5 10 15
Lys Gly Gln Asp Arg Trp Ser Gln Glu Asp Met Leu Thr Leu Leu Glu
20 25 30
Cys Met Lys Asn Asn Leu Pro Ser Asn Asp Ser Ser Lys Phe Lys Thr
35 40 45
Thr Glu Ser His Met Asp Trp Glu Lys Val Ala Phe Lys Asp Phe Ser
50 55 60
Gly Asp Met Cys Lys Leu Lys Trp Val Glu Ile Ser Asn Glu Val Arg
65 70 75 80
Lys Phe Arg Thr Leu Thr Glu Leu Ile Leu Asp Ala Gln Glu His Val
85 90 95
Lys Asn Pro Tyr Lys Gly Lys Lys Leu Lys Lys His Pro Asp Phe Pro
100 105 110
Lys Lys Pro Leu Thr Pro Tyr Phe Arg Phe Phe Met Glu Lys Arg Ala
115 120 125
Lys Tyr Ala Lys Leu His Pro Glu Met Ser Asn Leu Asp Leu Thr Lys
130 135 140
Ile Leu Ser Lys Lys Tyr Lys Glu Leu Pro Glu Lys Lys Lys Met Lys
145 150 155 160
Tyr Ile Gln Asp Phe Gln Arg Glu Lys Gln Glu Phe Glu Arg Asn Leu
165 170 175
Ala Arg Phe Arg Glu Asp His Pro Asp Leu Ile Gln Asn Ala Lys Lys
180 185 190
Ser Asp Ile Pro Glu Lys Pro Lys Thr Pro Gln Gln Leu Trp Tyr Thr
195 200 205
His Glu Lys Lys Val Tyr Leu Lys Val Arg Pro Asp Ala Thr Thr Lys
210 215 220
Glu Val Lys Asp Ser Leu Gly Lys Gln Trp Ser Gln Leu Ser Asp Lys
225 230 235 240
Lys Arg Leu Lys Trp Ile His Lys Ala Leu Glu Gln Arg Lys Glu Tyr
245 250 255
Glu Glu Ile Met Arg Asp Tyr Ile Gln Lys His Pro Glu Leu Asn Ile
260 265 270
Ser Glu Glu Gly Ile Thr Lys Ser Thr Leu Thr Lys Ala Glu Arg Gln
275 280 285
Leu Lys Asp Lys Phe Asp Gly Arg Pro Thr Lys Pro Pro Pro Asn Ser
290 295 300
Tyr Ser Leu Tyr Cys Ala Glu Leu Met Ala Asn Met Lys Asp Val Pro
305 310 315 320
Ser Thr Glu Arg Met Val Leu Cys Ser Gln Gln Trp Lys Leu Leu Ser
325 330 335
Gln Lys Glu Lys Asp Ala Tyr His Lys Lys Cys Asp Gln Lys Lys Lys
340 345 350
Asp Tyr Glu Val Glu Leu Leu Arg Phe Leu Glu Ser Leu Pro Glu Glu
355 360 365
Glu Gln Gln Arg Val Leu Gly Glu Glu Lys Met Leu Asn Ile Asn Lys
370 375 380
Lys Gln Ala Thr Ser Pro Ala Ser Lys Lys Pro Ala Gln Glu Gly Gly

```
385                 390                 395                 400
Lys Gly Gly Ser Glu Lys Pro Lys Arg Pro Val Ser Ala Met Phe Ile
                405                 410                 415
Phe Ser Glu Glu Lys Arg Arg Gln Leu Gln Glu Glu Arg Pro Glu Leu
            420                 425                 430
Ser Glu Ser Glu Leu Thr Arg Leu Leu Ala Arg Met Trp Asn Asp Leu
        435                 440                 445
Ser Glu Lys Lys Lys Ala Lys Tyr Lys Ala Arg Glu Ala Ala Leu Lys
    450                 455                 460
Ala Gln Ser Glu Arg Lys Pro Gly Gly Glu Arg Glu Glu Arg Gly Lys
465                 470                 475                 480
Leu Pro Glu Ser Pro Lys Arg Ala Glu Glu Ile Trp Gln Gln Ser Val
                485                 490                 495
Ile Gly Asp Tyr Leu Ala Arg Phe Lys Asn Asp Arg Val Lys Ala Leu
            500                 505                 510
Lys Ala Met Glu Met Thr Trp Asn Asn Met Glu Lys Lys Glu Lys Leu
        515                 520                 525
Met Trp Ile Lys Lys Ala Ala Glu Asp Gln Lys Arg Tyr Glu Arg Glu
    530                 535                 540
Leu Ser Glu Met Arg Ala Pro Pro Ala Ala Thr Asn Ser Ser Lys Lys
545                 550                 555                 560
Met Lys Phe Gln Gly Glu Pro Lys Lys Pro Pro Met Asn Gly Tyr Gln
                565                 570                 575
Lys Phe Ser Gln Glu Leu Leu Ser Asn Gly Glu Leu Asn His Leu Pro
            580                 585                 590
Leu Lys Glu Arg Met Val Glu Ile Gly Ser Arg Trp Gln Arg Ile Ser
        595                 600                 605
Gln Ser Gln Lys Glu His Tyr Lys Lys Leu Ala Glu Glu Gln Gln Lys
    610                 615                 620
Gln Tyr Lys Val His Leu Asp Leu Trp Val Lys Ser Leu Ser Pro Gln
625                 630                 635                 640
Asp Arg Ala Ala Tyr Lys Glu Tyr Ile Ser Asn Lys Arg Lys Ser Met
                645                 650                 655
Thr Lys Leu Arg Gly Pro Asn Pro Lys Ser Ser Arg Thr Thr Leu Gln
            660                 665                 670
Ser Lys Ser Glu Ser Glu Glu Asp Asp Glu Glu Asp Glu Asp Asp Glu
        675                 680                 685
Asp Glu Asp Glu Glu Glu Glu Asp Asp Glu Asn Gly Asp Ser Ser Glu
    690                 695                 700
Asp Gly Gly Asp Ser Ser Glu Ser Ser Ser Glu Asp Glu Ser Glu Asp
705                 710                 715                 720
Gly Asp Glu Asn Glu Glu Asp Asp Glu Asp Glu Asp Asp Asp Glu Asp
                725                 730                 735
Asp Asp Glu Asp Glu Asp Asn Glu Ser Glu Gly Ser Ser Ser Ser Ser
            740                 745                 750
Ser Ser Leu Gly Asp Ser Ser Asp Phe Asp Ser Asn
        755                 760

      <210> 68
      <211> 434
      <212> DNA
      <213> Homo sapien

      <400> 68
ctaagatgct ggatgctgaa gacatcgtcg gaactgcccg gccagatgag aaagccatta      60
tgacttatgt gtctagcttc tatcatgcct tctctggagc ccagaaggca gaaacagcag     120
ccaatcgcat ctgcaaagtg ttggcggtca atcaagagaa cgagcagctt atggaagact     180
atgagaagct ggccagtgat ctgttggagt ggatccgccg caccatccca tggctggaga     240
```

atcgggtgcc tgagaacacc atgcatgcca tgcagcagaa gctggaggac ttccgagact 300
atagacgcct gcacaagccg cccaaggtgc aggagaagtg ccagctggag atcaacttta 360
acacgctgca gaccaaactg cggctcagca accggcctgc cttcatgccc tccgagggca 420
ggatggtctc ggat 434

<210> 69
<211> 244
<212> DNA
<213> Homo sapien

<400> 69
aggcagcatg ctcgttgaga gtcatcacca ctccctaatc tcaagtacgc agggacacaa 60
acactgcgga aggccgcagg gtcctctgcc taggaaaacc agagaccttt gttcacttgt 120
ttatgtgctg accttccctc cactattgtc ctgtgaccct gccaaatccc cctttgtgag 180
aaacacccaa gaatgatcaa taaaaaataa attaatttag gaaaaaaaaa aaaaaaaact 240
cgag 244

<210> 70
<211> 437
<212> DNA
<213> Homo sapien

<400> 70
ctgggacggg agcgtccagc gggactcgaa ccccagatgt gaaggcgttt ctggaaagtc 60
cttggtccct ggatccagcg tcggccagcc cagagcccgt gccgcacatc cttgcgtcct 120
ccaggcagtg ggaccccgcg agctgcacgt ccctgggcac ggacaagtgt gaggcactgt 180
tggggctgtg ccaggtgcgg ggtgggctgc cccctttctc agaaccttcc agcctggtgc 240
cgtggccccc aggccggagt cttcctaagg ctgtgaggcc accccctgtcc tggcctccgt 300
tctcgcagca gcagaccttg cccgtgatga gcggggaggc ccttggctgg ctgggccagg 360
ctggttccct ggccatgggg gctgcacctc tgggggagcc agccaaggag gaccccatgc 420
tggcgcagga agccggg 437

<210> 71
<211> 271
<212> DNA
<213> Homo sapien

<400> 71
gcgcagagtt ctgtcgtcca ccatcgagtg aggaagagag cattggttcc cctgagatag 60
aagagatggc tctcttcagt gcccagtctc catacattaa cccgatcatc ccctttactg 120
gaccaatcca aggagggctg caggagggac ttcaggtgac cctccagggg actaccgaga 180
gttttgcaca aaagtttgtg gtgaactttt cagaacagct tcaatggaga tgacttggcc 240
ttccacttca accccggtta tgaggaagga g 271

<210> 72
<211> 290
<212> DNA
<213> Homo sapien

<400> 72
ccgagcccta cccggaggtc tccagaatcc ccaccgtcag ggatgcaac ggctccctgt 60
ctggtgccct ctcctgctgc gaggactcgg cccagggctc gggcccgccc aaggccccta 120
cggtggccga gggtcccagc tcctgccttc ggcggaacgt gatcagcgag agggagcgca 180
ggaagcggat gtcgttgagc tgtgagcgtc tgcgggccct gctgccccag ttcgatggcc 240
ggcgggagga catggcctcg gtcctggaga tgtctgttgc aattcctgcg 290

<210> 73
<211> 144

<212> PRT
<213> Homo sapien

<400> 73
Lys Met Leu Asp Ala Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu
1 5 10 15
Lys Ala Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly
20 25 30
Ala Gln Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala
35 40 45
Val Asn Gln Glu Asn Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala
50 55 60
Ser Asp Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn
65 70 75 80
Arg Val Pro Glu Asn Thr Met His Ala Met Gln Gln Lys Leu Glu Asp
85 90 95
Phe Arg Asp Tyr Arg Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys
100 105 110
Cys Gln Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu
115 120 125
Ser Asn Arg Pro Ala Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp
130 135 140

<210> 74
<211> 64
<212> PRT
<213> Homo sapien

<400> 74
Gly Ser Met Leu Val Glu Ser His His His Ser Leu Ile Ser Ser Thr
1 5 10 15
Gln Gly His Lys His Cys Gly Arg Pro Gln Gly Pro Leu Pro Arg Lys
20 25 30
Thr Arg Asp Leu Cys Ser Leu Val Tyr Val Leu Thr Phe Pro Pro Leu
35 40 45
Leu Ser Cys Asp Pro Ala Lys Ser Pro Phe Val Arg Asn Thr Gln Glu
50 55 60

<210> 75
<211> 145
<212> PRT
<213> Homo sapien

<400> 75
Gly Thr Gly Ala Ser Ser Gly Thr Arg Thr Pro Asp Val Lys Ala Phe
1 5 10 15
Leu Glu Ser Pro Trp Ser Leu Asp Pro Ala Ser Ala Ser Pro Glu Pro
20 25 30
Val Pro His Ile Leu Ala Ser Ser Arg Gln Trp Asp Pro Ala Ser Cys
35 40 45
Thr Ser Leu Gly Thr Asp Lys Cys Glu Ala Leu Leu Gly Leu Cys Gln
50 55 60
Val Arg Gly Gly Leu Pro Pro Phe Ser Glu Pro Ser Ser Leu Val Pro
65 70 75 80
Trp Pro Pro Gly Arg Ser Leu Pro Lys Ala Val Arg Pro Pro Leu Ser
85 90 95
Trp Pro Pro Phe Ser Gln Gln Gln Thr Leu Pro Val Met Ser Gly Glu
100 105 110

```
Ala Leu Gly Trp Leu Gly Gln Ala Gly Ser Leu Ala Met Gly Ala Ala
        115                 120                 125
Pro Leu Gly Glu Pro Ala Lys Glu Asp Pro Met Leu Ala Gln Glu Ala
    130                 135                 140
Gly
145

      &lt;210&gt; 76
      &lt;211&gt; 69
      &lt;212&gt; PRT
      &lt;213&gt; Homo sapien

      &lt;400&gt; 76
Ala Glu Phe Cys Arg Pro Pro Ser Ser Glu Glu Glu Ser Ile Gly Ser
 1               5                  10                  15
Pro Glu Ile Glu Glu Met Ala Leu Phe Ser Ala Gln Ser Pro Tyr Ile
            20                  25                  30
Asn Pro Ile Ile Pro Phe Thr Gly Pro Ile Gln Gly Gly Leu Gln Glu
        35                  40                  45
Gly Leu Gln Val Thr Leu Gln Gly Thr Thr Glu Ser Phe Ala Gln Lys
    50                  55                  60
Phe Val Val Asn Phe
65

      &lt;210&gt; 77
      &lt;211&gt; 96
      &lt;212&gt; PRT
      &lt;213&gt; Homo sapien

      &lt;400&gt; 77
Glu Pro Tyr Pro Glu Val Ser Arg Ile Pro Thr Val Arg Gly Cys Asn
 1               5                  10                  15
Gly Ser Leu Ser Gly Ala Leu Ser Cys Cys Glu Asp Ser Ala Gln Gly
            20                  25                  30
Ser Gly Pro Pro Lys Ala Pro Thr Val Ala Glu Gly Pro Ser Ser Cys
        35                  40                  45
Leu Arg Arg Asn Val Ile Ser Glu Arg Glu Arg Arg Lys Arg Met Ser
    50                  55                  60
Leu Ser Cys Glu Arg Leu Arg Ala Leu Leu Pro Gln Phe Asp Gly Arg
65                  70                  75                  80
Arg Glu Asp Met Ala Ser Val Leu Glu Met Ser Val Ala Ile Pro Ala
                85                  90                  95

      &lt;210&gt; 78
      &lt;211&gt; 2076
      &lt;212&gt; DNA
      &lt;213&gt; Homo sapien

      &lt;400&gt; 78
agaaaaagtc tatgtttgca gaaatacaga tccaagacaa agacaggatg ggcactgctg      60
gaaaagttat taaatgcaaa gcagctgtgc tttgggagca gaagcaaccc ttctccattg     120
aggaaataga agttgcccca ccaaagacta aagaagttcg cattaagatt ttggccacag     180
gaatctgtcg cacagatgac catgtgataa aaggaacaat ggtgtccaag tttccagtga     240
ttgtgggaca tgaggcaact gggattgtag agagcattgg agaaggagtg actacagtga     300
aaccaggtga caaagtcatc cctctctttc tgccacaatg tagagaatgc aatgcttgtc     360
gcaacccaga tggcaacctt tgcattagga gcgatattac tggtcgtgga gtactggctg     420
atggcaccac cagatttaca tgcaagggca aaccagtcca ccacttcatg aacaccagta     480
catttaccga gtacacagtg gtggatgaat cttctgttgc taagattgat gatgcagctc     540
```

```
ctcctgagaa agtctgttta attggctgtg ggttttccac tggatatggc gctgctgtta     600
aaactggcaa ggtcaaacct ggttccactt gcgtcgtctt tggcctgaga ggagttggcc     660
tgtcagtcat catgggctgt aagtcagctg gtgcatctag gatcattggg attgacctca     720
acaaagacaa atttgagaag gccatggctg taggtgccac tgagtgtatc agtcccaagg     780
actctaccaa acccatcagt gaggtgctgt cagaaatgac aggcaacaac gtgggataca     840
cctttgaagt tattgggcat cttgaaacca tgattgatgc cctggcatcc tgccacatga     900
actatgggac cagcgtggtt gtaggagttc ctccatcagc caagatgctc acctatgacc     960
cgatgttgct cttcactgga cgcacatgga agggatgtgt ctttggaggt ttgaaaagca    1020
gagatgatgt cccaaaacta gtgactgagt tcctggcaaa gaaatttgac ctggaccagt    1080
tgataactca tgtcttacca tttaaaaaaa tcagtgaagg atttgagctg ctcaattcag    1140
gacaaagcat tcgaacggtc ctgacgtttt gagatccaaa gtggcaggag gtctgtgttg    1200
tcatggtgaa ctggagtttc tcttgtgaga gttccctcat ctgaaatcat gtatctgtct    1260
cacaaataca agcataagta gaagatttgt tgaagacata gaacccttat aaagaattat    1320
taacctttat aaacatttaa agtcttgtga gcacctggga attagtataa taacaatgtt    1380
aatatttttg atttacattt tgtaaggcta taattgtatc ttttaagaaa acatacactt    1440
ggatttctat gttgaaatgg agatttttaa gagttttaac cagctgctgc agatatatat    1500
ctcaaaacag atatagcgta taaagatata gtaaatgcat ctcctagagt aatattcact    1560
taacacattg aaactattat tttttagatt tgaatataaa tgtatttttt aaacacttgt    1620
tatgagttaa cttggattac attttgaaat cagttcattc catgatgcat attactggat    1680
tagattaaga aagacagaaa agattaaggg acgggcacat ttttcaacga ttaagaatca    1740
tcattacata acttggtgaa actgaaaaag tatatcatat gggtacacaa ggctatttgc    1800
cagcatatat taatatttta gaaaatattc cttttgtaat actgaatata aacatagagc    1860
tagaatcata ttatcatact tatcataatg ttcaatttga tacagtagaa ttgcaagtcc    1920
ttaagtccct attcactgtg cttagtagtg actccattta ataaaaagtg tttttagttt    1980
ttaacaacta cactgatgta tttatatata tttataacat gttaaaaatt tttaaggaaa    2040
ttaaaaatta tataaaaaaa aaaaaaaaaa ctcgag                              2076
```

```
<210> 79
<211> 2790
<212> DNA
<213> Homo sapien

<400> 79
aagcagttga gtaggcagaa aaaagaacct cttcattaag gattaaaatg tataggccag      60
cacgtgtaac ttcgacttca agatttctga atccatatgt agtatgtttc attgtcgtcg     120
caggggtagt gatcctggca gtcaccatag ctctacttgt ttacttttta gcttttgatc     180
aaaaatctta cttttatagg agcagttttc aactcctaaa tgttgaatat aatagtcagt     240
taaattcacc agctacacag gaatacagga ctttgagtgg aagaattgaa tctctgatta     300
ctaaaacatt caaagaatca aatttaagaa atcagttcat cagagctcat gttgccaaac     360
tgaggcaaga tggtagtggt gtgagagcgg atgttgtcat gaaatttcaa ttcactagaa     420
ataacaatgg agcatcaatg aaaagcagaa ttgagtctgt tttacgacaa atgctgaata     480
actctggaaa cctggaaata aacccttcaa ctgagataac atcacttact gaccaggctg     540
cagcaaattg gcttattaat gaatgtgggg ccggtccaga cctaataaca ttgtctgagc     600
agagaatcct tggaggcact gaggctgagg agggaagctg gccgtggcaa gtcagtctgc     660
ggctcaataa tgcccaccac tgtggaggca gcctgatcaa taacatgtgg atcctgacag     720
cagctcactg cttcagaagc aactctaatc ctcgtgactg gattgccacg tctggtattt     780
ccacaacatt tcctaaacta agaatgagag taagaaatat tttaattcat aacaattata     840
aatctgcaac tcatgaaaat gacattgcac ttgtgagact tgagaacagt gtcaccttta     900
ccaaagatat ccatagtgtg tgtctcccag ctgctaccca gaatattcca cctggctcta     960
ctgcttatgt aacaggatgg ggcgctcaag aatatgctgg ccacacagtt ccagagctaa    1020
ggcaaggaca ggtcagaata ataagtaatg atgtatgtaa tgcaccacat agttataatg    1080
gagccatctt gtctggaatg ctgtgtgctg gagtacctca aggtggagtg gacgcatgtc    1140
agggtgactc tggtggccca ctagtacaag aagactcacg gcggctttgg tttattgtgg    1200
ggatagtaag ctggggagat cagtgtggcc tgccggataa gccaggagtg tatactcgag    1260
tgacagccta ccttgactgg attaggcaac aaactgggat ctagtgcaac aagtgcatcc    1320
ctgttgcaaa gtctgtatgc aggtgtgcct gtcttaaatt ccaaagcttt acatttcaac    1380
tgaaaaagaa actagaaatg tcctaattta acatcttgtt acataaatat ggtttaacaa    1440
acactgttta acctttcttt attattaaag gttttctatt ttctccagag aactatatga    1500
```

```
atgttgcata gtactgtggc tgtgtaacag aagaaacaca ctaaactaat tacaaagtta    1560
acaatttcat tacagttgtg ctaaatgccc gtagtgagaa gaacaggaac cttgagcatg    1620
tatagtagag gaacctgcac aggtctgatg ggtcagaggg gtcttctctg ggtttcactg    1680
aggatgagaa gtaagcaaac tgtggaaaca tgcaaaggaa aaagtgatag aataatattc    1740
aagacaaaaa gaacagtatg aggcaagaga aatagtatgt atttaaaatt tttggttact    1800
caatatctta tacttagtat gagtcctaaa attaaaaatg tgaaactgtt gtactatacg    1860
tataacctaa ccttaattat tctgtaagaa catgcttcca taggaaatag tggataattt    1920
tcagctattt aaggcaaaag ctaaaatagt tcactcctca actgagaccc aaagaattat    1980
agatattttt catgatgacc catgaaaaat atcactcatc tacataaagg agagactata    2040
tctattttat agagaagcta agaaatatac ctacacaaac ttgtcaggtg ctttacaact    2100
acatagtact ttttaacaac aaaataataa ttttaagaat gaaaaattta atcatcggga    2160
agaacgtccc actacagact tcctatcact ggcagttata tttttgagcg taaaagggtc    2220
gtcaaacgct aaatctaagt aatgaattga aagtttaaag aggggggaaga gttggtttgc    2280
aaaggaaaag tttaaatagc ttaatatcaa tagaatgatc ctgaagacag aaaaaacttt    2340
gtcactcttc ctctctcatt ttctttctct ctctctcccc ttctcataca catgcctccc    2400
cgaccaaaga atataatgta aattaaatcc actaaaatgt aatggcatga aaatctctgt    2460
agtctgaatc actaatattc ctgagttttt atgagctcct agtacagcta aagtttgcct    2520
atgcatgatc atctatgcgt cagagcttcc tccttctaca agctaactcc ctgcatctgg    2580
gcatcaggac tgctccatac atttgctgaa aacttcttgt atttcctgat gtaaaattgt    2640
gcaaacacct acaataaagc catctacttt tagggaaagg gagttgaaaa tgcaaccaac    2700
tcttggcgaa ctgtacaaac aaatctttgc tatactttat ttcaaataaa ttctttttga    2760
aatgaaaaaa aaaaaaaaaa aaaactcgag                                      2790
```

<210> 80
<211> 1460
<212> DNA
<213> Homo sapien

<400> 80

```
ctcaaagcag ttgagtaggc agaaaaaaga acctcttcat taaggattaa aatgtatagg      60
ccagcacgtg taacttcgac ttcaagattt ctgaatccat atgtagtatg tttcattgtc     120
gtcgcagggg tagtgatcct ggcagtcacc atagctctac ttgtttactt tttagctttt     180
gatcaaaaat cttactttta taggagcagt tttcaactcc taaatgttga atataatagt     240
cagttaaatt caccagctac acaggaatac aggactttga gtggaagaat tgaatctctg     300
attactaaaa cattcaaaga atcaaattta agaaatcagt tcatcagagc tcatgttgcc     360
aaactgaggc aagatggtag tggtgtgaga gcggatgttg tcatgaaatt tcaattcact     420
agaaataaca atggagcatc aatgaaaagc agaattgagt ctgttttacg acaaatgctg     480
aataactctg gaaacctgga aataaaccct tcaactgaga taacatcact tactgaccag     540
gctgcagcaa attggcttat taatgaatgt ggggccggtc cagacctaat aacattgtct     600
gagcagagaa tccttggagg cactgaggct gaggagggaa gctggccgtg gcaagtcagt     660
ctgcggctca ataatgccca ccactgtgga ggcagcctga tcaataacat gtggatcctg     720
acagcagctc actgcttcag aagcaactct aatcctcgtg actggattgc cacgtctggt     780
atttccacaa catttcctaa actaagaatg agagtaagaa atattttaat tcataacaat     840
tataaatctg caactcatga aaatgacatt gcacttgtga gacttgagaa cagtgtcacc     900
tttaccaaag atatccatag tgtgtgtctc ccagctgcta cccagaatat tccacctggc     960
tctactgctt atgtaacagg atggggcgct caagaatatg ctggccacac agttccagag    1020
ctaaggcaag gacaggtcag aataataagt aatgatgtat gtaatgcacc acatagttat    1080
aatggagcca tcttgtctgg aatgctgtgt gctggagtac ctcaaggtgg agtggacgca    1140
tgtcagggtg actctggtgg cccactagta caagaagact cacggcggct ttggtttatt    1200
gtggggatag taagctgggg agatcagtgt ggcctgccgg ataagccagg agtgtatact    1260
cgagtgacag cctaccttga ctggattagg caacaaactg ggatctagtg caacaagtgc    1320
atccctgttg caaagtctgt atgcaggtgt gcctgtctta aattccaaag ctttacattt    1380
caactgaaaa agaaactaga aatgtcctaa tttaacatct tgttacataa atatggttta    1440
acaaaaaaaa aaaaaaaaaa                                                 1460
```

<210> 81
<211> 386
<212> PRT

<213> Homo sapien

<400> 81
Met Phe Ala Glu Ile Gln Ile Gln Asp Lys Asp Arg Met Gly Thr Ala
1 5 10 15
Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp Glu Gln Lys Gln
20 25 30
Pro Phe Ser Ile Glu Glu Ile Glu Val Ala Pro Pro Lys Thr Lys Glu
35 40 45
Val Arg Ile Lys Ile Leu Ala Thr Gly Ile Cys Arg Thr Asp Asp His
50 55 60
Val Ile Lys Gly Thr Met Val Ser Lys Phe Pro Val Ile Val Gly His
65 70 75 80
Glu Ala Thr Gly Ile Val Glu Ser Ile Gly Glu Gly Val Thr Thr Val
85 90 95
Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Leu Pro Gln Cys Arg Glu
100 105 110
Cys Asn Ala Cys Arg Asn Pro Asp Gly Asn Leu Cys Ile Arg Ser Asp
115 120 125
Ile Thr Gly Arg Gly Val Leu Ala Asp Gly Thr Thr Arg Phe Thr Cys
130 135 140
Lys Gly Lys Pro Val His His Phe Met Asn Thr Ser Thr Phe Thr Glu
145 150 155 160
Tyr Thr Val Val Asp Glu Ser Ser Val Ala Lys Ile Asp Asp Ala Ala
165 170 175
Pro Pro Glu Lys Val Cys Leu Ile Gly Cys Gly Phe Ser Thr Gly Tyr
180 185 190
Gly Ala Ala Val Lys Thr Gly Lys Val Lys Pro Gly Ser Thr Cys Val
195 200 205
Val Phe Gly Leu Arg Gly Val Gly Leu Ser Val Ile Met Gly Cys Lys
210 215 220
Ser Ala Gly Ala Ser Arg Ile Ile Gly Ile Asp Leu Asn Lys Asp Lys
225 230 235 240
Phe Glu Lys Ala Met Ala Val Gly Ala Thr Glu Cys Ile Ser Pro Lys
245 250 255
Asp Ser Thr Lys Pro Ile Ser Glu Val Leu Ser Glu Met Thr Gly Asn
260 265 270
Asn Val Gly Tyr Thr Phe Glu Val Ile Gly His Leu Glu Thr Met Ile
275 280 285
Asp Ala Leu Ala Ser Cys His Met Asn Tyr Gly Thr Ser Val Val Val
290 295 300
Gly Val Pro Pro Ser Ala Lys Met Leu Thr Tyr Asp Pro Met Leu Leu
305 310 315 320
Phe Thr Gly Arg Thr Trp Lys Gly Cys Val Phe Gly Gly Leu Lys Ser
325 330 335
Arg Asp Asp Val Pro Lys Leu Val Thr Glu Phe Leu Ala Lys Lys Phe
340 345 350
Asp Leu Asp Gln Leu Ile Thr His Val Leu Pro Phe Lys Lys Ile Ser
355 360 365
Glu Gly Phe Glu Leu Leu Asn Ser Gly Gln Ser Ile Arg Thr Val Leu
370 375 380
Thr Phe
385

<210> 82
<211> 418
<212> PRT
<213> Homo sapien

<400> 82

```
Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro
 1               5                  10                  15
Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val
            20                  25                  30
Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr
        35                  40                  45
Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln
    50                  55                  60
Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile
65                  70                  75                  80
Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln
                85                  90                  95
Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val
            100                 105                 110
Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly
        115                 120                 125
Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn
    130                 135                 140
Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu
145                 150                 155                 160
Thr Asp Gln Ala Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly
                165                 170                 175
Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu
            180                 185                 190
Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn
        195                 200                 205
Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr
    210                 215                 220
Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala
225                 230                 235                 240
Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg
                245                 250                 255
Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp
            260                 265                 270
Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile
        275                 280                 285
His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser
    290                 295                 300
Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr
305                 310                 315                 320
Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val
                325                 330                 335
Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu
            340                 345                 350
Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser
        355                 360                 365
Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val
    370                 375                 380
Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly
385                 390                 395                 400
Val Tyr Thr Arg Val Thr Ala Tyr Leu Asp Trp Ile Arg Gln Gln Thr
                405                 410                 415
Gly Ile
```

<210> 83

<211> 418
<212> PRT
<213> Homo sapien

<400> 83
```
Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro
 1               5                  10                  15
Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val
            20                  25                  30
Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr
        35                  40                  45
Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln
    50                  55                  60
Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile
65                  70                  75                  80
Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln
                85                  90                  95
Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val
            100                 105                 110
Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly
        115                 120                 125
Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn
    130                 135                 140
Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu
145                 150                 155                 160
Thr Asp Gln Ala Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly
                165                 170                 175
Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu
            180                 185                 190
Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn
        195                 200                 205
Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr
    210                 215                 220
Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala
225                 230                 235                 240
Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg
                245                 250                 255
Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp
            260                 265                 270
Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile
        275                 280                 285
His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser
    290                 295                 300
Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr
305                 310                 315                 320
Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val
                325                 330                 335
Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu
            340                 345                 350
Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser
        355                 360                 365
Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val
    370                 375                 380
Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly
385                 390                 395                 400
Val Tyr Thr Arg Val Thr Ala Tyr Leu Asp Trp Ile Arg Gln Gln Thr
                405                 410                 415
Gly Ile
```

<210> 84
<211> 489
<212> DNA
<213> Homo sapien

<400> 84
aaaagggtaa gcttgatgat taccaggaac gaatgaacaa aggggaaagg cttaatcaag 60
atcagctgga tgccgtttct aagtaccagg aagtcacaaa taatttggag tttgcaaaag 120
aattacagag gagtttcatg gcactaagtc aagatattca gaaaacaata aagaagacag 180
cacgtcggga gcagcttatg agagaagaag ctgaacagaa acgtttaaaa actgtacttg 240
agctacagta tgttttggac aaattgggag atgatgaagt gcggactgac ctgaaacaag 300
gtttgaatgg agtgccaata ttgtccgaag aggagttgtc attgttggat gaattctata 360
agctagtaga ccctgaacgg gacatgagct tgaggttgaa tgaacagtat gaacatgcct 420
ccattcacct gtgggacctg ctggaaggga aggaaaaacc tgtatgtgga accacctata 480
aagttctaa 489

<210> 85
<211> 304
<212> DNA
<213> Homo sapien

<400> 85
gggacctgga ggaggccacg ctgcagcatg aagccacagc agccaccctg aggaagaagc 60
acgcggacag cgtggccgag ctcggggagc agatcgacaa cctgcagcgg gtgaagcaga 120
agctggagaa ggagaagagc gagatgaaga tggagatcga tgacctcgct tgtaacatgg 180
aggtcatctc caaatctaag ggaaaccttg agaagatgtg ccgcacactg gaggaccaag 240
tgagtgagct gaagacccag gaggaggaac agcagcggct gatcaatgaa ctgactgcgc 300
agag 304

<210> 86
<211> 296
<212> DNA
<213> Homo sapien

<400> 86
gaaaatcctt cctttgaatg ggaatctcca agcagttgaa ttgggcgaaa aaagaacctc 60
ttccttaagg attaaaatgt ttagggcaac acgtgttact tccacttcca gatttctgaa 120
tccatatgtt gtatgtttcc ttgtcctccc aggggttgtg atcctggcag tccccatagc 180
tctacttgtt tactttttag cttttgatca aaaatcttac ttttattgga gcaatttcc 240
actcccaaat gttgaatata atagtccgtt taattccccc gcttcaccgg gaattc 296

<210> 87
<211> 904
<212> DNA
<213> Homo sapien

<400> 87
gtgtccagga aacgattcat gaacataaca agcttgctgc aaattcagat catctcatgc 60
agattcaaaa atgtgagttg gtcttgatcc acacctaccc agttggtgaa gacagccttg 120
tatctgatcg ttctaaaaaa gagttgtccc cggttttaac cagtgaagtt catagtgttc 180
gtgcaggacg gcatcttgct accaaattga atattttagt acagcaacat tttgacttgg 240
cttcaactac tattacaaat attccaatga aggaagaaca gcatgctaac acatctgcca 300
attatgatgt ggagctactt catcacaaag atgcacatgt agatttcctg aaaagtggtg 360
attcgcatct aggtggcggc agtcgagaag gctcgtttaa agaaacaata acattaaagt 420
ggtgtacacc aaggacaaat aacattgaat tacactattg tactggagct tatcggattt 480
cacctgtaga tgtaaatagt agaccttcct cctgccttac taattttctt ctaaatggtc 540

gttctgtttt attggaacaa ccacgaaagt caggttctaa agtcattagt catatgctta 600
gtagccatgg aggagagatt tttttgcacg tccttagcag ttctcgatcc attctagaag 660
atccaccttc aattagtgaa ggatgtggag gaagagttac agactaccgg attacagatt 720
ttggtgaatt tatgagggga aaacagatta actccttttc tacaccccag atataaaatc 780
gatggaagtc ttgaggtccc tttggaaccg agccaaaaga tcagttaaaa aaacataccc 840
gttactggcc tatgatttca aaaacccacc atttttaaca tgcaagcggt agttccgtta 900
acca 904

<210> 88
<211> 387
<212> DNA
<213> Homo sapien

<400> 88
cgtctctccc ccagtttgcc gttcacccgg agcgctcggg acttgccgat agtggtgacg 60
gcggcaacat gtctgtggct ttcgcggccc cgaggcagcg aggcaagggg gagatcactc 120
ccgctgcgat tcagaagatg ttggatgaca ataaccatct tattcagtgt ataatggact 180
ctcagaataa aggaaagacc tcagagtgtt ctcagtatca gcagatgttg cacacaaact 240
tggtatacct tgctacaata gcagattcta atcaaaatat gcagtctctt ttaccagcac 300
cacccacaca gaatatgcct atgggtcctg gagggatgaa tcagagcggg cctcccccac 360
ctccacgctc tcacaacatg ccttcaa 387

<210> 89
<211> 481
<212> DNA
<213> Homo sapien

<400> 89
tgttcttgga cctgcggtgc tatagagcag gctcttctag gttggcagtt gccatggaat 60
ctggacccaa aatgttggcc cccgtttgcc tggtggaaaa taacaatgag cagctattgg 120
tgaaccagca agctatacag attcttgaaa agatttctca gccagtggtg gtggtggcca 180
ttgtaggact gtaccgtaca gggaaatcct acttgatgaa ccatctggca ggacagaatc 240
atggcttccc tctgggctcc acggtgcagt ctgaaaccaa gggcatctgg atgtggtgcg 300
tgccccaccc atccaagcca aaccacaccc tggtccttct ggacaccgaa ggtctgggcg 360
atgtggaaaa gggtgaccct aagaatgact cctggatctt tgccctggct gtgctcctgt 420
gcagcacctt tgtctacaac agcatgagca ccatcaacca ccaggccctg gagcagctgc 480
a 481

<210> 90
<211> 491
<212> DNA
<213> Homo sapien

<400> 90
tgaaaactgt tcttggacct gcggtgctat agagcaggtt ggcagttgcc atggaatctg 60
gacccaaaat gttggccccc gtttgcctgg tggaaaataa caatgagcag ctattggtga 120
accagcaagc tatacagatt cttgaaaaga tttctcagcc agtggtggtg gtggccattg 180
taggactgta ccgtacaggg aaatcctact tgatgaacca tctggcagga cagaatcatg 240
gcttccctct gggctccacg gtgcagtctg aaaccaaggg catctggatg tggtgcgtgc 300
cccacccatc caagccaaac cacaccctgg tccttctgga caccgaaggt ctgggcgatg 360
tggaaaaggg tgaccctaag aatgactcct ggatctttgc cctggctgtg ctcctgtgca 420
gcacctttgt ctacaacagc atgagcacca tcaaccacca agccctggag cagctgcatt 480
atgtgacgga c 491

<210> 91
<211> 488
<212> DNA
<213> Homo sapien

<400> 91
ttcgacagtc agccgcatct tcttttgcgt cgccagccga gccacatcgc tcagacacca 60
tggggaaggt gaaggtcgga gtcaacggat ttggtcgtat tgggcgcctg gtcaccaggg 120
ctgcttttaa ctctggtaaa gtggatattg ttgccatcaa tgaccccttc attgacctca 180
actacatggt ttacatgttc caatatgatt ccacccatgg caaattccat ggcaccgtcg 240
aggctgagaa cgggaagctt gtcatcaatg gaaatcccat caccatcttc caggagcgag 300
atccctccaa aatcaagtgg ggcgatgctg gcgctgagta cgtcgtggag tccactggcg 360
tcttcaccac catggagaag gctggggctc atttgcaggg gggagccaaa agggtcatca 420
tctctgcccc tctgctgatg ccccatgttc gtcatgggtg tgaaccatga gaagtatgac 480
acagcctc 488

<210> 92
<211> 384
<212> DNA
<213> Homo sapien

<400> 92
gacagtcagc cgcatcttct tttgcgtcgc cagccgagcc acatcgctca gacaccatgg 60
ggaaggtgaa ggtcggagtc aacggatttg gtcgtattgg gcgcctggtc accagggctg 120
cttttaactc tggtaaagtg gatattgttg ccatcaatga ccccttcatt gacctcaact 180
acatggttta catgttccaa tatgattcca cccatggcaa attccatggc accgtcgagg 240
ctgagaacgg gaagcttgtc atcaatggaa atcccatcac catcttccag gagcgagatc 300
cctccaaaat caagtggggc gatactggcg ctgagtacgt cgtggagtcc actggcgtct 360
tcaccaccat ggagaaggct gggg 384

<210> 93
<211> 162
<212> PRT
<213> Homo sapien

<400> 93
Lys Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg
1 5 10 15
Leu Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr
20 25 30
Asn Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu
35 40 45
Ser Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln
50 55 60
Leu Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu
65 70 75 80
Leu Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp
85 90 95
Leu Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu
100 105 110
Ser Leu Leu Asp Glu Phe Tyr Lys Leu Val Asp Pro Glu Arg Asp Met
115 120 125
Ser Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp
130 135 140
Asp Leu Leu Glu Gly Lys Glu Lys Pro Val Cys Gly Thr Thr Tyr Lys
145 150 155 160
Val Leu

<210> 94
<211> 100
<212> PRT

<213> Homo sapien

<400> 94

```
Asp Leu Glu Glu Ala Thr Leu Gln His Glu Ala Thr Ala Ala Thr Leu
 1               5                  10                  15
Arg Lys Lys His Ala Asp Ser Val Ala Glu Leu Gly Glu Gln Ile Asp
            20                  25                  30
Asn Leu Gln Arg Val Lys Gln Lys Leu Glu Lys Glu Lys Ser Glu Met
        35                  40                  45
Lys Met Glu Ile Asp Asp Leu Ala Cys Asn Met Glu Val Ile Ser Lys
    50                  55                  60
Ser Lys Gly Asn Leu Glu Lys Met Cys Arg Thr Leu Glu Asp Gln Val
65                  70                  75                  80
Ser Glu Leu Lys Thr Gln Glu Glu Glu Gln Gln Arg Leu Ile Asn Glu
                85                  90                  95
Leu Thr Ala Gln
            100
```

<210> 95
<211> 99
<212> PRT
<213> Homo sapien

<400> 95

```
Lys Ile Leu Pro Leu Asn Gly Asn Leu Gln Ala Val Glu Leu Gly Glu
 1               5                  10                  15
Lys Arg Thr Ser Ser Leu Arg Ile Lys Met Phe Arg Ala Thr Arg Val
            20                  25                  30
Thr Ser Thr Ser Arg Phe Leu Asn Pro Tyr Val Val Cys Phe Leu Val
        35                  40                  45
Leu Pro Gly Val Val Ile Leu Ala Val Pro Ile Ala Leu Leu Val Tyr
    50                  55                  60
Phe Leu Ala Phe Asp Gln Lys Ser Tyr Phe Tyr Trp Ser Asn Phe Pro
65                  70                  75                  80
Leu Pro Asn Val Glu Tyr Asn Ser Pro Phe Asn Ser Pro Ala Ser Pro
                85                  90                  95
Gly Ile Pro
```

<210> 96
<211> 257
<212> PRT
<213> Homo sapien

<400> 96

```
Val Gln Glu Thr Ile His Glu His Asn Lys Leu Ala Ala Asn Ser Asp
 1               5                  10                  15
His Leu Met Gln Ile Gln Lys Cys Glu Leu Val Leu Ile His Thr Tyr
            20                  25                  30
Pro Val Gly Glu Asp Ser Leu Val Ser Asp Arg Ser Lys Lys Glu Leu
        35                  40                  45
Ser Pro Val Leu Thr Ser Glu Val His Ser Val Arg Ala Gly Arg His
    50                  55                  60
Leu Ala Thr Lys Leu Asn Ile Leu Val Gln Gln His Phe Asp Leu Ala
65                  70                  75                  80
Ser Thr Thr Ile Thr Asn Ile Pro Met Lys Glu Glu Gln His Ala Asn
                85                  90                  95
Thr Ser Ala Asn Tyr Asp Val Glu Leu Leu His His Lys Asp Ala His
```

                100   105   110
Val Asp Phe Leu Lys Ser Gly Asp Ser His Leu Gly Gly Gly Ser Arg
            115   120   125
Glu Gly Ser Phe Lys Glu Thr Ile Thr Leu Lys Trp Cys Thr Pro Arg
        130   135   140
Thr Asn Asn Ile Glu Leu His Tyr Cys Thr Gly Ala Tyr Arg Ile Ser
145   150   155   160
Pro Val Asp Val Asn Ser Arg Pro Ser Ser Cys Leu Thr Asn Phe Leu
                165   170   175
Leu Asn Gly Arg Ser Val Leu Leu Glu Gln Pro Arg Lys Ser Gly Ser
                180   185   190
Lys Val Ile Ser His Met Leu Ser Ser His Gly Gly Glu Ile Phe Leu
            195   200   205
His Val Leu Ser Ser Ser Arg Ser Ile Leu Glu Asp Pro Pro Ser Ile
        210   215   220
Ser Glu Gly Cys Gly Gly Arg Val Thr Asp Tyr Arg Ile Thr Asp Phe
225   230   235   240
Gly Glu Phe Met Arg Gly Lys Gln Ile Asn Ser Phe Ser Thr Pro Gln
                245   250   255
Ile

<210> 97
<211> 128
<212> PRT
<213> Homo sapien

<400> 97
Ser Leu Pro Gln Phe Ala Val His Pro Glu Arg Ser Gly Leu Ala Asp
1   5   10   15
Ser Gly Asp Gly Gly Asn Met Ser Val Ala Phe Ala Ala Pro Arg Gln
                20   25   30
Arg Gly Lys Gly Glu Ile Thr Pro Ala Ala Ile Gln Lys Met Leu Asp
            35   40   45
Asp Asn Asn His Leu Ile Gln Cys Ile Met Asp Ser Gln Asn Lys Gly
        50   55   60
Lys Thr Ser Glu Cys Ser Gln Tyr Gln Gln Met Leu His Thr Asn Leu
65   70   75   80
Val Tyr Leu Ala Thr Ile Ala Asp Ser Asn Gln Asn Met Gln Ser Leu
                85   90   95
Leu Pro Ala Pro Pro Thr Gln Asn Met Pro Met Gly Pro Gly Gly Met
                100   105   110
Asn Gln Ser Gly Pro Pro Pro Pro Pro Arg Ser His Asn Met Pro Ser
            115   120   125

<210> 98
<211> 159
<212> PRT
<213> Homo sapien

<400> 98
Phe Leu Asp Leu Arg Cys Tyr Arg Ala Gly Ser Ser Arg Leu Ala Val
1   5   10   15
Ala Met Glu Ser Gly Pro Lys Met Leu Ala Pro Val Cys Leu Val Glu
                20   25   30
Asn Asn Asn Glu Gln Leu Leu Val Asn Gln Gln Ala Ile Gln Ile Leu
            35   40   45
Glu Lys Ile Ser Gln Pro Val Val Val Val Ala Ile Val Gly Leu Tyr

```
    50                  55                  60
Arg Thr Gly Lys Ser Tyr Leu Met Asn His Leu Ala Gly Gln Asn His
65                  70                  75                  80
Gly Phe Pro Leu Gly Ser Thr Val Gln Ser Glu Thr Lys Gly Ile Trp
                85                  90                  95
Met Trp Cys Val Pro His Pro Ser Lys Pro Asn His Thr Leu Val Leu
            100                 105                 110
Leu Asp Thr Glu Gly Leu Gly Asp Val Glu Lys Gly Asp Pro Lys Asn
        115                 120                 125
Asp Ser Trp Ile Phe Ala Leu Ala Val Leu Leu Cys Ser Thr Phe Val
    130                 135                 140
Tyr Asn Ser Met Ser Thr Ile Asn His Gln Ala Leu Glu Gln Leu
145                 150                 155

      <210> 99
      <211> 147
      <212> PRT
      <213> Homo sapien

      <400> 99
Met Glu Ser Gly Pro Lys Met Leu Ala Pro Val Cys Leu Val Glu Asn
 1               5                  10                  15
Asn Asn Glu Gln Leu Leu Val Asn Gln Gln Ala Ile Gln Ile Leu Glu
            20                  25                  30
Lys Ile Ser Gln Pro Val Val Val Val Ala Ile Val Gly Leu Tyr Arg
        35                  40                  45
Thr Gly Lys Ser Tyr Leu Met Asn His Leu Ala Gly Gln Asn His Gly
    50                  55                  60
Phe Pro Leu Gly Ser Thr Val Gln Ser Glu Thr Lys Gly Ile Trp Met
65                  70                  75                  80
Trp Cys Val Pro His Pro Ser Lys Pro Asn His Thr Leu Val Leu Leu
                85                  90                  95
Asp Thr Glu Gly Leu Gly Asp Val Glu Lys Gly Asp Pro Lys Asn Asp
            100                 105                 110
Ser Trp Ile Phe Ala Leu Ala Val Leu Leu Cys Ser Thr Phe Val Tyr
        115                 120                 125
Asn Ser Met Ser Thr Ile Asn His Gln Ala Leu Glu Gln Leu His Tyr
    130                 135                 140
Val Thr Asp
145

      <210> 100
      <211> 124
      <212> PRT
      <213> Homo sapien

      <400> 100
Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg
 1               5                  10                  15
Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala
            20                  25                  30
Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
        35                  40                  45
Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Glu Ala Glu Asn
    50                  55                  60
Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg
65                  70                  75                  80
Asp Pro Ser Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val
```

```
                85                  90                  95
Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu
            100                 105                 110
Gln Gly Gly Ala Lys Arg Val Ile Ile Ser Ala Pro
        115                 120

<210> 101
<211> 127
<212> PRT
<213> Homo sapien

<400> 101
Gln Ser Ala Ala Ser Ser Phe Ala Ser Pro Ala Glu Pro His Arg Ser
 1               5                  10                  15
Asp Thr Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile
            20                  25                  30
Gly Arg Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile
        35                  40                  45
Val Ala Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met
    50                  55                  60
Phe Gln Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Glu Ala
65                  70                  75                  80
Glu Asn Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln
                85                  90                  95
Glu Arg Asp Pro Ser Lys Ile Lys Trp Gly Asp Thr Gly Ala Glu Tyr
            100                 105                 110
Val Val Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly
        115                 120                 125

<210> 102
<211> 1225
<212> DNA
<213> Homo sapien

<400> 102
atggcggcgc ggtcgtcgtc gggggtggcg gcggcagagg gggcggcggc cctggcggca      60
gcggagacgg cagccgtgac ggtggcagcg gcggcgcggg acctgggcct gggggaatga     120
ggcggccgcg gcgggccagc ggcggagccg tgtagcggag aagctccccc tccctgcttc     180
ccttggccga gccgggggcg cgcgcgcacg cggccgtcca gagcgggctc cccacccctc     240
gactcctgcg acccgcaccg cacccccacc cgggcccgga ggatgatgaa gctcaagtcg     300
aaccagaccc gcacctacga cggcgacggc tacaagaagc gggccgcatg cctgtgtttc     360
cgcagcgaga gcgaggagga ggtgctactc gtgagcagta gtcgccatcc agacagatgg     420
attgtccctg gaggaggcat ggagcccgag gaggagccaa gtgtggcagc agttcgtgaa     480
gtctgtgagg aggctggagt aaaagggaca ttgggaagat tagttggaat tttgagaac      540
caggagagga agcacaggac gtatgtctat gtgctcattg tcactgaagt gctggaagac     600
tgggaagatt cagttaacat tggaaggaag agggaatggt ttaaaataga agacgccata     660
aaagtgctgc agtatcacaa acccgtgcag gcatcatatt ttgaaacatt gaggcaaggc     720
tactcagcca acaatggcac ccagtcgtg gccaccacat actcggtttc tgctcagagc      780
tcgatgtcag gcatcagatg actgaagact tcctgtaaga gaaatggaaa ttggaaacta     840
gactgaagtg caaatcttcc ctctcaccct ggctctttcc acttctcaca ggcctcctct     900
ttcaaataag gcatggtggg cagcaaagaa agggtgtatt gataatgttg ctgtttggtg     960
ttaagtgatg gggctttttc ttctgttttt attgagggtg ggggttgggt gtgtaatttg    1020
taagtacttt tgtgcatgat ctgtccctcc ctcttcccac ccctgcagtc ctctgaagag    1080
aggccaacag ccttcccctg ccttggattc tgaagtgttc ctgtttgtct tatcctggcc    1140
ctggccagac gttttctttg atttttaatt tttttttttt attaaaagat accagtatga    1200
gaaaaaaaaa aaaaaaaaac tcgag                                           1225

<210> 103
```

<211> 741
<212> DNA
<213> Homo sapien

<400> 103
agaaacctca atcggattca gcaaaggaat ggtgttatta tcactacata ccaaatgtta 60
atcaataact ggcagcaact ttcaagcttt aggggccaag agtttgtgtg ggactatgtc 120
atcctcgatg aagcacataa aataaaaacc tcatctacta agtcagcaat atgtgctcgt 180
gctattcctg caagtaatcg cctcctcctc acaggaaccc caatccagaa taatttacaa 240
gaactatggt ccctatttga ttttgcttgt caagggtccc tgctgggaac attaaaaact 300
tttaagatgg agtatgaaaa tcctattact agagcaagag agaaggatgc taccccagga 360
gaaaaagcct tgggatttaa aatatctgaa aacttaatgg caatcataaa accctatttt 420
ctcaggagga ctaaagaaga cgtacagaag aaaaagtcaa gcaacccaga ggccagactt 480
aatgaaaaga atccagatgt tgatgccatt tgtgaaatgc cttccctttc caggagaaat 540
gatttaatta tttggatacg acttgtgcct ttacaagaag aaatatacag gaaatttgtg 600
tctttagatc atatcaagga gttgctaatg gagacgcgct cacctttggc tgagctaggt 660
gtcttaaaga agctgtgtga tcatcctagg ctgctgtctg cacgggcttg ttgtttgcta 720
aatcttggga cattctctgc t 741

<210> 104
<211> 321
<212> DNA
<213> Homo sapien

<400> 104
ttgctctgcg tcatcaaaga caccaaactg ctgtgctata aaagttccaa ggaccagcag 60
cctcagatgg aactgccact ccaaggctgt aacattacgt acatcccgaa agacagcaaa 120
aagaagaagc acgagctgaa gattactcag cagggcacgg acccgcttgt tctcgccgtc 180
cagagcaagg aacaggccga gcagtggctg aaggtgatca aagaagccta cagtggttgt 240
agtggccccg tggattcaga gtgtcctcct ccaccaagct ccccggtgca caaggcagaa 300
ctggagaaga aactgtcttc a 321

<210> 105
<211> 389
<212> DNA
<213> Homo sapien

<400> 105
cagcactggc cacactataa aattcaggtt cagaaaaaca gggtaagtca cagacagcaa 60
cgcttccagc atttattttc tttgcaccca tgggcaattt gagaaaattt acctttagaa 120
cgaactctgt taaaggtaca gacagtacaa tactttttat tcagaaggtt tctgcataaa 180
ggtgatagtc ttttgactta atatattatt gtctcctgcc ttgtgtttct ggaatgaatg 240
aaggtcatta tttagaagat aatctgggtt gtatttgtgt cgtcagattg aattttcatt 300
gcacatgcta cttaatgtct ttaccaaata ataacaaagg gaaagaaaac caaatataga 360
tgtataataa ggaaaagctg gcctataga 389

<210> 106
<211> 446
<212> DNA
<213> Homo sapien

<400> 106
gccacatttg ccctggtcat agtttaaaca ccaggtcctg tgtcacatct ttttggtgcc 60
acaagtatca ctccattgtt cagagagtaa tgtattagtt ctgcccaatt cattcttcac 120
ttttatttct tccatttcat tagcatttat atcagctcaa gaagttaagg ttagaaaatt 180
ttccacttca aattttcagt acagaaatgt gctgtgatgt ttgacaagac tatttcatag 240
taagtgagtt aatgtttatt ggcctctgct ctcctctgtg tcagacctag gaagcctgag 300
gattacttag ttgttctgtc tctgggtcca caggcagaat ttggcccatc caaagactgg 360

ccaagtgcca aaaaaaggcc tgattaggcc ctgaaattca gtgaaattct gcctgaagaa 420
acctcttatt gaatttgaaa accata 446

<210> 107
<211> 467
<212> DNA
<213> Homo sapien

<400> 107
ccgccgctgc cgtcgccttc ctgggattgg agtctcgagc tttcttcgtt cgttcgccgg 60
cgggttcgcg cccttctcgc gcctcggggc tgcgaggctg gggaaggggt tggagggggc 120
tgttgatcgc cgcgtttaag ttgcgctcgg ggcggccatg tcggccggcg aggtcgagcg 180
cctagtgtcg gagctgagcg gcgggaccgg aggggatgag gaggaagagt ggctctatgg 240
cgatgaagat gaagttgaaa ggccagaaga agaaaatgcc agtgctaatc ctccatctgg 300
aattgaagat gaaactgctg aaaatggtgt accaaaaccg aaagtgactg agaccgaaga 360
tgatagtgat agtgacagcg atgatgatga agatgatgtg catgtcacta taggagacat 420
taaaacggga gcaccacagt atgggagtta tggtacagca cctgtaa 467

<210> 108
<211> 491
<212> DNA
<213> Homo sapien

<400> 108
gaaagataca acttccccaa cccaaacccg tttgtggagg acgacatgga taagaatgaa 60
atcgcctctg ttgcgtaccg ttaccgcagg tggaagcttg gagatgatat tgaccttatt 120
gtccgttgtg agcacgatgg cgtcatgact ggagccaacg gggaagtgtc cttcatcaac 180
atcaagacac tcaatgagtg ggattccagg cactgtaatg gcgttgactg gcgtcagaag 240
ctggactctc agcgaggggc tgtcattgcc acggagctga agaacaacag ctacaagttg 300
gcccggtgga cctgctgtgc tttgctggct ggatctgagt acctcaagct tggttatgtg 360
tctcggtacc acgtgaaaga ctcctcacgc cacgtcatcc taggcaccca gcagttcaag 420
cctaatgagt ttgccagcca gatcaacctg agcgtggaga atgcctgagg cattttacgc 480
tgcgtcattg a 491

<210> 109
<211> 489
<212> DNA
<213> Homo sapien

<400> 109
ctcagatagt actgaaccct ttatcaacta tgtttttttca gtctgacaac caaggcggct 60
actaagtgac taaggggcag gtagtataca gtgtggataa gcaggacaaa ggggtgattc 120
acatcccagg caggacagag caggagatca tgagatttca tcactcagga tggcttgtga 180
tttattttat tttattcttt ttttttttg agatggagtc tcactcttgc ccaggctgga 240
gtgcagtggt gcgatcttgg ctcactgcaa cctctgcctc ctgggttcaa gcagttctcc 300
tgcctcagcc tcccaagtag ctgggattac aggcgtccgc caccatgccc agccaatttt 360
tgtactttta gtagagatgg ggtttcacca tgttggccag gctggtctcg aactcctgac 420
ctcaggtgat ccactcgcct cggcctccca aagtgctggg attataggca tgcgccacca 480
tgcccgggc 489

<210> 110
<211> 391
<212> DNA
<213> Homo sapien

<400> 110
gcggagtccg ctggctgacc cgagcgctgg tctccgccgg gaaccctggg gcatggagag 60
gtctgagtac ctcggccgcg gcgcacgctg catcgcggag ccaggctgcc gctgtcccag 120

```
tggagttcca ggagcaccac ctgagtgagg tgcagaatat ggcatctgag gagaagctgg     180
agcaggtgct gagttccatg aaggagaaca aagtggccat cattggaaag attcataccc     240
cgatggagta taagggggag ctagcctcct atgatatgcg gctgaggcgt aagttggact     300
tatttgccaa cgtaatccat gtgaagtcac ttcctgggta tatgactcgg cacaacaatc     360
tagacctggt gatcattcga gagcagacag a                                    391

      <210> 111
      <211> 172
      <212> PRT
      <213> Homo sapien

      <400> 111
Met Met Lys Leu Lys Ser Asn Gln Thr Arg Thr Tyr Asp Gly Asp Gly
 1               5                  10                  15
Tyr Lys Lys Arg Ala Ala Cys Leu Cys Phe Arg Ser Glu Ser Glu Glu
            20                  25                  30
Glu Val Leu Leu Val Ser Ser Ser Arg His Pro Asp Arg Trp Ile Val
        35                  40                  45
Pro Gly Gly Gly Met Glu Pro Glu Glu Glu Pro Ser Val Ala Ala Val
    50                  55                  60
Arg Glu Val Cys Glu Glu Ala Gly Val Lys Gly Thr Leu Gly Arg Leu
65                  70                  75                  80
Val Gly Ile Phe Glu Asn Gln Glu Arg Lys His Arg Thr Tyr Val Tyr
                85                  90                  95
Val Leu Ile Val Thr Glu Val Leu Glu Asp Trp Glu Asp Ser Val Asn
            100                 105                 110
Ile Gly Arg Lys Arg Glu Trp Phe Lys Ile Glu Asp Ala Ile Lys Val
        115                 120                 125
Leu Gln Tyr His Lys Pro Val Gln Ala Ser Tyr Phe Glu Thr Leu Arg
    130                 135                 140
Gln Gly Tyr Ser Ala Asn Asn Gly Thr Pro Val Val Ala Thr Thr Tyr
145                 150                 155                 160
Ser Val Ser Ala Gln Ser Ser Met Ser Gly Ile Arg
                165                 170

      <210> 112
      <211> 247
      <212> PRT
      <213> Homo sapien

      <400> 112
Arg Asn Leu Asn Arg Ile Gln Gln Arg Asn Gly Val Ile Ile Thr Thr
 1               5                  10                  15
Tyr Gln Met Leu Ile Asn Asn Trp Gln Gln Leu Ser Ser Phe Arg Gly
            20                  25                  30
Gln Glu Phe Val Trp Asp Tyr Val Ile Leu Asp Glu Ala His Lys Ile
        35                  40                  45
Lys Thr Ser Ser Thr Lys Ser Ala Ile Cys Ala Arg Ala Ile Pro Ala
    50                  55                  60
Ser Asn Arg Leu Leu Leu Thr Gly Thr Pro Ile Gln Asn Asn Leu Gln
65                  70                  75                  80
Glu Leu Trp Ser Leu Phe Asp Phe Ala Cys Gln Gly Ser Leu Leu Gly
                85                  90                  95
Thr Leu Lys Thr Phe Lys Met Glu Tyr Glu Asn Pro Ile Thr Arg Ala
            100                 105                 110
Arg Glu Lys Asp Ala Thr Pro Gly Glu Lys Ala Leu Gly Phe Lys Ile
        115                 120                 125
Ser Glu Asn Leu Met Ala Ile Ile Lys Pro Tyr Phe Leu Arg Arg Thr
```

```
    130                 135                 140
Lys Glu Asp Val Gln Lys Lys Lys Ser Ser Asn Pro Glu Ala Arg Leu
145                 150                 155                 160
Asn Glu Lys Asn Pro Asp Val Asp Ala Ile Cys Glu Met Pro Ser Leu
                165                 170                 175
Ser Arg Arg Asn Asp Leu Ile Ile Trp Ile Arg Leu Val Pro Leu Gln
            180                 185                 190
Glu Glu Ile Tyr Arg Lys Phe Val Ser Leu Asp His Ile Lys Glu Leu
        195                 200                 205
Leu Met Glu Thr Arg Ser Pro Leu Ala Glu Leu Gly Val Leu Lys Lys
    210                 215                 220
Leu Cys Asp His Pro Arg Leu Leu Ser Ala Arg Ala Cys Cys Leu Leu
225                 230                 235                 240
Asn Leu Gly Thr Phe Ser Ala
                245

      <210> 113
      <211> 107
      <212> PRT
      <213> Homo sapien

      <400> 113
Leu Leu Cys Val Ile Lys Asp Thr Lys Leu Leu Cys Tyr Lys Ser Ser
 1               5                  10                  15
Lys Asp Gln Gln Pro Gln Met Glu Leu Pro Leu Gln Gly Cys Asn Ile
            20                  25                  30
Thr Tyr Ile Pro Lys Asp Ser Lys Lys Lys Lys His Glu Leu Lys Ile
        35                  40                  45
Thr Gln Gln Gly Thr Asp Pro Leu Val Leu Ala Val Gln Ser Lys Glu
    50                  55                  60
Gln Ala Glu Gln Trp Leu Lys Val Ile Lys Glu Ala Tyr Ser Gly Cys
65                  70                  75                  80
Ser Gly Pro Val Asp Ser Glu Cys Pro Pro Pro Pro Ser Ser Pro Val
                85                  90                  95
His Lys Ala Glu Leu Glu Lys Lys Leu Ser Ser
            100                 105

      <210> 114
      <211> 155
      <212> PRT
      <213> Homo sapien

      <400> 114
Glu Arg Tyr Asn Phe Pro Asn Pro Asn Pro Phe Val Glu Asp Asp Met
 1               5                  10                  15
Asp Lys Asn Glu Ile Ala Ser Val Ala Tyr Arg Tyr Arg Arg Trp Lys
            20                  25                  30
Leu Gly Asp Asp Ile Asp Leu Ile Val Arg Cys Glu His Asp Gly Val
        35                  40                  45
Met Thr Gly Ala Asn Gly Glu Val Ser Phe Ile Asn Ile Lys Thr Leu
    50                  55                  60
Asn Glu Trp Asp Ser Arg His Cys Asn Gly Val Asp Trp Arg Gln Lys
65                  70                  75                  80
Leu Asp Ser Gln Arg Gly Ala Val Ile Ala Thr Glu Leu Lys Asn Asn
                85                  90                  95
Ser Tyr Lys Leu Ala Arg Trp Thr Cys Cys Ala Leu Leu Ala Gly Ser
            100                 105                 110
Glu Tyr Leu Lys Leu Gly Tyr Val Ser Arg Tyr His Val Lys Asp Ser
```

```
        115                 120                 125
Ser Arg His Val Ile Leu Gly Thr Gln Gln Phe Lys Pro Asn Glu Phe
    130                 135                 140
Ala Ser Gln Ile Asn Leu Ser Val Glu Asn Ala
145                 150                 155

      <210> 115
      <211> 129
      <212> PRT
      <213> Homo sapien

      <400> 115
Gly Val Arg Trp Leu Thr Arg Ala Leu Val Ser Ala Gly Asn Pro Gly
 1               5                  10                  15
Ala Trp Arg Gly Leu Ser Thr Ser Ala Ala Ala His Ala Ala Ser Arg
            20                  25                  30
Ser Gln Ala Ala Ala Val Pro Val Glu Phe Gln Glu His His Leu Ser
        35                  40                  45
Glu Val Gln Asn Met Ala Ser Glu Glu Lys Leu Glu Gln Val Leu Ser
    50                  55                  60
Ser Met Lys Glu Asn Lys Val Ala Ile Ile Gly Lys Ile His Thr Pro
65                  70                  75                  80
Met Glu Tyr Lys Gly Glu Leu Ala Ser Tyr Asp Met Arg Leu Arg Arg
                85                  90                  95
Lys Leu Asp Leu Phe Ala Asn Val Ile His Val Lys Ser Leu Pro Gly
            100                 105                 110
Tyr Met Thr Arg His Asn Asn Leu Asp Leu Val Ile Ile Arg Glu Gln
        115                 120                 125
Thr


      <210> 116
      <211> 550
      <212> DNA
      <213> Homo sapien

      <400> 116
gaattcggca ccagcctcag agcccccag cccggctacc accccctgcg gaaaggtacc      60
catctgcatt cctgcccgtc gggacctggt ggacagtcca gcctccttgg cctctagcct     120
tggctcaccg ctgcctagag ccaaggagct catcctgaat gaccttcccg ccagcactcc     180
tgcctccaaa tcctgtgact cctccccgcc ccaggacgct tccaccccca ggcccagctc     240
ggccagtcac ctctgccagc ttgctgccaa gccagcacct tccacggaca gcgtcgccct     300
gaggagcccc ctgactctgt ccagtccctt caccacgtcc ttcagcctgg gctcccacag     360
cactctcaac ggagacctct ccgtgcccag ctcctacgtc agcctccacc tgtcccccca     420
ggtcagcagc tctgtggtgt acggacgctc ccccgtgatg gcatttgagt ctcatcccca     480
tctccgaggg tcatccgtct cttcctccct acccagcatc cctgggggaa agccggccta     540
ctccttccac                                                            550

      <210> 117
      <211> 154
      <212> DNA
      <213> Homo sapien

      <400> 117
ttctgaggga aagccgagtg gagtgggcga cccggcggcg gtgacaatga gttttcttgg      60
aggctttttt ggtcccattt gtgagattga tgttgccctt aatgatgggg aaaccaggaa     120
aatggcagaa atgaaaactg aggatggcaa agta                                 154
```

<210> 118
<211> 449
<212> DNA
<213> Homo sapien

<400> 118
gaattcggca ccagggcccg cagcccgagt gtcgccgcca tggcttcgcc gcagctctgc 60
cgcgcgctgg tgtcggcgca atgggtggcg gaggcgctgc gggccccgcg cgctgggcag 120
cctctgcagc tgctggacgc ctcctggtac ctgccgaagc tggggcgcga cgcgcgacgc 180
gagttcgagg agcgccacat cccgggcgcc gctttcttcg acatcgacca gtgcagcgac 240
cgcacctcgc cctacgacca catgctgccc ggggccgagc atttcgcgga gtacgcaggc 300
cgcctgggcg tgggcgcggc cacccacgtc gtgatctacg acgccagcga ccagggcctc 360
tactccgccc cgcgcgtctg gtggatgttc cgcgccttcg gccaccacgc cgtgtcactg 420
cttgatggcg gcctccgcca ctggctgcg 449

<210> 119
<211> 642
<212> DNA
<213> Homo sapien

<400> 119
gaattcggca cgagcagtaa cccgaccgcc gctggtcttc gctggacacc atgaatcaca 60
ctgtccaaac cttcttctct cctgtcaaca gtggccagcc ccccaactat gagatgctca 120
aggaggagca cgaggtggct gtgctggggg cgccccacaa ccctgctccc ccgacgtcca 180
ccgtgatcca catccgcagc gagacctccg tgcccgacca tgtcgtctgg tccctgttca 240
acaccctctt catgaacccc tgctgcctgg gcttcatagc attcgcctac tccgtgaagt 300
ctagggacag gaagatggtt ggcgacgtga ccggggccca ggcctatgcc tccaccgcca 360
agtgcctgaa catctgggcc ctgattctgg gcatcctcat gaccattctg ctcatcgtca 420
tcccagtgct gatcttccag gcctatggat agatcaggag gcatcactga ggccaggagc 480
tctgcccatg acctgtatcc cacgtactcc aacttccatt cctcgccctg cccccggagc 540
cgagtcctgt atcagccctt tatcctcaca cgcttttcta caatggcatt caataaagtg 600
cacgtgtttc tggtgaaaaa aaaaaaaaaa aaaaaactcg ag 642

<210> 120
<211> 603
<212> DNA
<213> Homo sapien

<400> 120
gaattcggca cgagccacaa cagccactac gactgcatcc actggatcca cggccacccc 60
gtcctccacc ccgggaacag ctccccctcc caaagtgctg accagcccgg ccaccacacc 120
catgtccacc atgtccacaa tccacacctc ctctactcca gagaccaccc acacctccac 180
agtgctgacc accacagcca ccatgacaag ggccaccaat tccacggcca caccctcctc 240
cactctgggg acgacccgga tcctcactga gctgaccaca acagccacta caactgcagc 300
cactggatcc acggccaccc tgtcctccac cccagggacc acctggatcc tcacagagcc 360
gagcactata gccaccgtga tggtgcccac cggttccacg gccaccgcct cctccactct 420
gggaacagct cacacccccа aagtggtgac caccatggcc actatgccca cagccactgc 480
ctccacggtt cccagctcgt ccaccgtggg gaccacccgc acccctgcag tgctccccag 540
cagcctgcca accttcagcg tgtccactgt gtcctcctca gtcctcacca ccctgagacc 600
cac 603

<210> 121
<211> 178
<212> PRT
<213> Homo sapien

<400> 121
Ser Glu Pro Pro Ser Pro Ala Thr Thr Pro Cys Gly Lys Val Pro Ile

1 5 10 15
Cys Ile Pro Ala Arg Arg Asp Leu Val Asp Ser Pro Ala Ser Leu Ala
20 25 30
Ser Ser Leu Gly Ser Pro Leu Pro Arg Ala Lys Glu Leu Ile Leu Asn
35 40 45
Asp Leu Pro Ala Ser Thr Pro Ala Ser Lys Ser Cys Asp Ser Ser Pro
50 55 60
Pro Gln Asp Ala Ser Thr Pro Arg Pro Ser Ser Ala Ser His Leu Cys
65 70 75 80
Gln Leu Ala Ala Lys Pro Ala Pro Ser Thr Asp Ser Val Ala Leu Arg
85 90 95
Ser Pro Leu Thr Leu Ser Ser Pro Phe Thr Thr Ser Phe Ser Leu Gly
100 105 110
Ser His Ser Thr Leu Asn Gly Asp Leu Ser Val Pro Ser Ser Tyr Val
115 120 125
Ser Leu His Leu Ser Pro Gln Val Ser Ser Ser Val Val Tyr Gly Arg
130 135 140
Ser Pro Val Met Ala Phe Glu Ser His Pro His Leu Arg Gly Ser Ser
145 150 155 160
Val Ser Ser Ser Leu Pro Ser Ile Pro Gly Gly Lys Pro Ala Tyr Ser
165 170 175
Phe His

<210> 122
<211> 36
<212> PRT
<213> Homo sapien

<400> 122
Met Ser Phe Leu Gly Gly Phe Phe Gly Pro Ile Cys Glu Ile Asp Val
1 5 10 15
Ala Leu Asn Asp Gly Glu Thr Arg Lys Met Ala Glu Met Lys Thr Glu
20 25 30
Asp Gly Lys Val
35

<210> 123
<211> 136
<212> PRT
<213> Homo sapien

<400> 123
Met Ala Ser Pro Gln Leu Cys Arg Ala Leu Val Ser Ala Gln Trp Val
1 5 10 15
Ala Glu Ala Leu Arg Ala Pro Arg Ala Gly Gln Pro Leu Gln Leu Leu
20 25 30
Asp Ala Ser Trp Tyr Leu Pro Lys Leu Gly Arg Asp Ala Arg Arg Glu
35 40 45
Phe Glu Glu Arg His Ile Pro Gly Ala Ala Phe Phe Asp Ile Asp Gln
50 55 60
Cys Ser Asp Arg Thr Ser Pro Tyr Asp His Met Leu Pro Gly Ala Glu
65 70 75 80
His Phe Ala Glu Tyr Ala Gly Arg Leu Gly Val Gly Ala Ala Thr His
85 90 95
Val Val Ile Tyr Asp Ala Ser Asp Gln Gly Leu Tyr Ser Ala Pro Arg
100 105 110
Val Trp Trp Met Phe Arg Ala Phe Gly His His Ala Val Ser Leu Leu

```
        115                 120                 125
Asp Gly Gly Leu Arg His Trp Leu
    130                 135

      <210> 124
      <211> 133
      <212> PRT
      <213> Homo sapien

      <400> 124
Met Asn His Thr Val Gln Thr Phe Phe Ser Pro Val Asn Ser Gly Gln
 1               5                  10                  15
Pro Pro Asn Tyr Glu Met Leu Lys Glu Glu His Glu Val Ala Val Leu
            20                  25                  30
Gly Ala Pro His Asn Pro Ala Pro Pro Thr Ser Thr Val Ile His Ile
        35                  40                  45
Arg Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe Asn
    50                  55                  60
Thr Leu Phe Met Asn Pro Cys Cys Leu Gly Phe Ile Ala Phe Ala Tyr
65                  70                  75                  80
Ser Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly Ala
                85                  90                  95
Gln Ala Tyr Ala Ser Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu Ile
            100                 105                 110
Leu Gly Ile Leu Met Thr Ile Leu Leu Ile Val Ile Pro Val Leu Ile
        115                 120                 125
Phe Gln Ala Tyr Gly
    130

      <210> 125
      <211> 195
      <212> PRT
      <213> Homo sapien

      <400> 125
Thr Thr Ala Thr Thr Thr Ala Ser Thr Gly Ser Thr Ala Thr Pro Ser
 1               5                  10                  15
Ser Thr Pro Gly Thr Ala Pro Pro Pro Lys Val Leu Thr Ser Pro Ala
            20                  25                  30
Thr Thr Pro Met Ser Thr Met Ser Thr Ile His Thr Ser Ser Thr Pro
        35                  40                  45
Glu Thr Thr His Thr Ser Thr Val Leu Thr Thr Thr Ala Thr Met Thr
    50                  55                  60
Arg Ala Thr Asn Ser Thr Ala Thr Pro Ser Ser Thr Leu Gly Thr Thr
65                  70                  75                  80
Arg Ile Leu Thr Glu Leu Thr Thr Thr Ala Thr Thr Thr Ala Ala Thr
                85                  90                  95
Gly Ser Thr Ala Thr Leu Ser Ser Thr Pro Gly Thr Thr Trp Ile Leu
            100                 105                 110
Thr Glu Pro Ser Thr Ile Ala Thr Val Met Val Pro Thr Gly Ser Thr
        115                 120                 125
Ala Thr Ala Ser Ser Thr Leu Gly Thr Ala His Thr Pro Lys Val Val
    130                 135                 140
Thr Thr Met Ala Thr Met Pro Thr Ala Thr Ala Ser Thr Val Pro Ser
145                 150                 155                 160
Ser Ser Thr Val Gly Thr Thr Arg Thr Pro Ala Val Leu Pro Ser Ser
                165                 170                 175
Leu Pro Thr Phe Ser Val Ser Thr Val Ser Ser Ser Val Leu Thr Thr
```

180 185 190
Leu Arg Pro
195

<210> 126
<211> 509
<212> DNA
<213> Homo sapien

<400> 126
gaattcggca cgagccaagt accccctgag gaatctgcag cctgcatctg agtacaccgt 60
atccctcgtg gccataaagg gcaaccaaga gagccccaaa gccactggag tctttaccac 120
actgcagcct gggagctcta ttccacctta caacaccgag gtgactgaga ccaccattgt 180
gatcacatgg acgcctgctc caagaattgg ttttaagctg ggtgtacgac caagccaggg 240
aggagaggca ccacgagaag tgacttcaga ctcaggaagc atcgttgtgt ccggcttgac 300
tccaggagta gaatacgtct acaccatcca agtcctgaga gatggacagg aaagagatgc 360
gccaattgta aacaaagtgg tgacaccatt gtctccacca acaaacttgc atctggaggc 420
aaaccctgac actggagtgc tcacagtctc ctggagagga gcaccacccc agacattact 480
gggtatagaa ttaccacaac ccctacaaa 509

<210> 127
<211> 500
<212> DNA
<213> Homo sapien

<400> 127
gaattcggca cgagccactg atgtccgggg agtcagccag gagcttgggg aagggaagcg 60
cgcccccggg gccggtcccg gagggctcga tccgcatcta cagcatgagg ttctgcccgt 120
ttgctgagag gacgcgtcta gtcctgaagg ccaagggaat caggcatgaa gtcatcaata 180
tcaacctgaa aaataagcct gagtggttct ttaagaaaaa tccctttggt ctggtgccag 240
ttctggaaaa cagtcagggt cagctgatct acgagtctgc catcacctgt gagtacctgg 300
atgaagcata cccagggaag aagctgttgc cggatgaccc ctatgagaaa gcttgccaga 360
agatgatctt agagttgttt tctaaggtgc catccttggt aggaagcttt attagaagcc 420
aaaataaaga agactatgct ggcctaaaag aagaatttcg taaagaattt accaagctag 480
aggaggttct gactaataag 500

<210> 128
<211> 500
<212> DNA
<213> Homo sapien

<400> 128
agctttcctc tgctgccgct cggtcacgct tgtgcccgaa ggaggaaaca gtgacagacc 60
tggagactgc agttctctat ccttcacaca gctctttcac catgcctgga tcacttcctt 120
tgaatgcaga agcttgctgg ccaaaagatg tgggaattgt tgcccttgag atctattttc 180
cttctcaata tgttgatcaa gcagagttgg aaaaatatga tggtgtagat gctggaaagt 240
ataccattgg cttgggccag gccaagatgg gcttctgcac agatagagaa gatattaact 300
ctctttgcat gactgtggtt cagaatctta tggagagaaa taacctttcc tatgattgca 360
ttgggcggct ggaagttgga acagagacaa tcatcgacaa atcaaagtct gtgaagacta 420
atttgatgca gctgtttgaa gagtctggga atacagatat agaaggaatc gacacaacta 480
atgcatgcta tggaggcaca 500

<210> 129
<211> 497
<212> DNA
<213> Homo sapien

<400> 129

gaattcggca cgagcagagg tctccagagc cttctctctc ctgtgcaaaa tggcaactct 60
taaggaaaaa ctcattgcac cagttgcgga agaagaggca acagttccaa acaataagat 120
cactgtagtg ggtgttggac aagttggtat ggcgtgtgct atcagcattc tgggaaagtc 180
tctggctgat gaacttgctc ttgtggatgt tttggaagat aagcttaaag gagaaatgat 240
ggatctgcag catgggagct tatttcttca gacacctaaa attgtggcag ataaagatta 300
ttctgtgacc gccaattcta agattgtagt ggtaactgca ggagtccgtc agcaagaagg 360
ggagagtcgg ctcaatctgg tgcagagaaa tgttaatgtc ttcaaattca ttattcctca 420
gatcgtcaag tacagtcctg attgcatcat aattgtggtt tccaacccag tggacattct 480
tacgtatgtt acctgga 497

<210> 130
<211> 383
<212> DNA
<213> Homo sapien

<400> 130
gaattcggca cgagggccgc ggctgccgac tgggtcccct gccgctgtcg ccaccatggc 60
tccgcaccgc cccgcgcccg cgctgctttg cgcgctgtcc ctggcgctgt gcgcgctgtc 120
gctgcccgtc cgcgcggcca ctgcgtcgcg gggggcgtcc caggcggggg cgcccaggg 180
gcgggtgccc gaggcgcggc ccaacagcat ggtggtggaa caccccgagt tcctcaaggc 240
agggaaggag cctggcctgc agatctggcg tgtggagaaa gttcgatctg gtggcccgtg 300
cccaccaacc tttatggaga cttcttcacg ggcgacgcct acgtcatcct gaagacagtg 360
cagcttaaga acggaaaatc ttg 383

<210> 131
<211> 509
<212> DNA
<213> Homo sapien

<400> 131
gaattcggca cgagagtcag ccgcatcttc ttttgcgtcg ccagccgagc cacatcgctc 60
agacaccatg gggaaggtga aggtcggagt caacggattt ggtcgtattg ggcgcctggt 120
caccagggct gcttttaact ctggtaaagt ggatattgtt gccatcaatg accccttcat 180
tgacctcaac tacatggttt acatgttcca atatgattcc acccatggca aattccatgg 240
caccgtcaag gctgagaacg ggaagcttgt catcaatgga aatcccatca ccatcttcca 300
ggagcgagat ccctccaaaa tcaagtgggg cgatgctggc gctgagtacg tcgtggagtc 360
cactggccgt cttcaccacc atggagaagg ctggggctca tttgcagggg ggagccaaaa 420
gggtcatcat ctctgccccc tctgctgacg cccccatgtt cgtcatgggt gtgaaccatg 480
agaagtatga caacagcctc aagatcatc 509

<210> 132
<211> 357
<212> DNA
<213> Homo sapien

<400> 132
gaattcggca cgagtaagaa gaagccccta gaccacagct ccacaccatg gactggacct 60
ggaggatcct cttcttggtg gcagcagcaa caggtgccca ctcccaggtg caactggtgc 120
aatctgggtc tgagttgaag aagcctgggg cctcagtgaa ggtttcctgc aaggcttctg 180
gacacatctt cagtatctat ggtttgaatt gggtgcgaca ggcccctggt caaggccttg 240
agtggatggg atggatcaaa gtcgacactg cgaacccaac gtatgcccag ggcttcacag 300
gacgatttgt cttctccctg gacacctctg tcagcacggc atatctgcag atcagca 357

<210> 133
<211> 468
<212> DNA
<213> Homo sapien

<400> 133
gaattcggca cgaggcgccc cgaaccgtcc tcctgctgct ctcggcggcc ctggccctga 60
ccgagacctg ggccggctcc cactccatga ggtatttcga caccgccatg tcccggcccg 120
gccgcgggga gccccgcttc atctcagtgg gctacgtgga cgacacgcag ttcgtgaggt 180
tcgacagcga cgccgcgagt ccgagagagg agccgcgggc gccgtggata gagcaggagg 240
ggccggagta ttgggaccgg aacacacaga tcttcaagac caacacacag actgaccgag 300
agagcctgcg gaacctgcgc ggctactaca accagagcga ggccgggtct cacaccctcc 360
agagcatgta cggctgcgac gtggggccgg acgggcgcct cctccgcggg cataaccagt 420
acgcctacga cggcaaggat tacatcgccc tgaacgagga cctgcgct 468

<210> 134
<211> 214
<212> DNA
<213> Homo sapien

<400> 134
gaattcggca cgagctgcgt cctgctgagc tctgttctct ccagcacctc ccaacccact 60
agtgcctggt tctcttgctc caccaggaac aagccaccat gtctcgccag tcaagtgtgt 120
ccttccggag cgggggcagt cgtagcttca gcaccgcctc tgccatcacc ccgtctgtct 180
cccgcaccag cttcacctcc gtgtcccggt ccgg 214

<210> 135
<211> 355
<212> DNA
<213> Homo sapien

<400> 135
gaattcggca cgaggtgaac aggacccgtc gccatgggcc gtgtgatccg tggacagagg 60
aagggcgccg ggtctgtgtt ccgcgcgcac gtgaagcacc gtaaaggcgc tgcgcgcctg 120
cgcgccgtgg atttcgctga gcggcacggc tacatcaagg gcatcgtcaa ggacatcatc 180
cacgacccgg gccgcggcgc gcccctcgcc aaggtggtct tccgggatcc gtatcggttt 240
aagaagcgga cggagctgtt cattgccgcc gagggcattc acacgggcca gtttgtgtat 300
tgcggcaaga aggcccagct caacattggc aatgtgctcc ctgtgggcac catgc 355

<210> 136
<211> 242
<212> DNA
<213> Homo sapien

<400> 136
gaattcggca cgagccagct cctaaccgcg agtgatccgc cagcctccgc ctcccgaggt 60
gcccggattg cagacggagt ctccttcact cagtgctcaa tggtgcccag gctggagtgc 120
agtggtgtga tctcggctcg ctacaacatc cacctcccag cagcctgcct tggcctccca 180
aagtgccgag attgcagctc tctgcccggc cgccacccct gtctgggaag tgaggatgct 240
gt 242

<210> 137
<211> 424
<212> DNA
<213> Homo sapien

<400> 137
gaattcggca cgagcccaga tcccgaggtc cgacagcgcc cggcccagat ccccacgcct 60
gccaggagca agccgagagc cagccggccg gcgcactccg actccgagca gtctctgtcc 120
ttcgacccga gccccgcgcc ctttccggga cccctgcccc gcgggcagcg ctgccaacct 180
gccggccatg gagaccccgt cccagcggcg cgccacccgc agcggggcgc aggccagctc 240
cactccgctg tcgcccaccc gcatcacccg gctgcaggag aaggaggacc tgcaggagct 300
caatgatcgc ttggcggtct acatcgaccg tgtgcgctcg ctggaaacgg agaacgcagg 360

gctgcgcctt cgcatcaccg agtctgaaga ggtggtcagc cgcgaggtgt ccggcatcaa 420
ggcc 424

<210> 138
<211> 448
<212> DNA
<213> Homo sapien

<400> 138
gaattcggca cgagcctgtg ttccaggagc cgaatcagaa atgtcatcct caggcacgcc 60
agacttacct gtcctactca ccgatttgaa gattcaatat actaagatct tcataaacaa 120
tgaatggcat gattcagtga gtggcaagaa atttcctgtc tttaatcctg caactgagga 180
ggagctctgc caggtagaag aaggagataa ggaggatgtt gacaaggcag tgaaggccgc 240
aagacaggct tttcagattg gatccccgtg gcgtactatg gatgcttccg agagggggcg 300
actattatac aagttggctg atttaatcga aagagatcgt ctgctgctgg ccgacaatgg 360
agtcaatgaa tggtggaaaa ctctattcca atgcatatct gaatgattta gcaggctgca 420
tcaaaacatt gcgctactgt gcaggttg 448

<210> 139
<211> 510
<212> DNA
<213> Homo sapien

<400> 139
gaattcggca cgaggttccg tgcagctcac ggagaagcga atggacaaag tcggcaagta 60
ccccaaggag ctgcgcaagt gctgcgagga cggcatgcgg gagaacccca tgaggttctc 120
gtgccagcgc cggacccgtt tcatctccct ggcgaggcgt gcaagaaggt cttcctggac 180
tgctgcaact acatcacaga gctgcggcgg cagcacgcgc gggccagcca cctggcctgc 240
caggagtaac ctggatgagg acatcattgc agaagagaac atcgtttccc gaagtgagtt 300
cccagagagc tggctgtgga acgttgagga cttgaaagag ccaccgaaaa atggaatctc 360
tacgaagctc atgaatatat ttttgaaaga ctccatcacc acgtgggaga ttctggctgt 420
gagcatgtcg gacaagaaag ggatctgtgt ggcagacccc ttcgaggtca cagtaatgca 480
ggacttcttc atcgacctgc ggctacccta 510

<210> 140
<211> 360
<212> DNA
<213> Homo sapien

<400> 140
gaattcggca cgagcggtaa ctaccccggc tgcgcacagc tcggcgctcc ttcccgctcc 60
ctcacacacc ggcctcagcc cgcaccggca gtagaagatg gtgaaagaaa caacttacta 120
cgatgttttg gggggtcaaac ccaatgctac tcaggaagaa ttgaaaaagg cttataggaa 180
actggctttg aagtaccatc ctgataagaa cccaaatgaa ggagagaagt ttaaacagat 240
ttctcaagct tacgaagttc tctctgatgc aaagaaaagg gaattatatg acaaaggagg 300
agaacaggca attaaagagg gtggagcagg tggcggtttt ggctccccca tggacatctt 360

<210> 141
<211> 483
<212> DNA
<213> Homo sapien

<400> 141
gaattcggca cgagagcaga ggctgatctt tgctggaaaa cagctggaag atgggctgca 60
ccctgtctga ctacaacatc cagaaagagt ccaccctgca cctggtgctc cgtctcagag 120
gtgggatgca aatcttcgtg aagacactca ctggcaagac catcaccctt gaggtggagc 180
ccagtgacac catcgagaac gtcaaagcaa agatccagga caaggaaggc attcctcctg 240
accagcagag gttgatcttt gccggaaagc agctggaaga tgggcgcacc ctgtctgact 300

acaacatcca gaaagagtct accctgcacc tggtgctccg tctcagaggt gggatgcaga 360
tcttcgtgaa gaccctgact ggtaagacca tcaccctcga ggtggagccc agtgacacca 420
tcgagaatgt caaggcaaag atccaagata aggaaggcat tcctcctgat cagcagaggt 480
tga 483

<210> 142
<211> 500
<212> DNA
<213> Homo sapien

<400> 142
gaattcggca cgaggcggcg acgaccgccg ggagcgtgtg cagcggcggc ggcggaagtg 60
gccggcgagc ccggtccccg ccggcaccat gcttcccttg tcactgctga agacggctca 120
gaatcacccc atgttggtgg agctgaaaaa tggggagacg tacaatggac acctggtgag 180
ctgcgacaac tggatgaaca ttaacctgcg agaagtcatc tgcacgtcca gggacgggga 240
caagttctgg cggatgcccg agtgctacat ccgcggcagc accatcaagt acctgcgcat 300
ccccgacgag atcatcgaca tggtcaagga ggaggtggtg gccaagggcc gcggccgcgg 360
aggcctgcag cagcagaagc agcagaaagg ccgcggcatg ggcggcgctg gccgaggtgt 420
gtttggtggc cggggccgag gtgggatccc gggcacaggc agaagccagc cagagaagaa 480
gcctggcaga caggcgggca 500

<210> 143
<211> 400
<212> DNA
<213> Homo sapien

<400> 143
gaattcggca cgagctcgga tgtcagcagg cgtcccaacc cagcaggaac tggctcaatt 60
ctcagaagaa agcgatcggc cccgaggcag gaaggccggc tccggtgcag ggcgcgccgc 120
ctgcgggctg cttcgggcca gggtcgaccc gagggccagc gcaagcagcg gcaacaggag 180
cgccaggagg acatgaggct ctgcctgcag tcagcaactt ggaatattca gacttcagac 240
cagcatcaca gattataacc ctccgtaaat catctgcatc ccagctccca tcaaaagcca 300
gcctgaagga cccatggaca cgtgactcca gtgttctcaa caacatctta gatcaagttg 360
gtttgcacaa catttgcatc tacttgggac aaagcaagaa 400

<210> 144
<211> 243
<212> DNA
<213> Homo sapien

<400> 144
gaattcggca cgagccagct cctaaccgcg agtgatccgc cagcctccgc ctcccgaggt 60
gcccggattg cagacggagt ctccttcact cagtgctcaa tggtgcccag gctggagtgc 120
agtggtgtga tctcggctcg ctacaacatc cacctcccag cagcctgcct tggcctccca 180
aagtgccgag attgcagcct ctgcccggcc gtcaccccgt ctgggaagtg aggagcgttt 240
ctg 243

<210> 145
<211> 450
<212> DNA
<213> Homo sapien

<400> 145
gaattcggca cgaggacagc aggaccgtgg aggccgcggc aggggtggca gtggtggcgg 60
cggcggcggc ggcggtggtg gttacaaccg cagcagtggt ggctatgaac ccagaggtcg 120
tggaggtggc cgtggaggca gaggtggcat gggcggaagt gaccgtggtg gcttcaataa 180
atttggtggc cctcgggacc aaggatcacg tcatgactcc gaacaggata attcagacaa 240
caacaccatc tttgtgcaag gcctgggtga gaatgttaca attgagtctg tggctgatta 300

cttcaagcag attggtatta ttaagacaaa caagaaaacg ggacagccca tgattaattt 360
gtacacagac agggaaactg gcaagctgaa gggagaggca acggtctctt ttgatgaccc 420
accttcagct aaagcagcct attgactggt 450

<210> 146
<211> 451
<212> DNA
<213> Homo sapien

<400> 146
gaattcggca cgagccatcg agtccctgcc tttcgacttg cagagaaatg tctcgctgat 60
gcgggagatc gacgcgaaat accaagagat cctgaaggag ctagacgagt gctacgagcg 120
cttcagtcgc gagacagacg gggcgcagaa gcggcggatg ctgcactgtg tgcagcgcgc 180
gctgatccgc accaggagct gggcgacgag aagatccaga tcgtgagcca gatggtggag 240
ctggtggaga accgcacgcg gcaggtggac agccacgtgg agctgttcga ggcgcagcag 300
gagctgggcg acacagcggg caacagcggc aaggctggcg cggacaggcc caaaggcgag 360
gcggcagcgc aggctgacaa gcccaacagc aagcgctcac ggcggcagcg caacaacgag 420
aaccgtgaga acgcgtccag caaccacgac c 451

<210> 147
<211> 400
<212> DNA
<213> Homo sapien

<400> 147
gaattcggca cgagctcgga tgtcagcagg cgtcccaacc cagcaggaac tggctcaatt 60
ctcagaagaa agcgatcggc cccgaggcag gaaggccggc tccggtgcag ggcgcgccgc 120
ctgcgggctg cttcgggcca gggtcgaccc gagggccagc gcaagcagcg gcaacaggag 180
cgccaggagg acatgaggct ctgcctgcag tcagcaactt ggaatattca gacttcagac 240
cagcatcaca gattataacc ctccgtaaat catctgcatc ccagctccca tcaaaagcca 300
gcctgaagga cccatggaca cgtgactcca gtgttctcaa caacatctta gatcaagttg 360
gtttgcacaa catttgcatc tacttgggac aaagcaagaa 400

<210> 148
<211> 503
<212> DNA
<213> Homo sapien

<400> 148
aaaagaattc ggcacgagcg gcgccgctca tccccctctc ccagcagatt cccactggaa 60
attcgttgta tgaatcttat tacaagcagg tcgatccggc atacacaggg agggtggggg 120
cgagtgaagc tgcgcttttt ctaaagaagt ctggcctctc ggacattatc cttgggaaga 180
tatgggactt ggccgatcca gaaggtaaag ggttcttgga caaacagggt ttctatgttg 240
cactgagact ggtggcctgt gcacagagtg gccatgaagt taccttgagc aatctgaatt 300
tgagcatgcc accgcctaaa tttcacgaca ccagcagccc tctgatggtc acaccgccct 360
ctgcagaggc ccactgggct gtgagggtgg aagaaaaggc caaatttgat gggatttttg 420
aaagcctctt gcccatcaat ggtttgctct ctggagacaa agtcaagcca gtcctcatga 480
actcaaagct gcctcttgat gtc 503

<210> 149
<211> 1061
<212> DNA
<213> Homo sapien

<400> 149
gaattcggca cgaggccttt tccagcaacc ccaaggtcca ggtggaggcc atcgaagggg 60
gagccctgca gaagctgctg gtcatcctgg ccacggagca gccgctcact gcaaagaaga 120
aggtcctgtt tgcactgtgc tccctgctgc gccacttccc ctatgcccag cggcagttcc 180

tgaagctcgg ggggctgcag gtcctgagga ccctggtgca ggagaagggc acggaggtgc 240
tcgccgtgcg cgtggtcaca ctgctctacg acctggtcac ggagaagatg ttcgccgagg 300
aggaggctga gctgacccag gagatgtccc cagagaagct gcagcagtat cgccaggtac 360
acctcctgcc aggcctgtgg gaacagggct ggtgcgagat cacggcccac ctcctggcgc 420
tgcccgagca tgatgcccgt gagaaggtgc tgcagacact gggcgtcctc ctgaccacct 480
gccgggaccg ctaccgtcag gacccccagc tcggcaggac actggccagc ctgcaggctg 540
agtaccaggt gctggccagc ctggagctgc aggatggtga ggacgagggc tacttccagg 600
agctgctggg ctctgtcaac agcttgctga aggagctgag atgaggcccc acaccagtac 660
tggactggga tgccgctagt gaggctgagg ggtgccagcg tgggtgggct tctcaggcag 720
gaggacatct tggcagtgct ggcttggcca ttaaatggaa acctgaaggc catcctcttt 780
ctgctgtgtg tctgtgtaga ctgggcacag ccctgtggcc gggggtcag gtgagtggtt 840
gggtgatggg ctctgctgac gtgcagggct cagcccaggg catccaggaa caggctccag 900
ggcaggaacc tgggcccagg agttgcaagt ctctgcttct taccaagcag cagctctgta 960
ccttgggaag tcgcttaatt gctctgagct tgtttcctca tctgtcagga gtgccattaa 1020
aggagaaaaa tcacgtaaaa aaaaaaaaaa aaaaactcga g 1061

<210> 150
<211> 781
<212> DNA
<213> Homo sapien

<400> 150
gaattcggca cgagaaatgg cggcaggggt cgaagcggca gccgaagtgg cggcgacaga 60
acccaaaatg gaggaagaga gcggcgcgcc ctgcgtgccg agcggcaacg gagctccggg 120
cccgaagggt gaagaacgac ctactcagaa tgagaagagg aaggagaaaa acataaaaag 180
aggaggcaat cgctttgagc catattccaa cccaactaaa agatacagag ccttcattac 240
aaatatacct tttgatgtga aatggcagtc acttaaagac ctggttaaag aaaaagttgg 300
tgaggtaaca tacgtggagc tcttaatgga cgctgaagga aagtcaaggg gatgtgctgt 360
tgttgaattc aagatggagg agagcatgaa aaaagctgct gaagttctaa acaagcatag 420
tctgagtgga aggccactga aagtcaagga agatcctgat ggtgaacatg caaggagagc 480
aatgcaaaag gctggaagac ttggaagcac agtatttgta gcaaatctgg attataaagt 540
tggctggaag aaactgaagg aagtatttag tatggctggt gtggtggtcc gagcagacat 600
tctggaagat aaagatggga aaagtcgtgg aataggcatt gtgacttttg aacagtccat 660
tgaagctgtg caagcaatat ctatgtttaa tggccagttg ctgtttgata gaccgatgca 720
cgtcaagatg gatgagaggg ctttaccaaa gggagacttt tttcctcctg aacgccacag 780
c 781

<210> 151
<211> 3275
<212> DNA
<213> Homo sapien

<400> 151
cttaagtgga tcctgcatca ggagggagca gacaccggag aaagaaaaac aagttgtgct 60
gtttgaggaa gcaagttgga cctgcactcc agcctgtgga gatgaaccta ggactgtgat 120
tctgctatcc agtatgttgg ctgaccacag gctcaaactg gaggattata aggatcgcct 180
gaaaagtgga gagcatctta atccagacca gttggaagct gtagagaaat atgaagaagt 240
gctacataat ttggaatttg ccaaggagct tcaaaaaacc ttttctgggt tgagcctaga 300
tctactaaaa gcgcaaaaga aggcccagag aagggagcac atgctaaaac ttgaggctga 360
gaagaaaaag cttcgaacta tacttcaagt tcagtatgta ttgcagaact tgacacagga 420
gcacgtacaa aaagacttca aagggggttt gaatggtgca gtgtatttgc cttcaaaaga 480
acttgactac ctcattaagt tttcaaaact gacctgccct gaaagaaatg aaagtctgag 540
acaaacactt gaaggatcta ctgtctaaat tgctgaactc aggctatttt gaaagtatcc 600
cagttcccaa aaatgccaag gaaaaggaag taccactgga ggaagaaatg ctaatacaat 660
cagagaaaaa aacacaatta tcgaagactg aatctgtcaa agagtcagag tctctaatgg 720
aatttgccca gccagagata caaccacaag agtttcttaa cagacgctat atgacagaag 780
tagattattc aaacaaacaa ggcgaagagc aacccttggga agcagattat gctagaaaac 840
caaatctccc aaaacgttgg gatatgctta ctgaaccaga tggtcaagag aagaaacagg 900

agtcctttaa gtcctgggag gcttctggta agcaccagga ggtatccaag cctgcagttt 960
ccttagaaca gaggaaacaa gacacctcaa aactcaggtc tactctgccg gaagagcaga 1020
agaagcagga gatctccaaa tccaagccat ctcctagcca gtggaagcaa gatacaccta 1080
aatccaaagc agggtatgtt caagaggaac aaaagaaaca ggagacacca aagctgtggc 1140
cagttcagct gcagaaagaa caagatccaa agaagcaaac tccaaagtct tggacacctt 1200
ccatgcagag cgaacagaac accaccaagt catggaccac tcccatgtgt gaagaacagg 1260
attcaaaaca gccagagact ccaaaatcct gggaaaacaa tgttgagagt caaaaacact 1320
ctttaacatc acagtcacag atttctccaa agtcctgggg agtagctaca gcaagcctca 1380
taccaaatga ccagctgctg cccaggaagt tgaacacaga acccaaagat gtgcctaagc 1440
ctgtgcatca gcctgtaggt tcttcctcta cccttccgaa ggatccagta ttgaggaaag 1500
aaaaactgca ggatctgatg actcagattc aaggaacttg taactttatg caagagtctg 1560
ttcttgactt tgacaaacct tcaagtgcaa ttccaacgtc acaaccgcct tcagctactc 1620
caggtagccc cgtagcatct aaagaacaaa atctgtccag tcaaagtgat tttcttcaag 1680
agccgttaca ggtatttaac gttaatgcac ctctgcctcc acgaaaagaa caagaaataa 1740
aagaatcccc ttattcacct ggctacaatc aaagtttac cacagcaagt acacaaacac 1800
caccccagtg ccaactgcca tctatacatg tagaacaaac tgtccattct caagagactg 1860
cagcaaatta tcatcctgat ggaactattc aagtaagcaa tggtagcctt gccttttacc 1920
cagcacagac gaatgtgttt cccagaccta ctcagccatt tgtcaatagc cggggatctg 1980
ttagaggatg tactcgtggt gggagattaa taaccaattc ctatcggtcc cctggtggtt 2040
ataaaggttt tgatacttat agaggactcc cttcaatttc caatggaaat tatagccagc 2100
tgcagttcca agctagagag tattctggag caccttattc ccaaagggat aatttccagc 2160
agtgttataa gcgaggaggg acatctggtg gtccacgagc aaattcgaga gcagggtgga 2220
gtgattcttc tcaggtgagc agcccagaaa gagacaacga aacctttaac agtggtgact 2280
ctggacaagg agactcccgt agcatgaccc ctgtggatgt gccagtgaca aatccagcag 2340
ccaccatact gccagtacac gtctaccctc tgcctcagca gatgcgagtt gccttctcag 2400
cagccagaac ctctaatctg gcccctggaa ctttagacca acctattgtg tttgatcttc 2460
ttctgaacaa cttaggagaa actttgatc ttcagcttgg tagatttaat tgcccagtga 2520
atggcactta cgttttcatt tttcacatgc taaagctggc agtgaatgtg ccactgtatg 2580
tcaacctcat gaagaatgaa gaggtcttgg tatcagccta tgccaatgat ggtgctccag 2640
accatgaaac tgctagcaat catgcaattc ttcagctctt ccagggagac cagatatggt 2700
tacgtctgca caggggagca atttatggaa gtagctggaa atattctacg ttttcaggct 2760
atcttcttta tcaagattga aagtcagtac agtattgaca ataaaaggat ggtgttctaa 2820
ttagtgggat tgaaggaaaa gtagtctttg ccctcatgac tgattggttt aggaaaatgt 2880
ttttgttcct agagggagga ggtccttact tttttgtttt ccttcctgag gtgaaaaatc 2940
aagctgaatg acaattagca ctaatctggc actttataaa ttgtgatgta gcctcgctag 3000
tcaagctgtg aatgtatatt gtttgcactt aatccttaac tgtattaacg ttcagcttac 3060
taaactgact gcctcaagtc caggcaagtt acaatgcctt gttgtgcctc aataaaaaag 3120
ttacatgcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3180
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3240
aaaaaaaaaa aaaaaaaaaa aaaaaaaaac tcgag 3275

<210> 152
<211> 2179
<212> DNA
<213> Homo sapien

<400> 152
gaattcggca ccaggcacta ttaaatgtga ggcagcctcc atctactaca acatttgtgc 60
tgaatcaaat aaatcatctt ccacccttgg gatctacaat tgtaatgact aaaacaccac 120
ctgtaacaac caacaggcaa accatcactt taactaagtt tatccagact actgcaagca 180
cacgcccgtc agtctcagca ccaacagtac gaaatgccat gacctctgca ccttcaaaag 240
accaagttca gcttaaagat ctactgaaaa ataatagtct taatgaactg atgaaactaa 300
agccacctgc taatattgct cagccagtag caacagcagc tactgatgta agcaatggta 360
cagtaaagaa agagtcttct aataaagaag gagctagaat gtggataaac gacatgaaga 420
tgaggagttt ttccccaacc atgaaggttc ctgttgtaaa agaagatgat gaaccagagg 480
aagaagatga agaagaaatg ggtcatgcag aaacctatgc agaatacatg ccaataaaat 540
taaaaattgg cctacgtcat ccagatgctg tagtggaaac cagctcttta tccagtgtta 600
ctcctcctga tgtttggtac aaaacatcca tttctgagga aaccattgat aatggctggt 660

```
tatcagcatt gcagcttgag gcaattacat atgcagccca gcaacatgaa actttcctac     720
ctaatggaga tcgtgctggc ttcttaatag gtgatggtgc cggtgtagga aaaggaagga     780
cgatagcagg aatcatctat gaaaattatt tgttgagtag aaaacgagca ttgtggttta     840
gtgtttcaaa tgacttaaag tatgatgctg aaagagattt aagggatatt ggagcaaaaa     900
acattttggt tcattcgtta aataagttta aatacggaaa aatttcttcc aaacataatg     960
ggagtgtgaa aaagggtgtt atttttgcta cttactcttc acttattggt gaaagccagt    1020
ctggcggcaa gtataaaact aggttaaaac aacttctgca ttggtgcggt gatgacttcg    1080
atggagtgat agtgtttgat gagtgtcata aagccaaaaa cttatgtcct gttggttctt    1140
caaagccaac caagacaggc ttagcagttt tagagcttca gaacaaattg ccaaaagcca    1200
gagttgttta tgctagtgca actggtgctt ctgaaccacg caacatggcc tatatgaacc    1260
gtcttggcat atggggtgag ggtactccat ttagagaatt cagtgatttt attcaagcag    1320
tagaacggag aggagttggt gccatggaaa tagttgctat ggatatgaag cttagaggaa    1380
tgtacattgc tcgacaactg agctttactg gagtgacctt caaaattgag gaagttcttc    1440
tttctcagag ctacgttaaa atgtataaca aagctgtcaa gctgtgggtc attgccagag    1500
agcggtttca gcaagctgca gatctgattg atgctgagca acgaatgaag aagtccatgt    1560
ggggtcagtt ctggtctgct caccagaggt tcttcaaata cttatgcata gcatccaaag    1620
ttaaaagggt tgtgcaacta gctcgagagg aaatcaagaa tggaaaatgt gttgtaattg    1680
gtctgcagtc tacaggagaa gctagaacat tagaagcttt ggaagagggc gggggagaat    1740
tgaatgattt tgtttcaact gccaaaggtg tgttgcagtc actcattgaa aaacattttc    1800
ctgctccaga caggaaaaaa ctttatagtt tactaggaat cgatttgaca gctccaagta    1860
acaacagttc gccaagagat agtccttgta aagaaaataa aataaagaag cggaaaggtg    1920
aagaaataac tcgagaagcc aaaaaagcac gaaaagtagg tggccttact ggtagcagtt    1980
ctgacgacag tggaagtgaa tctgatgcct ctgataatga agaaagtgac tatgagagct    2040
ctaaaaacat gagttctgga gatgatgacg atttcaaccc atttttagat gagtctaatg    2100
aggatgatga aaatgatccc tggttaatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa    2160
aaaaaaaaaa aaactcgag                                                 2179
```

<210> 153
<211> 2109
<212> DNA
<213> Homo sapien

<400> 153

```
cagagagccc caggcatcga ggagaaggcg gcggagaatg gggccctggg gtcccccgag      60
agagaagaga aagtgctgga gaatggggag ctgacacccc caaggaggga ggagaaagcg     120
ctggagaatg gggagctgag gtccccagag gccggggaga aggtgctggt gaatgggggc     180
ctgacacccc caaagagcga ggacaaggtg tcagagaatg gggcctgag attccccagg      240
aacacggaga ggccaccaga gactgggcct tggagagccc cagggccctg ggagaagacg     300
cccgagagtt ggggtccagc ccccacgatc ggggagccag ccccagagac ctctctggag     360
agagcccctg cacccagcgc agtggtctcc tcccggaacg gcggggagac agcccctggc     420
cccctggcc cagcccccaa gaacgggacg ctggaacccg ggaccgagag gagagccccc      480
gagactgggg gggcgccgag agccccaggg gctgggaggc tggacctcgg gagtgggggc     540
cgagccccag tgggcacggg gacggccccc ggcggcggcc ccggaagcgg cgtggacgca     600
aaggccggat gggtagacaa cacgaggccg cagccaccgc cgccaccgct gccaccgcca     660
ccggaggcac agccgaggag gctggagcca gcgcccccga gagccaggcc ggaggtggcc     720
cccgagggag agcccggggc cccagacagc agggccggcg gagacacggc actcagcgga     780
gacggggacc cccccaagcc cgagaggaag ggccccgaga tgccacgact attcttggac     840
ttgggacccc ctcaggggaa cagcgagcag atcaaagcca ggctctcccg gctctcgctg     900
gcgctgccgc cgctcacgct cacgccattc ccggggccgg gcccgcggcg gcccccgtgg     960
gagggcgcgg acgccggggc ggctggcggg gaggccggcg gggcgggagc gccggggccg    1020
gcggaggagg acggggagga cgaggacgag gacgaggagg aggacgagga ggcggcggcg    1080
ccgggcgcgg cggcggggcc gcggggcccc gggagggcgc gagcagcccc ggtgcccgtc    1140
gtggtgagca gcgccgacgc ggacgcggcc cgcccgctgc gggggctgct caagtctccg    1200
cgcggggccg acgagccaga ggacagcgag ctggagagga agcgcaagat ggtctccttc    1260
cacggggacg tgaccgtcta cctcttcgac caggagacgc caaccaacga gctgagcgtc    1320
caggcccccc ccgagggggga cacggacccg tcaacgcctc cagcgccccc gacacctccc    1380
caccccgcca cccccggaga tgggtttccc agcaacgaca gcggctttgg aggcagtttc    1440
gagtgggcgg aggatttccc cctcctcccc cctccaggcc ccccgctgtg cttctcccgc    1500
```

ttctccgtct cgcctgcgct ggagaccccg gggccacccg cccgggcccc cgacgcccgg 1560
cccgcaggcc ccgtggagaa ttgattcccc gaagacccga ccccgctgca ccctcagaag 1620
aggggttgag aatggaatcc tctgtggatg acggcgccac tgccaccacc gcagacgccg 1680
cctctgggga ggcccccgag gctgggccct cccccctccca ctcccctacc atgtgccaaa 1740
cgggaggccc cgggcccccg cccccccagc cccccagatg gctcccctga ccccccctgac 1800
cccctcggag ccaaatgagg caggaatccc cccgcccctc catagagagc cgcctttctc 1860
ggaactgaac tgaactcttt tgggcctgga gcccctcgac acagcggagg tccctcctca 1920
cccactcctg gcccaagaca ggggccgcag gcttcgggga cccggacccc ccatttcgcg 1980
tctccccttt ccctccccag cccggcccct ggaggggcct ctggttcaaa ccttcgcgtg 2040
gcattttcac attatttaaa aaagacaaaa acaacttttt ggaggaaaaa aaaaaaaaaa 2100
aaactcgag 2109

<210> 154
<211> 1411
<212> DNA
<213> Homo sapien

<400> 154
gaattcggca ccaggggaga tgaggaagtt cgatgttcct agcatggagt ctacccttaa 60
ccagccagcc atgctagaga cgttatactc agatccacat taccgagccc atttccccaa 120
cccaagacct gatacaaata aggatgtata caaagtattg ccagaatcca agaaggcacc 180
gggcagtggt gcagtatttg agaggaacgg accacatgct agcagtagtg ggtgctccc 240
tttgggactc cagcctgcgc ctggactttc caagtcacta tcctctcagg tgtggcaacc 300
aagtcctgac ccttggcatc ctggagaaca atcctgtgaa ctcagtactt gtcgacagca 360
gttggaattg atccgtttac agatggagca aatgcagctt cagaacggag ccatgtgtca 420
ccatcctgct gctttcgctc cattactgcc caccctagag ccagcacagt ggctcagcat 480
cctgaacagt aacgagcatc tcctgaagga gaaggagctc ctcattgaca agcaaaggaa 540
gcatatctct cagctggagc agaaagtgcg agagagtgaa ctgcaagtcc acagtgccct 600
tttgggccgc cctgcccccct ttggggatgt ctgcttattg aggctacagg agttgcagcg 660
agagaacact ttcttacggg cacagtttgc acagaagaca gaagccctga gcaaggagaa 720
gatggagctt gaaaagaaac tctctgcatc tgaagttgaa attcagctca ttagggagtc 780
tctaaaagtg acactacaga agcattcgga ggaggggaag aaacaggagg aaagggtcaa 840
aggtcgtgat aaacatatca ataatttgaa aaagaaatgt cagaaggaat cagagcagaa 900
ccgggagaag cagcagcgta ttgaaacctt ggagcgctat ctagctgacc tgcccaccct 960
agaagaccat cagaaacaga cggagcagct taaggacgct gaattaaaga acacagaact 1020
gcaagagaga gtggctgagc tggagacttt gctggaggac acccaggcaa cctgcagaga 1080
gaaggaggtt cagctggaaa gtctgagaca aagagaagca gacctctcct ctgctagaca 1140
taggtaatgc cctgtgtact tgggggaagg agggagttcg gttctggtgc tctgttaact 1200
cttgtgtgtt caacagtgtt catttcaagt tcctttcttc taagagcttt gtgttctttg 1260
aattgaaagt cacttatggc cgggtgtggt ggcgcacacc tttaatccca gcacttggga 1320
gtcagaggca ggctaatttc tgagtttcag gacagccagg gctatacaga gaaaccctgt 1380
ctcaaacaaa aaaaaaaaaa aaaaactcga g 1411

<210> 155
<211> 678
<212> DNA
<213> Homo sapien

<400> 155
ctggagtgaa gggagctagt ggtaaaggga gctggtggag gggtggcggc aggggtaagg 60
ggcaggggac accctctaga cggagagcgg gctccgaggt cctggctggc cctcggtgcg 120
cccgcccctg tgttggtccc acaatccctg gcaatgagag gccagggttt attggacaga 180
gtcagttgtg ggttcagag ggtcagcaat caatcaatcc tccgaatcca gagatttaga 240
cccagtcgtc cgtattagga ctggaggggg gtcaataggt tcagtgtttg agatgccaag 300
ggaacctgtc ttttgatttg ggttcaaca tacagagttc aggtacctgc aggaatttgc 360
ccccctaggc acagggggtg gtctttacca ttttcgagac cagatcctgg ctgggagccc 420
cgaggcattc ttcgtgctca atgctgatgt ctgctccgac ttccccttga gtgctatgtt 480
ggaagcccac cgacgccagc gtcacccttt cttactcctt ggcactacgg ctaacaggac 540

gcaatccctc aactacggct gcatcgttga gaatccacag acacacgagg tattgcacta 600
tgtggagaaa cccagcacat ttatcagtga catcatcaac tgcggcacct acctcttttc 660
tcctgaagcc ttgaagcc 678

<210> 156
<211> 2668
<212> DNA
<213> Homo sapien

<400> 156
gggaaggcgg ctgcgctgct gggcgggggc gggagctgga gccggagctg gagccggggc 60
cggggcccgg gtcagcgctt gagccgggag aagagtttga gatcgtggac cgaagccagc 120
tgcccggccc aggcgacctg cggagcgcaa cgaggccgcg ggcggccgag ggctggtcgg 180
cgcccatcct gaccctggca cgcagggcca ccgggaacct gtcggcgagc tgcgggagcg 240
cgctgcgcgc ggccgcgggg ctgggcggcg gggacagcgg ggacggcacg gcgcgcgcag 300
cttctaagtg ccagatgatg gaggagcgtg ccaacctgat gcacatgatg aaactcagca 360
tcaaggtgtt gctccagtcg gctctgagcc tgggccgcag cctggatgcg gaccatgccc 420
ccttgcagca gttctttgta gtgatggagc actgcctcaa acatgggctg aaagttaaga 480
agagttttat tggccaaaat aaatcattct ttggtccttt ggagctggtg gagaaacttt 540
gtccagaagc atcagatata gcgactagtg tcagaaatct tccagaatta aagacagctg 600
tgggaagagg ccgagcgtgg ctttatcttg cactcatgca aaagaaactg gcagattatc 660
tgaaagtgct tatagacaat aaacatctct taagcgagtt ctatgagcct gaggctttaa 720
tgatggagga agaagggatg gtgattgttg gtctgctggt gggactcaat gttctcgatg 780
ccaatctctg cttgaaagga gaagacttgg attctcaggt tggagtaata gatttttccc 840
tctaccttaa ggatgtgcag gatcttgatg gtggcaagga gcatgaaaga attactgatg 900
tccttgatca aaaaaattat gtggaagaac ttaaccggca cttgagctgc acagttgggg 960
atcttcaaac caagatagat ggcttggaaa agactaactc aaagcttcaa gaagagcttt 1020
cagctgcaac agaccgaatt tgctcacttc aagaagaaca gcagcagtta agagaacaaa 1080
atgaattaat tcgagaaaga agtgaaaaga gtgtagagat aacaaaacag gataccaaag 1140
ttgagctgga gacttacaag caaactcggc aaggtctgga tgaaatgtac agtgatgtgt 1200
ggaagcagct aaaagaggag aagaaagtcc ggttggaact ggaaaaagaa ctggagttac 1260
aaattggaat gaaaaccgaa atggaaattg caatgaagtt actggaaaag gacacccacg 1320
agaagcagga cacactagtt gccctccgcc agcagctgga agaagtcaaa gcgattaatt 1380
tacagatgtt tcacaaagct cagaatgcag agagcagttt gcagcagaag aatgaagcca 1440
tcacatcctt tgaaggaaaa accaaccaag ttatgtccag catgaaacaa atggaagaaa 1500
ggttgcagca ctcggagcgg gcgaggcagg gggctgagga gcggagccac aagctgcagc 1560
aggagctggg cgggaggatc ggcgccctgc agctgcagct ctcccagctg cacgagcaat 1620
gctcaagcct ggagaaagaa ttgaaatcag aaaaagagca aagacaggct cttcagcgcg 1680
aattacagca cgagaaagac acttcctctc tactcaggat ggagctgcaa caagtggaag 1740
gactgaaaaa ggagttgcgg gagcttcagg acgagaaggc agagctgcag aagatctgcg 1800
aggagcagga acaagccctc caggaaatgg gcctgcacct cagccagtcc aagctgaaga 1860
tggaagatat aaaagaagtg aaccaggcac tgaagggcca cgcctggctg aaagatgacg 1920
aagcgacaca ctgtaggcag tgtgagaagg agttctccat ttcccggaga aagcaccact 1980
gccggaactg tggccacatc ttctgcaaca cctgctccag caacgagctg gccctgccct 2040
cctaccccaa gccggtgcga gtgtgcgaca gctgccacac cctgctcctg cagcgctgct 2100
cctccacggc ctcctgaacg tccgtcctca ggagcacagc ctcacggaca gtgccaaacc 2160
ctgtgggtct ccaggggctt gggaaatgtg ttctttccca agagtatcaa aggaaagaat 2220
caaatttctt gcccggtcac tggcactcca gaagacagcg tgccggaacc ggcagctctc 2280
acctttctgt gacttgttcg gaattaactc ctctggatgg aaacttccat cttacttggt 2340
tacatcacgg ctctggttca gatacaactt catgattttg ctactatcat ttttcacttt 2400
tcaaagaatt taacctattt tacagcagtt cagttctgct agtgagtagt tttcctctcc 2460
taccttcctt ctaaaaacct gattcatgca cagcgtttga cacacatgga gtctgccagt 2520
gtgccttctc tgcttcagac aagagatctg ccatttcatg cccttgtgac tacctatcat 2580
tggccctgca ataaaatcat ttatttttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2640
aaaaaaaaaa aaaaaaaaaa aactcgag 2668

<210> 157
<211> 2313

<212> DNA
<213> Homo sapien

<400> 157
gaattcggca ccaggccggg cgggcgcctc agccatggcc ctgcgcaagg aactgctcaa 60
gtccatctgg tacgccttta ccgcgctgga cgtggagaag agtggcaaag tctccaagtc 120
ccagctcaag gtgctgtccc acaacctgta cacggtcctg cacatccccc atgaccccgt 180
ggccctggag gaacacttcc gagatgatga tgacggccct gtgtccagcc agggatacat 240
gccctacctc aacaagtaca tcctggacaa ggtggaggag ggggcttttg ttaaagagca 300
ctttgatgag ctgtgctgga cgctgacggc caagaagaac tatcgggcag atagcaacgg 360
gaacagtatg ctctccaatc aggatgcctt ccgcctctgg tgcctcttca acttcctgtc 420
tgaggacaag taccctctga tcatggttcc tgatgaggtg gaatacctgc tgaaaaaggt 480
actcagcagc atgagcttgg aggtgagctt gggtgagctg gaggagcttc tggcccagga 540
ggcccaggtg gcccagacca ccgggggct cagcgtctgg cagttcctgg agctcttcaa 600
ttcgggccgc tgcctgcggg gcgtgggccg ggacaccctc agcatggcca tccacgaggt 660
ctaccaggag ctcatccaag atgtcctgaa gcagggctac ctgtggaagc gagggcacct 720
gagaaggaac tgggccgaac gctggttcca gctgcagccc agctgcctct gctactttgg 780
gagtgaagag tgcaaagaga aaaggggcat tatcccgctg gatgcacact gctgcgtgga 840
ggtgctgcca gaccgcgacg gaaagcgctg catgttctgt gtgaagacag ccacccgcac 900
gtatgagatg agcgcctcag acacgcgcca gcgccaggag tggacagctg ccatccagat 960
ggcgatccgg ctgcaggccg aggggaagac gtccctacac aaggacctga agcagaaacg 1020
gcgcgagcag cgggagcagc gggagcggcg ccgggcggcc aaggaagagg agctgctgcg 1080
gctgcagcag ctgcaggagg agaaggagcg gaagctgcag gagctggagc tgctgcagga 1140
ggcgcagcgg caggccgagc ggctgctgca ggaggaggag gaacggcgcc gcagccagca 1200
ccgcgagctg cagcaggcgc tcgagggcca actgcgcgag gcggagcagg cccgggcctc 1260
catgcaggct gagatggagc tgaaggagga ggaggctgcc cggcagcggc agcgcatcaa 1320
ggagctggag gagatgcagc agcggttgca ggaggccctg caactagagg tgaaagctcg 1380
gcgagatgaa gaatctgtgc gaatcgctca gaccagactg ctggaagagg aggaagagaa 1440
gctgaagcag ttgatgcagc tgaaggagga gcaggagcgc tacatcgaac gggcgcagca 1500
ggagaaggaa gagctgcagc aggagatggc acagcagagc cgctccctgc agcaggccca 1560
gcagcagctg gaggaggtgc ggcagaaccg gcagagggct gacgaggatg tggaggctgc 1620
ccagagaaaa ctgcgccagg ccagcaccaa cgtgaaacac tggaatgtcc agatgaaccg 1680
gctgatgcat ccaattgagc ctggagataa gcgtccggtc acaagcagct ccttctcagg 1740
cttccagccc cctctgcttg cccaccgtga ctcctcccta aagcgcctga cccgctgggg 1800
atcccagggc aacaggaccc cctcgcccaa cagcaatgag cagcagaagt ccctcaatgg 1860
tggggatgag gctcctgccc cggcttccac ccctcaggaa gataaactgg atccagcacc 1920
agaaaattag cctctcttag ccccttgttc ttcccaatgt catatccacc aggacctggc 1980
cacagctggc ctgtgggtga tcccagctct tactaggaga gggagctgag gtcctggtgc 2040
caggggccca ggccctccaa ccataaacag tccaggatgg aacctggttc acccttcata 2100
ccagctccaa gccccagacc atgggagctg tctgggatgt tgatccttga gaacttggcc 2160
ctgtgcttta gacccaagga cccgattcct gggctaggaa agagagaaca agcaagccgg 2220
ggctacctgc cccaggtgg ccaccaagtt gtggaagcac atttctaaat aaaaactgct 2280
cttagaatga aaaaaaaaa aaaaaaactc gag 2313

<210> 158
<211> 2114
<212> DNA
<213> Homo sapien

<400> 158
gaattcggca cgaggaagaa ctcgcctctg ttgagtgtaa gtagccaaac aataaccaag 60
gagaataaca gaaatgtcca tttggagcac tcagagcaga atcctggttc atcagcaggt 120
gacacctcag cagcgcacca ggtggtttta ggagaaaact tgatagccac agccctttgt 180
ctttctggca gtgggtctca gtctgatttg aaggatgtgg ccagcacagc aggagaggag 240
ggggacacaa gccttcggga gagcctccat ccagtcactc ggtctcttaa ggcagggtgc 300
catactaagc agcttgcctc caggaattgc tctgaagaga aatccccaca aacctccatc 360
ctaaaggaag gtaacaggga cacaagcttg gatttccgac ctgtagtgtc tccagcaaat 420
ggggttgaag gagtccgagt ggatcaggat gatgatcaag atagctcttc cctgaagctt 480

tctcagaaca ttgctgtaca gactgacttt aagacagctg attcagaggt aaacacagat 540
caagatattg aaaagaattt ggataaaatg atgacagaga gaaccctgtt gaaagagcgt 600
taccaggagg tcctggacaa acagaggcaa gtggagaatc agctccaagt gcaattaaag 660
cagcttcagc aaaggagaga agaggaaatg aagaatcacc aggagatatt aaaggctatt 720
caggatgtga caataaagcg ggaagaaaca aagaagaaga tagagaaaga gaagaaggag 780
tttttgcaga aggagcagga tctgaaagct gaaattgaga agctttgtga gaagggcaga 840
agagaggtgt gggaaatgga actggataga ctcaagaatc aggatggcga aataaatagg 900
aacattatgg aagagactga acgggcctgg aaggcagaga tcttatcact agagagccgg 960
aaagagttac tggtactgaa actagaagaa gcagaaaaag aggcagaatt gcaccttact 1020
tacctcaagt caactccccc aacactggag acagttcgtt ccaaacagga gtgggagacg 1080
agactgaatg gagttcggat aatgaaaaag aatgttcgtg accaatttaa tagtcatatc 1140
cagttagtga ggaacggagc caagctgagc agccttcctc aaatccctac tcccacttta 1200
cctccacccc catcagagac agacttcatg cttcaggtgt ttcaacccag tccctctctg 1260
gctcctcgga tgcccttctc cattgggcag gtcacaatgc ccatggttat gcccagtgca 1320
gatccccgct ccttgtcttt cccaatcctg aaccctgccc tttcccagcc cagccagcct 1380
tcctcacccc ttcctggctc ccatggcaga aatagccctg gcttgggttc ccttgtcagc 1440
cctggtgccg aattcggcac gaggtaccac tggtctgtgt gctagaggag ggtgttgcca 1500
tagaaccagt ggccacagtt gtggtggtgg tggtcagcac tgtgggggtg tgggtggtcc 1560
ccgggacgga ggaggggtc accgtgaagc cactggttgt gggtgtggtg gttgtgctga 1620
tccacactgg aggcgtgcgt gccgtccctg ggctgaagga gggggtgact gtgaagcccg 1680
tggttgtggt agtcggcact ttggtagtgt gagctgttcc tggggtggaa gagggggtgg 1740
ccacagagcc ggtggccctg gttgtggtgg ccgtggtggt aagcactgtg gaggtgtggg 1800
cagtctctgg agtggaggag ggtgtggctg tggacatggt ggccgtgggt gtggtggtct 1860
gtgataggcg ggtccaggtg gtgcccaggg aggaggaggg gatggctgta aagctggtag 1920
ctgtgggtgt ggtggctgtg cttctcagtg ctggaagggc ggttgcagtc cctggactgg 1980
agaagggagt ggctttggag ctggtgactg tgggtgtcgt ggccgtggtg ctcacatgtg 2040
gggtgccagc agttgcctgg gtggaggagg cggtggccgt ggatccggtg ggcaccgtca 2100
cgggagtact tcta 2114

<210> 159
<211> 278
<212> DNA
<213> Homo sapien

<400> 159
gaattcggca caggtaactt tgcctggggt atttaaaaaa aaaaaaaaaa aaaaaaaaag 60
tcaaatatct gagtactaat ttcctgaaaa gtatgttccg atagatgaac agatcattaa 120
tgcagaatga gaatcactcc taaaataggt aatggtaaaa attaaattga caattacctc 180
tctctatgca gaaggaaata tcacctatat gacatcatca tcatctattg atacttgctg 240
gcagtgctaa taatggtttt aatgccaatt tgtaagaa 278

<210> 160
<211> 848
<212> DNA
<213> Homo sapien

<400> 160
gaattcggca cgagccccag aggagctcgg cctgcgctgc gccacgatgt ccggggagtc 60
agccaggagc ttggggaagg gaagcgcgcc cccggggccg gtcccggagg gctcgatccg 120
catctacagc atgaggttct gcccgtttgc tgagaggacg cgtctagtcc tgaaggccaa 180
gggaatcagg catgaagtca tcaatatcaa cctgaaaaat aagcctgagt ggttctttaa 240
gaaaaatccc tttggtctgg tgccagttct ggaaaacagt cagggtcagc tgatctacga 300
gtctgccatc acctgtgagt acctggatga agcataccca gggaagaagc tgttgccgga 360
tgacccctat gagaaagctt gccagaagat gatcttagag ttgttttcta aggtgccatc 420
cttggtagga agctttatta gaagccaaaa taaagaagac tatgctggcc taaaagaaga 480
atttcgtaaa gaatttacca agctagagga ggttctgact aataagaaga cgaccttctt 540
tggtggcaat tctatctcta tgattgatta cctcatctgg ccctggtttg aacggctgga 600
agcaatgaag ttaaatgagt gtgtagacca cactccaaaa ctgaaactgt ggatggcagc 660

catgaaggaa gatcccacag tctcagccct gcttactagt gagaaagact ggcaaggttt 720
cctagagctc tacttacaga acagccctga ggcctgtgac tatgggctct gaagggggca 780
ggagtcagca ataaagctat gtctgatatt ttccttcact aaaaaaaaaa aaaaaaaaaa 840
aactcgag 848

<210> 161
<211> 432
<212> DNA
<213> Homo sapien

<400> 161
gaattcggca cgagggcaga ccaagatcct ggaggaggac ctggaacaga tcaagctgtc 60
cttgagagag cgaggccggg agctgaccac tcagaggcag ctgatgcagg aacgggcaga 120
ggaagggaag ggcccaagta aagcacagcg cgggagccta gagcacatga agctgatcct 180
gcgtgataag gagaaggagg tggaatgtca gcaggagcat atccatgaac tccaggagct 240
caaagaccag ctggagcagc agctccaggg cctgcacagg aaggtaggtg agaccagcct 300
cctcctgtcc cagcgagagc aggaaatagt ggtcctgcag cagcaactgc aggaagccag 360
ggaacaaggg gagctgaagg agcagtcact tcagagtcaa ctggatgagg cccagagagc 420
cctagcccag ag 432

<210> 162
<211> 433
<212> DNA
<213> Homo sapien

<400> 162
gattcggcac gagccggagc tgggttgctc ctgctcccgt ctccaagtcc tggtacctcc 60
ttcaagctgg gagagggctc tagtccctgg ttctgaacac tctggggttc tcgggtgcag 120
gccgccatga gcaaacggaa ggcgccgcag gagactctca acgggggaat caccgacatg 180
ctcacagaac tcgcaaactt tgagaagaac gtgagccaag ctatccacaa gtacaatgct 240
tacagaaaag cagcatctgt tatagcaaaa tacccacaca aaataaagag tggagctgaa 300
gctaagaaat tgcctggagt aggaacaaaa attgctgaaa agattgatga gtttttagca 360
actggaaaat tacgtaaact ggaaaagatt cggcaggatg atacgagttc atccatcaat 420
ttcctgactc gag 433

<210> 163
<211> 432
<212> DNA
<213> Homo sapien

<400> 163
gaattcggca ccagatgagg ccaacgaggt gacggacagc gcgtacatgg gctccgagag 60
cacctacagt gagtgtgaga ccttcacgga cgaggacacc agcaccctgg tgcaccctga 120
gctgcaacct gaaggggacg cagacagtgc cggcggctcg gccgtgccct ctgagtgcct 180
ggacgccatg gaggagcccg accatggtgc cctgctgctg ctcccaggca ggcctcaccc 240
ccatggccag tctgtcatca cggtgatcgg gggcgaggag cactttgagg actacggtga 300
aggcagtgag gcggagctgt ccccagagac cctatgcaac gggcagctgg gctgcagtga 360
ccccgctttc ctcacgccca gtccgacaaa gcggctctcc agcaagaagg tggcaaggta 420
cctgcaccag tc 432

<210> 164
<211> 395
<212> DNA
<213> Homo sapien

<400> 164
gacacttgaa tcatgggtga cgttaaaaat tttctgtatg cctggtgtgg caaaaggaag 60
atgaccccat cctatgaaat tagagcagtg ggaacaaaaa acaggcagaa attcatgtgt 120

```
gaggttcagg tggaaggtta taattacact ggcatgggaa attccaccaa taaaaaagat     180
gcacaaagca atgctgccag agactttgtt aactatttgg ttcgaataaa tgaaataaag     240
agtgaagaag ttccagcttt tggggtagca tctccgcccc cacttactga tactcctgac     300
actacagcaa atgctgaagg catcttgttg acatcgaata tgactttgat aataaatacc     360
ggttcctgaa aaaaaaaaaa aaaaaaaaac tcgag                                395

      <210> 165
      <211> 503
      <212> DNA
      <213> Homo sapien

      <400> 165
gaattcggca ccaggaacgc tcggtgagag gcggaggagc ggtaactacc ccggttgcgc      60
acagctcggc gctccttccc gctccctcac acaccggcct cagcccgcac cggcagtaga     120
agatggtgaa agaaacaact tactacgatg ttttgggggt caaacccaat gctactcagg     180
aagaattgaa aaaggcttat aggaaactgg ccttgaagta ccatcctgat aagaacccaa     240
atgaaggaga gaagtttaaa cagatttctc aagcttacga agttctctct gatgcaaaga     300
aaagggaatt atatgacaaa ggaggagaac aggcaattaa agagggtgga gcaggtggcg     360
gttttggctc cccccatggac atctttgata tgttttttgg aggaggagga aggatgcaga     420
gagaaaggag aggtaaaaat gttgtacatc agctctcagt aaccctagaa gacttatata     480
atggtgcaac aagaaaactg gct                                            503

      <210> 166
      <211> 893
      <212> DNA
      <213> Homo sapien

      <400> 166
gaattcggca cgagaggaac ttctcttgac gagaagagag accaaggagg ccaagcaggg      60
gctgggccag aggtgccaac atggggaaac tgaggctcgg ctcggaaggg tgagagtgag     120
actacatctc aaaaaaaaaa aaaaaaaaaa aaaagaaaga aaagaaaaga aaaaagaaag     180
aacggaagta gttgtaggta gtggtatggt ggtatgagtc tgtttctgt tacttataac      240
aacaacaaca acaaaaaacg ctgaaactgg gtaatttata aagaaaagga aaaaaagcag     300
aaaaaaatca ggaagaagag aaaggaaaag aagacaaata aatgaaattt atgtattaca     360
gttctgaagg ctgagacatc ccaggtcaag ggtccacact tggcgagggc tttcttgctg     420
gtggagactc tttgtggagt cctgggacag tgcagaagga tcacgcctcc ctaccgctcc     480
aagcccagcc ctcagccatg gcatgccccc tggatcaggc cattggcctc ctcgtggcca     540
tcttccacaa gtactccggc agggagggtg acaagcacac cctgagcaag aaggagctga     600
aggagctgat ccagaaggag ctcaccattg gctcgaagct gcaggatgct gaaattgcaa     660
ggctgatgga agacttggac cggaacaagg accaggaggt gaacttccag gagtatgtca     720
ccttcctggg ggccttggct ttgatctaca atgaagccct caagggctga aaataaatag     780
ggaagatgga gacaccctct gggggtcctc tctgagtcaa atccagtggt gggtaattgt     840
acaataaatt ttttttggtc aaatttaaaa aaaaaaaaaa aaaaaaactc gag            893

      <210> 167
      <211> 549
      <212> DNA
      <213> Homo sapien

      <400> 167
gaattcggca cgagcccaga tcccgaggtc cgacagcgcc cggcccagat ccccacgcct      60
gccaggagca agccgagagc cagccggccg gcgcactccg actccgagca gtctctgtcc     120
ttcgacccga gccccgcgcc ctttccggga cccctgcccc gcgggcagcg ctgccaacct     180
gccggccatg gagaccccgt cccagcggcg cgccacccgc agcggggcgc aggccagctc     240
cactccgctg tcgcccaccc gcatcacccg gctgcaggag aaggaggacc tgcaggagct     300
caatgatcgc ttggcggtct acatcgaccg tgtgcgctcg ctggaaacgg agaacgcagg     360
gctgcgcctt cgcatcaccg agtctgaaga ggtggtcagc cgcgaggtgt ccggcatcaa     420
ggccgcctac gaggccgagc tcggggatgc ccgcaagacc cttgactcag tagccaagga     480
```

gcgcgcccgc ctgcagctgg agctgagcaa agtgcgtgaa gagtttaagg agctgaaagc 540
gcgcaatac 549

<210> 168
<211> 547
<212> DNA
<213> Homo sapien

<400> 168
gaattcggca cgagatggcg gcaggggtcg aagcggcggc ggaggtggcg gcgacggaga 60
tcaaaatgga ggaagagagc ggcgcgcccg gcgtgccgag cggcaacggg gctccgggcc 120
ctaagggtga aggagaacga cctgctcaga atgagaagag gaaggagaaa aacataaaaa 180
gaggaggcaa tcgctttgag ccatatgcca atccaactaa aagatacaga gccttcatta 240
caaacatacc ttttgatgtg aaatggcagt cacttaaaga cctggttaaa gaaaaagttg 300
gtgaggtaac atacgtggag ctcttaatgg acgctgaagg aaagtcaagg ggatgtgctg 360
ttgttgaatt caagatggaa gagagcatga aaaaagctgc ggaagtccta aacaagcata 420
gtctgagcgg aagaccactg aaagtcaaag aagatcctga tggtgaacat gccaggagag 480
caatgcaaaa ggctggaaga cttggaagca cagtatttgt agcaaatctg gattataaag 540
ttggctg 547

<210> 169
<211> 547
<212> DNA
<213> Homo sapien

<400> 169
gaattcggca ccaggagtcc gactgtgctc gctgctcagc gccgcacccg gaagatgagg 60
ctcgccgtgg gagccctgct ggtctgcgcc gtcctggggc tgtgtctggc tgtccctgat 120
aaaactgtga gatggtgtgc agtgtcggag catgaggcca ctaagtgcca gagtttccgc 180
gaccatatga aaagcgtcat tccatccgat ggtcccagtg ttgcttgtgt gaagaaagcc 240
tcctaccttg attgcatcag ggccattgcg gcaaacgaag cggatgctgt gacactggat 300
gcaggtttgg tgtatgatgc ttacctggct cccaataacc tgaagcctgt ggtggcagag 360
ttctatgggt caaaagagga tccacagact ttctattatg ctgttgctgt ggtgaagaag 420
gatagtggct tccagatgaa ccagcttcga ggcaagaagt cctgccacac gggtctaggc 480
aggtccgctg ggtggaacat ccccataggc ttactttact gtgacttacc tgagccacgt 540
aaacctc 547

<210> 170
<211> 838
<212> DNA
<213> Homo sapien

<400> 170
gaattcggca ccagaggagc tcggcctgcg ctgcgccacg atgtccgggg agtcagccag 60
gagcttgggg aagggaagcg cgcccccggg gccggtcccg gagggctcga tccgcatcta 120
cagcatgagg ttctgcccgt ttgctgagag gacgcgtcta gtcctgaagg ccaagggaat 180
caggcatgaa gtcatcaata tcaacctgaa aaataagcct gagtggttct ttaagaaaaa 240
tccctttggt ctggtgccag ttctggaaaa cagtcagggt cagctgatct acgagtctgc 300
catcacctgt gagtacctgg atgaagcata cccagggaag aagctgttgc cggatgaccc 360
ctatgagaaa gcttgccaga agatgatctt agagttgttt tctaaggtgc catccttggt 420
aggaagcttt attagaagcc aaaataaaga agactatgat ggcctaaaag aagaatttcg 480
taaagaattt accaagctag aggaggttct gactaataag aagacgacct tctttggtgg 540
caattctatc tctatgattg attacctcat ctggccctgg tttgaacggc tggaagcaat 600
gaagttaaat gagtgtgtag accacactcc aaaactgaaa ctgtggatgg cagccatgaa 660
ggaagatccc acagtctcag ccctgcttac tagtgagaaa gactggcaag gtttcctaga 720
gctctactta cagaacagcc ctgaggcctg tgactatggg ctctgaaggg ggcaggagtc 780
agcaataaag ctatgtctga tattttcctt cactaaaaaa aaaaaaaaaa aactcgag 838

<210> 171
<211> 547
<212> DNA
<213> Homo sapien

<400> 171
gaattcggca ccagcgggat ttgggtcgca gttcttgttt gtggattgct gtgatcgtca 60
cttgacaatg cagatcttcg tgaagactct gactggtaag accatcaccc tcgaggttga 120
gcccagtgac accatcgaga atgtcaaggc aaagatccaa gataaggaag gcatccctcc 180
tgaccagcag aggctgatct ttgctggaaa acagctggaa gatgggcgca ccctgtctga 240
ctacaacatc cagaaagagt ccaccctgca cctggtgctc cgtctcagag gtgggatgca 300
aatcttcgtg aagacactca ctggcaagac catcaccctt gaggtcgagc ccagtgacac 360
catcgagaac gtcaaagcaa agatccagga caaggaaggc attcctcctg accagcagag 420
gttgatcttt gccggaaagc agctggaaga tgggcgcacc ctgtctgact acaacatcca 480
gaaagagtct accctgcacc tggtgctccg tctcagaggt gggatgcaga tcttcgtgaa 540
gaccctg 547

<210> 172
<211> 608
<212> DNA
<213> Homo sapien

<400> 172
gaattcggca ccagagactt ctccctctga ggcctgcgca cccctcctca tcagcctgtc 60
caccctcatc tacaatggtg ccctgccatg tcagtgcaac cctcaaggtt cactgagttc 120
tgagtgcaac cctcatggtg gtcagtgcct gtgcaagcct ggagtggttg ggcgccgctg 180
tgacctctgt gcccctggct actatggctt tggccccaca ggctgtcaag gcgcttgcct 240
gggctgccgt gatcacacag gggtgagca ctgtgaaagg tgcattgctg gtttccacgg 300
ggacccacgg ctgccatatg gggccagtg ccggccctgt ccctgtcctg aaggccctgg 360
gagccaacgg cactttgcta cttcttgcca ccaggatgaa tattcccagc agattgtgtg 420
ccactgccgg gcaggctata cggggctgcg atgtgaagct tgtgcccctg ggcactttgg 480
ggacccatca aggccaggtg gccggtgcca actgtgtgag tgcagtggga acattgaccc 540
aatggatcct gatgcctgtg accccccacac ggggcaatgc ctgcgctgtt tacaccacac 600
agagggtc 608

<210> 173
<211> 543
<212> DNA
<213> Homo sapien

<400> 173
gaattcggca ccagagatca tccgccagca gggtctggcc tcctacgact acgtgcgccg 60
ccgcctcacg gctgaggacc tgttcgaggc tcggatcatc tctctcgaga cctacaacct 120
gctccgggag ggcaccagga gcctccgtga ggctctcgag gcggagtccg cctggtgcta 180
cctctatggc acgggctccg tggctggtgt ctacctgccc ggttccaggc agacactgag 240
catctaccag gctctcaaga aagggctgct gagtgccgag gtggcccgcc tgctgctgga 300
ggcacaggca gccacaggct tcctgctgga cccggtgaag ggggaacggc tgactgtgga 360
tgaagctgtg cggaagggcc tcgtggggcc cgaactgcac gaccgcctgc tctcggctga 420
gcgggcggtc accggctacc gtgaccccta caccgagcag accatctcgc tcttccaggc 480
catgaagaag gaactgatcc ctactgagga ggccctgcgg ctgtggatgc ccagctggcc 540
acc 543

<210> 174
<211> 548
<212> DNA
<213> Homo sapien

<400> 174

```
gaattcggca cgagaaatgg cggcaggggt cgaagcggcg gcggaggtgg cggcgacgga      60
gatcaaaatg gaggaagaga gcggcgcgcc cggcgtgccg agcggcaacg gggctccggg     120
ccctaagggt gaaggagaac gacctgctca gaatgagaag aggaaggaga aaaacataaa     180
aagaggaggc aatcgctttg agccatatgc caatccaact aaaagataca gagccttcat     240
tacaaacata ccttttgatg tgaaatggca gtcacttaaa gacctggtta aagaaaaagt     300
tggtgaggta acatacgtgg agctcttaat ggacgctgaa ggaaagtcaa ggggatgtgc     360
tgttgttgaa ttcaagatgg aagagagcat gaaaaaagct gcggaagtcc taaacaagca     420
tagtctgagc ggaagaccac tgaaagtcaa agaagatcct gatggtgaac atgccaggag     480
agcaatgcaa aaggtgatgg ctacgactgg tgggatgggt atgggaccag gtggcccagg     540
aatgatta                                                              548
```

<210> 175
<211> 604
<212> DNA
<213> Homo sapien

<400> 175

```
gaattcggca ccagaggacc tccaggacat gttcatcgtc cataccatcg aggagattga      60
gggcctgatc tcagcccatg accagttcaa gtccaccctg ccggacgccg atagggagcg     120
cgaggccatc ctggccatcc acaaggaggc ccagaggatc gctgagagca accacatcaa     180
gctgtcgggc agcaacccct acaccaccgt caccccgcaa atcatcaact ccaagtggga     240
gaaggtgcag cagctggtgc caaaacggga ccatgccctc ctggaggagc agagcaagca     300
gcagtccaac gagcacctgc gccgccagtt cgccagccag gccaatgttg tggggccctg     360
gatccagacc aagatggagg agatcgggcg catctccatt gagatgaacg ggaccctgga     420
ggaccagctg agccacctga agcagtatga acgcagcatc gtggactaca agcccaacct     480
ggacctgctg gagcagcagc accagcttat ccaggaggcc ctcatcttcg acaacaagca     540
caccaactat accatggagc acatccgcgt gggctgggag cagctgctca ccaccattgc     600
ccgg                                                                  604
```

<210> 176
<211> 486
<212> DNA
<213> Homo sapien

<400> 176

```
gaattcggca ccagccaagc tcactattga atccacgccg ttcaatgtcg cagaggggaa      60
ggaggttctt ctactcgccc acaacctgcc ccagaatcgt attggttaca gctggtacaa     120
aggcgaaaga gtggatggca acagtctaat tgtaggatat gtaataggaa ctcaacaagc     180
taccccaggg cccgcataca gtggtcgaga gacaatatac cccaatgcat ccctgctgat     240
ccagaacgtc acccagaatg acacaggatt ctataccta caagtcataa agtcagatct      300
tgtgaatgaa gaagcaaccg gacagttcca tgtataccg gagctgccca agccctccat      360
ctccagcaac aactccaacc ccgtggagga caaggatgct gtggccttca cctgtgaacc     420
tgaggttcag aacacaacct acctgtggtg ggtaaatggt cagagcctcc cggtcagtcc     480
caaggc                                                                486
```

<210> 177
<211> 387
<212> DNA
<213> Homo sapien

<400> 177

```
gaattcggca ccagggacag cagaccagac agtcacagca gccttgacaa aacgttcctg      60
gaactcaagc tcttctccac agaggaggac agagcagaca gcagagacca tggagtctcc     120
ctcggcccct ccccacagat ggtgcatccc ctggcagagg ctcctgctca cagcctcact     180
tctaaccttc tggaacccgc ccaccactgc caagctcact attgaatcca cgccgttcaa     240
tgtcgcagag gggaaggagg tgcttctact tgtccacaat ctgccccagc atctttttgg     300
ctacagctgg tacaaaggtg aaagagtgga tggcaaccgt caaattatag gatatgtaat     360
aggaactcaa caagctaccc cagggcc                                         387
```

<210> 178
<211> 440
<212> DNA
<213> Homo sapien

<400> 178
gaattcggca cgaggagaag cagaaaaaca aggaatttag ccagacttta gaaaatgaga 60
aaaatacctt actgagtcag atatcaacaa aggatggtga actaaaaatg cttcaggagg 120
aagtaaccaa aatgaacctg ttaaatcagc aaatccaaga agaactctct agagttacca 180
aactaaagga gacagcagaa gaagagaaag atgatttgga agagaggctt atgaatcaat 240
tagcagaact taatggaagc attgggaatt actgtcagga tgttacagat gcccaaataa 300
aaaatgagct attggaatct gaaatgaaga accttaaaaa gtgtgtgagt gaattggaag 360
aagaaaagca gcagttagtc aaggaaaaaa ctaaggtgga atcagaaata cgaaaggaat 420
atttggagaa aatacaaggt 440

<210> 179
<211> 443
<212> DNA
<213> Homo sapien

<400> 179
gaattcggca ccagcggggg gctacggcgg cggctacggc ggcgtcctga ccgcgtccga 60
cgggctgctg gcgggcaacg agaagctaac catgcagaac ctcaacgacc gcctggcctc 120
ctacctggac aaggtgcgcg ccctggaggc ggccaacggc gagctagagg tgaagatccg 180
cgactggtac cagaagcagg ggcctgggcc ctcccgcgac tacagccact actacacgac 240
catccaggac ctgcgggaca agattcttgg tgccaccatt gagaactcca ggattgtcct 300
gcagatcgac aacgcccgtc tggctgcaga tgacttccga accaagtttg agacggaaca 360
ggctctgcgc atgagcgtgg aggccgacat caacggcctg cgcagggtgc tggatgagct 420
gaccctggcc aggaccgacc tgg 443

<210> 180
<211> 403
<212> DNA
<213> Homo sapien

<400> 180
gaattcggca cgaggttatg agagtcgact tcaatgttcc tatgaagaac aaccagataa 60
caaacaacca gaggattaag gctgctgtcc caagcatcaa attctgcttg gacaatggag 120
ccaagtcggt agtccttatg agccacctag gccggcctga tggtgtgccc atgcctgaca 180
agtactcctt agagccagtt gctgtagaac tcagatctct gctgggcaag gatgttctgt 240
tcttgaagga ctgtgtaggc ccagaagtgg agaaagcctg tgccaaccca gctgctgggt 300
ctgtcatcct gctggagaac ctccgctttc atgtggagga agaagggaag ggaaaagatg 360
cttctgggaa caaggttaaa gccgagccag ccaaaataga agc 403

<210> 181
<211> 493
<212> DNA
<213> Homo sapien

<400> 181
gaattcggca ccagcagagg tctccagagc cttctctctc ctgtgcaaaa tggcaactct 60
taaggaaaaa ctcattgcac cagttgcgga agaagaggca acagttccaa acaataagat 120
cactgtagtg ggtgttggac aagttggtat ggcgtgtgct atcagcattc tgggaaagtc 180
tctggctgat gaacttgctc ttgtggatgt tttggaagat aagcttaaag gagaaatgat 240
ggatctgcag catgggagct tatttcttca gacacctaaa attgtggcag ataaagatta 300
ttctgtgacc gccaattcta agattgtagt ggtaactgca ggagtccgtc agcaagaagg 360
ggagagtcgg ctcaatctgg tgcagagaaa tgttaatgtc ttcaaattca ttattcctca 420

gatcgtcaag tacagtcctg attgcatcat aattgtggtt tccaacccag tggacattct 480
tacgtatgtt acc 493

<210> 182
<211> 209
<212> PRT
<213> Homo sapien

<400> 182
Ala Phe Ser Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly
1 5 10 15
Ala Leu Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr
20 25 30
Ala Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe
35 40 45
Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu
50 55 60
Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val
65 70 75 80
Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu
85 90 95
Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln Gln Tyr
100 105 110
Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp Cys Glu
115 120 125
Ile Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg Glu Lys
130 135 140
Val Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp Arg Tyr
145 150 155 160
Arg Gln Asp Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln Ala Glu
165 170 175
Tyr Gln Val Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp Glu Gly
180 185 190
Tyr Phe Gln Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys Glu Leu
195 200 205
Arg

<210> 183
<211> 255
<212> PRT
<213> Homo sapien

<400> 183
Met Ala Ala Gly Val Glu Ala Ala Ala Glu Val Ala Ala Thr Glu Pro
1 5 10 15
Lys Met Glu Glu Glu Ser Gly Ala Pro Cys Val Pro Ser Gly Asn Gly
20 25 30
Ala Pro Gly Pro Lys Gly Glu Glu Arg Pro Thr Gln Asn Glu Lys Arg
35 40 45
Lys Glu Lys Asn Ile Lys Arg Gly Gly Asn Arg Phe Glu Pro Tyr Ser
50 55 60
Asn Pro Thr Lys Arg Tyr Arg Ala Phe Ile Thr Asn Ile Pro Phe Asp
65 70 75 80
Val Lys Trp Gln Ser Leu Lys Asp Leu Val Lys Glu Lys Val Gly Glu
85 90 95
Val Thr Tyr Val Glu Leu Leu Met Asp Ala Glu Gly Lys Ser Arg Gly
100 105 110

Cys Ala Val Val Glu Phe Lys Met Glu Glu Ser Met Lys Lys Ala Ala
        115   120   125
Glu Val Leu Asn Lys His Ser Leu Ser Gly Arg Pro Leu Lys Val Lys
    130   135   140
Glu Asp Pro Asp Gly Glu His Ala Arg Arg Ala Met Gln Lys Ala Gly
145   150   155   160
Arg Leu Gly Ser Thr Val Phe Val Ala Asn Leu Asp Tyr Lys Val Gly
                165   170   175
Trp Lys Lys Leu Lys Glu Val Phe Ser Met Ala Gly Val Val Val Arg
            180   185   190
Ala Asp Ile Leu Glu Asp Lys Asp Gly Lys Ser Arg Gly Ile Gly Ile
        195   200   205
Val Thr Phe Glu Gln Ser Ile Glu Ala Val Gln Ala Ile Ser Met Phe
    210   215   220
Asn Gly Gln Leu Leu Phe Asp Arg Pro Met His Val Lys Met Asp Glu
225   230   235   240
Arg Ala Leu Pro Lys Gly Asp Phe Phe Pro Pro Glu Arg His Ser
                245   250   255

<210> 184
<211> 188
<212> PRT
<213> Homo sapien

<400> 184
Leu Ser Gly Ser Cys Ile Arg Arg Glu Gln Thr Pro Glu Lys Glu Lys
 1   5   10   15
Gln Val Val Leu Phe Glu Glu Ala Ser Trp Thr Cys Thr Pro Ala Cys
            20   25   30
Gly Asp Glu Pro Arg Thr Val Ile Leu Leu Ser Ser Met Leu Ala Asp
        35   40   45
His Arg Leu Lys Leu Glu Asp Tyr Lys Asp Arg Leu Lys Ser Gly Glu
    50   55   60
His Leu Asn Pro Asp Gln Leu Glu Ala Val Glu Lys Tyr Glu Glu Val
65   70   75   80
Leu His Asn Leu Glu Phe Ala Lys Glu Leu Gln Lys Thr Phe Ser Gly
                85   90   95
Leu Ser Leu Asp Leu Leu Lys Ala Gln Lys Lys Ala Gln Arg Arg Glu
            100   105   110
His Met Leu Lys Leu Glu Ala Glu Lys Lys Lys Leu Arg Thr Ile Leu
        115   120   125
Gln Val Gln Tyr Val Leu Gln Asn Leu Thr Gln Glu His Val Gln Lys
    130   135   140
Asp Phe Lys Gly Gly Leu Asn Gly Ala Val Tyr Leu Pro Ser Lys Glu
145   150   155   160
Leu Asp Tyr Leu Ile Lys Phe Ser Lys Leu Thr Cys Pro Glu Arg Asn
                165   170   175
Glu Ser Leu Arg Gln Thr Leu Glu Gly Ser Thr Val
            180   185

<210> 185
<211> 746
<212> PRT
<213> Homo sapien

<400> 185
Asp Lys His Leu Lys Asp Leu Leu Ser Lys Leu Leu Asn Ser Gly Tyr
 1   5   10   15

```
Phe Glu Ser Ile Pro Val Pro Lys Asn Ala Lys Glu Lys Glu Val Pro
            20                  25                  30
Leu Glu Glu Glu Met Leu Ile Gln Ser Glu Lys Lys Thr Gln Leu Ser
        35                  40                  45
Lys Thr Glu Ser Val Lys Glu Ser Glu Ser Leu Met Glu Phe Ala Gln
    50                  55                  60
Pro Glu Ile Gln Pro Gln Glu Phe Leu Asn Arg Arg Tyr Met Thr Glu
65                  70                  75                  80
Val Asp Tyr Ser Asn Lys Gln Gly Glu Glu Gln Pro Trp Glu Ala Asp
                85                  90                  95
Tyr Ala Arg Lys Pro Asn Leu Pro Lys Arg Trp Asp Met Leu Thr Glu
            100                 105                 110
Pro Asp Gly Gln Glu Lys Lys Gln Glu Ser Phe Lys Ser Trp Glu Ala
        115                 120                 125
Ser Gly Lys His Gln Glu Val Ser Lys Pro Ala Val Ser Leu Glu Gln
    130                 135                 140
Arg Lys Gln Asp Thr Ser Lys Leu Arg Ser Thr Leu Pro Glu Glu Gln
145                 150                 155                 160
Lys Lys Gln Glu Ile Ser Lys Ser Lys Pro Ser Pro Ser Gln Trp Lys
                165                 170                 175
Gln Asp Thr Pro Lys Ser Lys Ala Gly Tyr Val Gln Glu Glu Gln Lys
            180                 185                 190
Lys Gln Glu Thr Pro Lys Leu Trp Pro Val Gln Leu Gln Lys Glu Gln
        195                 200                 205
Asp Pro Lys Lys Gln Thr Pro Lys Ser Trp Thr Pro Ser Met Gln Ser
    210                 215                 220
Glu Gln Asn Thr Thr Lys Ser Trp Thr Thr Pro Met Cys Glu Glu Gln
225                 230                 235                 240
Asp Ser Lys Gln Pro Glu Thr Pro Lys Ser Trp Glu Asn Asn Val Glu
                245                 250                 255
Ser Gln Lys His Ser Leu Thr Ser Gln Ser Gln Ile Ser Pro Lys Ser
            260                 265                 270
Trp Gly Val Ala Thr Ala Ser Leu Ile Pro Asn Asp Gln Leu Leu Pro
        275                 280                 285
Arg Lys Leu Asn Thr Glu Pro Lys Asp Val Pro Lys Pro Val His Gln
    290                 295                 300
Pro Val Gly Ser Ser Ser Thr Leu Pro Lys Asp Pro Val Leu Arg Lys
305                 310                 315                 320
Glu Lys Leu Gln Asp Leu Met Thr Gln Ile Gln Gly Thr Cys Asn Phe
                325                 330                 335
Met Gln Glu Ser Val Leu Asp Phe Asp Lys Pro Ser Ser Ala Ile Pro
            340                 345                 350
Thr Ser Gln Pro Pro Ser Ala Thr Pro Gly Ser Pro Val Ala Ser Lys
        355                 360                 365
Glu Gln Asn Leu Ser Ser Gln Ser Asp Phe Leu Gln Glu Pro Leu Gln
    370                 375                 380
Val Phe Asn Val Asn Ala Pro Leu Pro Pro Arg Lys Glu Gln Glu Ile
385                 390                 395                 400
Lys Glu Ser Pro Tyr Ser Pro Gly Tyr Asn Gln Ser Phe Thr Thr Ala
                405                 410                 415
Ser Thr Gln Thr Pro Pro Gln Cys Gln Leu Pro Ser Ile His Val Glu
            420                 425                 430
Gln Thr Val His Ser Gln Glu Thr Ala Ala Asn Tyr His Pro Asp Gly
        435                 440                 445
Thr Ile Gln Val Ser Asn Gly Ser Leu Ala Phe Tyr Pro Ala Gln Thr
    450                 455                 460
Asn Val Phe Pro Arg Pro Thr Gln Pro Phe Val Asn Ser Arg Gly Ser
465                 470                 475                 480
```

```
Val Arg Gly Cys Thr Arg Gly Gly Arg Leu Ile Thr Asn Ser Tyr Arg
                485                 490                 495
Ser Pro Gly Gly Tyr Lys Gly Phe Asp Thr Tyr Arg Gly Leu Pro Ser
            500                 505                 510
Ile Ser Asn Gly Asn Tyr Ser Gln Leu Gln Phe Gln Ala Arg Glu Tyr
        515                 520                 525
Ser Gly Ala Pro Tyr Ser Gln Arg Asp Asn Phe Gln Gln Cys Tyr Lys
    530                 535                 540
Arg Gly Gly Thr Ser Gly Gly Pro Arg Ala Asn Ser Arg Ala Gly Trp
545                 550                 555                 560
Ser Asp Ser Ser Gln Val Ser Ser Pro Glu Arg Asp Asn Glu Thr Phe
                565                 570                 575
Asn Ser Gly Asp Ser Gly Gln Gly Asp Ser Arg Ser Met Thr Pro Val
            580                 585                 590
Asp Val Pro Val Thr Asn Pro Ala Ala Thr Ile Leu Pro Val His Val
        595                 600                 605
Tyr Pro Leu Pro Gln Gln Met Arg Val Ala Phe Ser Ala Ala Arg Thr
    610                 615                 620
Ser Asn Leu Ala Pro Gly Thr Leu Asp Gln Pro Ile Val Phe Asp Leu
625                 630                 635                 640
Leu Leu Asn Asn Leu Gly Glu Thr Phe Asp Leu Gln Leu Gly Arg Phe
                645                 650                 655
Asn Cys Pro Val Asn Gly Thr Tyr Val Phe Ile Phe His Met Leu Lys
            660                 665                 670
Leu Ala Val Asn Val Pro Leu Tyr Val Asn Leu Met Lys Asn Glu Glu
        675                 680                 685
Val Leu Val Ser Ala Tyr Ala Asn Asp Gly Ala Pro Asp His Glu Thr
    690                 695                 700
Ala Ser Asn His Ala Ile Leu Gln Leu Phe Gln Gly Asp Gln Ile Trp
705                 710                 715                 720
Leu Arg Leu His Arg Gly Ala Ile Tyr Gly Ser Ser Trp Lys Tyr Ser
                725                 730                 735
Thr Phe Ser Gly Tyr Leu Leu Tyr Gln Asp
            740                 745

      <210> 186
      <211> 705
      <212> PRT
      <213> Homo sapien

      <400> 186
Ala Leu Leu Asn Val Arg Gln Pro Pro Ser Thr Thr Thr Phe Val Leu
 1               5                  10                  15
Asn Gln Ile Asn His Leu Pro Pro Leu Gly Ser Thr Ile Val Met Thr
            20                  25                  30
Lys Thr Pro Pro Val Thr Thr Asn Arg Gln Thr Ile Thr Leu Thr Lys
        35                  40                  45
Phe Ile Gln Thr Thr Ala Ser Thr Arg Pro Ser Val Ser Ala Pro Thr
    50                  55                  60
Val Arg Asn Ala Met Thr Ser Ala Pro Ser Lys Asp Gln Val Gln Leu
65                  70                  75                  80
Lys Asp Leu Leu Lys Asn Asn Ser Leu Asn Glu Leu Met Lys Leu Lys
                85                  90                  95
Pro Pro Ala Asn Ile Ala Gln Pro Val Ala Thr Ala Ala Thr Asp Val
            100                 105                 110
Ser Asn Gly Thr Val Lys Lys Glu Ser Ser Asn Lys Glu Gly Ala Arg
        115                 120                 125
Met Trp Ile Asn Asp Met Lys Met Arg Ser Phe Ser Pro Thr Met Lys
```

```
    130                 135                 140
Val Pro Val Val Lys Glu Asp Asp Glu Pro Glu Glu Glu Asp Glu Glu
145                 150                 155                 160
Glu Met Gly His Ala Glu Thr Tyr Ala Glu Tyr Met Pro Ile Lys Leu
                165                 170                 175
Lys Ile Gly Leu Arg His Pro Asp Ala Val Val Glu Thr Ser Ser Leu
            180                 185                 190
Ser Ser Val Thr Pro Pro Asp Val Trp Tyr Lys Thr Ser Ile Ser Glu
        195                 200                 205
Glu Thr Ile Asp Asn Gly Trp Leu Ser Ala Leu Gln Leu Glu Ala Ile
    210                 215                 220
Thr Tyr Ala Ala Gln Gln His Glu Thr Phe Leu Pro Asn Gly Asp Arg
225                 230                 235                 240
Ala Gly Phe Leu Ile Gly Asp Gly Ala Gly Val Gly Lys Gly Arg Thr
                245                 250                 255
Ile Ala Gly Ile Ile Tyr Glu Asn Tyr Leu Leu Ser Arg Lys Arg Ala
            260                 265                 270
Leu Trp Phe Ser Val Ser Asn Asp Leu Lys Tyr Asp Ala Glu Arg Asp
        275                 280                 285
Leu Arg Asp Ile Gly Ala Lys Asn Ile Leu Val His Ser Leu Asn Lys
    290                 295                 300
Phe Lys Tyr Gly Lys Ile Ser Ser Lys His Asn Gly Ser Val Lys Lys
305                 310                 315                 320
Gly Val Ile Phe Ala Thr Tyr Ser Ser Leu Ile Gly Glu Ser Gln Ser
                325                 330                 335
Gly Gly Lys Tyr Lys Thr Arg Leu Lys Gln Leu Leu His Trp Cys Gly
            340                 345                 350
Asp Asp Phe Asp Gly Val Ile Val Phe Asp Glu Cys His Lys Ala Lys
        355                 360                 365
Asn Leu Cys Pro Val Gly Ser Ser Lys Pro Thr Lys Thr Gly Leu Ala
    370                 375                 380
Val Leu Glu Leu Gln Asn Lys Leu Pro Lys Ala Arg Val Val Tyr Ala
385                 390                 395                 400
Ser Ala Thr Gly Ala Ser Glu Pro Arg Asn Met Ala Tyr Met Asn Arg
                405                 410                 415
Leu Gly Ile Trp Gly Glu Gly Thr Pro Phe Arg Glu Phe Ser Asp Phe
            420                 425                 430
Ile Gln Ala Val Glu Arg Arg Gly Val Gly Ala Met Glu Ile Val Ala
        435                 440                 445
Met Asp Met Lys Leu Arg Gly Met Tyr Ile Ala Arg Gln Leu Ser Phe
    450                 455                 460
Thr Gly Val Thr Phe Lys Ile Glu Glu Val Leu Leu Ser Gln Ser Tyr
465                 470                 475                 480
Val Lys Met Tyr Asn Lys Ala Val Lys Leu Trp Val Ile Ala Arg Glu
                485                 490                 495
Arg Phe Gln Gln Ala Ala Asp Leu Ile Asp Ala Glu Gln Arg Met Lys
            500                 505                 510
Lys Ser Met Trp Gly Gln Phe Trp Ser Ala His Gln Arg Phe Phe Lys
        515                 520                 525
Tyr Leu Cys Ile Ala Ser Lys Val Lys Arg Val Val Gln Leu Ala Arg
    530                 535                 540
Glu Glu Ile Lys Asn Gly Lys Cys Val Val Ile Gly Leu Gln Ser Thr
545                 550                 555                 560
Gly Glu Ala Arg Thr Leu Glu Ala Leu Glu Glu Gly Gly Gly Glu Leu
                565                 570                 575
Asn Asp Phe Val Ser Thr Ala Lys Gly Val Leu Gln Ser Leu Ile Glu
            580                 585                 590
Lys His Phe Pro Ala Pro Asp Arg Lys Lys Leu Tyr Ser Leu Leu Gly
```

```
        595                 600                 605
Ile Asp Leu Thr Ala Pro Ser Asn Asn Ser Ser Pro Arg Asp Ser Pro
    610                 615                 620
Cys Lys Glu Asn Lys Ile Lys Lys Arg Lys Gly Glu Glu Ile Thr Arg
625                 630                 635                 640
Glu Ala Lys Lys Ala Arg Lys Val Gly Gly Leu Thr Gly Ser Ser Ser
                645                 650                 655
Asp Asp Ser Gly Ser Glu Ser Asp Ala Ser Asp Asn Glu Glu Ser Asp
            660                 665                 670
Tyr Glu Ser Ser Lys Asn Met Ser Ser Gly Asp Asp Asp Asp Phe Asn
        675                 680                 685
Pro Phe Leu Asp Glu Ser Asn Glu Asp Asp Glu Asn Asp Pro Trp Leu
    690                 695                 700
Ile
705

      <210> 187
      <211> 595
      <212> PRT
      <213> Homo sapien

      <400> 187
Glu Ser Pro Arg His Arg Gly Glu Gly Gly Gly Glu Trp Gly Pro Gly
 1               5                  10                  15
Val Pro Arg Glu Arg Arg Glu Ser Ala Gly Glu Trp Gly Ala Asp Thr
            20                  25                  30
Pro Lys Glu Gly Gly Glu Ser Ala Gly Glu Trp Gly Ala Glu Val Pro
        35                  40                  45
Arg Gly Arg Gly Glu Gly Ala Gly Glu Trp Gly Pro Asp Thr Pro Lys
    50                  55                  60
Glu Arg Gly Gln Gly Val Arg Glu Trp Gly Pro Glu Ile Pro Gln Glu
65                  70                  75                  80
His Gly Glu Ala Thr Arg Asp Trp Ala Leu Glu Ser Pro Arg Ala Leu
                85                  90                  95
Gly Glu Asp Ala Arg Glu Leu Gly Ser Ser Pro His Asp Arg Gly Ala
            100                 105                 110
Ser Pro Arg Asp Leu Ser Gly Glu Ser Pro Cys Thr Gln Arg Ser Gly
        115                 120                 125
Leu Leu Pro Glu Arg Arg Gly Asp Ser Pro Trp Pro Pro Trp Pro Ser
    130                 135                 140
Pro Gln Glu Arg Asp Ala Gly Thr Arg Asp Arg Glu Glu Ser Pro Arg
145                 150                 155                 160
Asp Trp Gly Gly Ala Glu Ser Pro Arg Gly Trp Glu Ala Gly Pro Arg
                165                 170                 175
Glu Trp Gly Pro Ser Pro Ser Gly His Gly Asp Gly Pro Arg Arg Arg
            180                 185                 190
Pro Arg Lys Arg Arg Gly Arg Lys Gly Arg Met Gly Arg Gln His Glu
        195                 200                 205
Ala Ala Ala Thr Ala Ala Thr Ala Ala Thr Ala Thr Gly Gly Thr Ala
    210                 215                 220
Glu Glu Ala Gly Ala Ser Ala Pro Glu Ser Gln Ala Gly Gly Gly Pro
225                 230                 235                 240
Arg Gly Arg Ala Arg Gly Pro Arg Gln Gln Gly Arg Arg Arg His Gly
                245                 250                 255
Thr Gln Arg Arg Arg Gly Pro Pro Gln Ala Arg Glu Glu Gly Pro Arg
            260                 265                 270
Asp Ala Thr Thr Ile Leu Gly Leu Gly Thr Pro Ser Gly Glu Gln Arg
        275                 280                 285
```

Ala Asp Gln Ser Gln Ala Leu Pro Ala Leu Ala Gly Ala Ala Ala Ala
    290   295   300
His Ala His Ala Ile Pro Gly Ala Gly Pro Ala Ala Ala Pro Val Gly
305   310   315   320
Gly Arg Gly Arg Arg Gly Gly Trp Arg Gly Gly Arg Arg Gly Gly Ser
                325   330   335
Ala Gly Ala Gly Gly Gly Gly Arg Gly Gly Arg Gly Arg Gly Arg Gly
            340   345   350
Gly Gly Arg Gly Gly Gly Gly Ala Gly Arg Gly Gly Gly Ala Ala Gly
        355   360   365
Pro Arg Glu Gly Ala Ser Ser Pro Gly Ala Arg Arg Gly Glu Gln Arg
    370   375   380
Arg Arg Gly Arg Gly Pro Pro Ala Ala Gly Ala Ala Gln Val Ser Ala
385   390   395   400
Arg Gly Arg Arg Ala Arg Gly Gln Arg Ala Gly Glu Glu Ala Gln Asp
                405   410   415
Gly Leu Leu Pro Arg Gly Arg Asp Arg Leu Pro Leu Arg Pro Gly Asp
            420   425   430
Ala Asn Gln Arg Ala Glu Arg Pro Gly Pro Pro Arg Gly Gly His Gly
        435   440   445
Pro Val Asn Ala Ser Ser Ala Pro Asp Thr Ser Pro Pro Arg His Pro
    450   455   460
Arg Arg Trp Val Ser Gln Gln Arg Gln Arg Leu Trp Arg Gln Phe Arg
465   470   475   480
Val Gly Gly Gly Phe Pro Pro Pro Pro Pro Ser Arg Pro Pro Ala Val
                485   490   495
Leu Leu Pro Leu Leu Arg Leu Ala Cys Ala Gly Asp Pro Gly Ala Thr
            500   505   510
Arg Pro Gly Pro Arg Arg Pro Ala Arg Arg Pro Arg Gly Glu Leu Ile
        515   520   525
Pro Arg Arg Pro Asp Pro Ala Ala Pro Ser Glu Glu Gly Leu Arg Met
    530   535   540
Glu Ser Ser Val Asp Asp Gly Ala Thr Ala Thr Thr Ala Asp Ala Ala
545   550   555   560
Ser Gly Glu Ala Pro Glu Ala Gly Pro Ser Pro Ser His Ser Pro Thr
                565   570   575
Met Cys Gln Thr Gly Gly Pro Gly Pro Pro Pro Pro Gln Pro Pro Arg
            580   585   590
Trp Leu Pro
        595

<210> 188
<211> 376
<212> PRT
<213> Homo sapien

<400> 188
Glu Met Arg Lys Phe Asp Val Pro Ser Met Glu Ser Thr Leu Asn Gln
 1   5   10   15
Pro Ala Met Leu Glu Thr Leu Tyr Ser Asp Pro His Tyr Arg Ala His
            20   25   30
Phe Pro Asn Pro Arg Pro Asp Thr Asn Lys Asp Val Tyr Lys Val Leu
        35   40   45
Pro Glu Ser Lys Lys Ala Pro Gly Ser Gly Ala Val Phe Glu Arg Asn
    50   55   60
Gly Pro His Ala Ser Ser Ser Gly Val Leu Pro Leu Gly Leu Gln Pro
65   70   75   80
Ala Pro Gly Leu Ser Lys Ser Leu Ser Ser Gln Val Trp Gln Pro Ser

```
                85                  90                  95
Pro Asp Pro Trp His Pro Gly Glu Gln Ser Cys Glu Leu Ser Thr Cys
            100                 105                 110
Arg Gln Gln Leu Glu Leu Ile Arg Leu Gln Met Glu Gln Met Gln Leu
        115                 120                 125
Gln Asn Gly Ala Met Cys His His Pro Ala Ala Phe Ala Pro Leu Leu
    130                 135                 140
Pro Thr Leu Glu Pro Ala Gln Trp Leu Ser Ile Leu Asn Ser Asn Glu
145                 150                 155                 160
His Leu Leu Lys Glu Lys Glu Leu Leu Ile Asp Lys Gln Arg Lys His
                165                 170                 175
Ile Ser Gln Leu Glu Gln Lys Val Arg Glu Ser Glu Leu Gln Val His
            180                 185                 190
Ser Ala Leu Leu Gly Arg Pro Ala Pro Phe Gly Asp Val Cys Leu Leu
        195                 200                 205
Arg Leu Gln Glu Leu Gln Arg Glu Asn Thr Phe Leu Arg Ala Gln Phe
    210                 215                 220
Ala Gln Lys Thr Glu Ala Leu Ser Lys Glu Lys Met Glu Leu Glu Lys
225                 230                 235                 240
Lys Leu Ser Ala Ser Glu Val Glu Ile Gln Leu Ile Arg Glu Ser Leu
                245                 250                 255
Lys Val Thr Leu Gln Lys His Ser Glu Glu Gly Lys Lys Gln Glu Glu
            260                 265                 270
Arg Val Lys Gly Arg Asp Lys His Ile Asn Asn Leu Lys Lys Lys Cys
        275                 280                 285
Gln Lys Glu Ser Glu Gln Asn Arg Glu Lys Gln Gln Arg Ile Glu Thr
    290                 295                 300
Leu Glu Arg Tyr Leu Ala Asp Leu Pro Thr Leu Glu Asp His Gln Lys
305                 310                 315                 320
Gln Thr Glu Gln Leu Lys Asp Ala Glu Leu Lys Asn Thr Glu Leu Gln
                325                 330                 335
Glu Arg Val Ala Glu Leu Glu Thr Leu Leu Glu Asp Thr Gln Ala Thr
            340                 345                 350
Cys Arg Glu Lys Glu Val Gln Leu Glu Ser Leu Arg Gln Arg Glu Ala
        355                 360                 365
Asp Leu Ser Ser Ala Arg His Arg
    370                 375

      <210> 189
      <211> 160
      <212> PRT
      <213> Homo sapien

      <400> 189
Met Leu Glu Ala His Arg Arg Gln Arg His Pro Phe Leu Leu Leu Gly
 1               5                  10                  15
Thr Thr Ala Asn Arg Thr Gln Ser Leu Asn Tyr Gly Cys Ile Val Glu
            20                  25                  30
Asn Pro Gln Thr His Glu Val Leu His Tyr Val Glu Lys Pro Ser Thr
        35                  40                  45
Phe Ile Ser Asp Ile Ile Asn Cys Gly Ile Tyr Leu Phe Ser Pro Glu
    50                  55                  60
Ala Leu Lys Pro Leu Arg Asp Val Phe Gln Arg Asn Gln Gln Asp Gly
65                  70                  75                  80
Gln Leu Glu Asp Ser Pro Gly Leu Trp Pro Gly Ala Gly Thr Ile Arg
                85                  90                  95
Leu Glu Gln Asp Val Phe Ser Ala Leu Ala Gly Gln Gly Gln Ile Tyr
            100                 105                 110
```

```
Val His Leu Thr Asp Gly Ile Trp Ser Gln Ile Lys Ser Ala Gly Ser
        115                 120                 125
Ala Leu Tyr Ala Ser Arg Leu Tyr Leu Ser Arg Tyr Gln Asp Thr His
    130                 135                 140
Pro Glu Arg Leu Ala Lys His Thr Pro Gly Gly Pro Trp Ile Arg Gly
145                 150                 155                 160

      <210> 190
      <211> 146
      <212> PRT
      <213> Homo sapien

      <400> 190
Met Asp Pro Arg Ala Ser Leu Leu Leu Leu Gly Asn Val Tyr Ile His
 1               5                  10                  15
Pro Thr Ala Lys Val Ala Pro Ser Ala Val Leu Gly Pro Asn Val Ser
            20                  25                  30
Ile Gly Lys Gly Val Thr Val Gly Glu Gly Val Arg Leu Arg Glu Ser
        35                  40                  45
Ile Val Leu His Gly Ala Thr Leu Gln Glu His Thr Cys Val Leu His
    50                  55                  60
Ser Ile Val Gly Trp Gly Ser Thr Val Gly Arg Trp Ala Arg Val Glu
65                  70                  75                  80
Gly Thr Pro Ser Asp Pro Asn Pro Asn Asp Pro Arg Ala Arg Met Asp
                85                  90                  95
Ser Glu Ser Leu Phe Lys Asp Gly Lys Leu Leu Pro Ala Ile Thr Ile
            100                 105                 110
Leu Gly Cys Arg Val Arg Ile Pro Ala Glu Val Leu Ile Leu Asn Ser
        115                 120                 125
Ile Val Leu Pro His Lys Glu Leu Ser Arg Ser Phe Thr Asn Gln Ile
    130                 135                 140
Ile Leu
145

      <210> 191
      <211> 704
      <212> PRT
      <213> Homo sapien

      <400> 191
Glu Gly Gly Cys Ala Ala Gly Arg Gly Arg Glu Leu Glu Pro Glu Leu
 1               5                  10                  15
Glu Pro Gly Pro Gly Pro Gly Ser Ala Leu Glu Pro Gly Glu Glu Phe
            20                  25                  30
Glu Ile Val Asp Arg Ser Gln Leu Pro Gly Pro Gly Asp Leu Arg Ser
        35                  40                  45
Ala Thr Arg Pro Arg Ala Ala Glu Gly Trp Ser Ala Pro Ile Leu Thr
    50                  55                  60
Leu Ala Arg Arg Ala Thr Gly Asn Leu Ser Ala Ser Cys Gly Ser Ala
65                  70                  75                  80
Leu Arg Ala Ala Ala Gly Leu Gly Gly Gly Asp Ser Gly Asp Gly Thr
                85                  90                  95
Ala Arg Ala Ala Ser Lys Cys Gln Met Met Glu Glu Arg Ala Asn Leu
            100                 105                 110
Met His Met Met Lys Leu Ser Ile Lys Val Leu Leu Gln Ser Ala Leu
        115                 120                 125
Ser Leu Gly Arg Ser Leu Asp Ala Asp His Ala Pro Leu Gln Gln Phe
    130                 135                 140
```

```
Phe Val Val Met Glu His Cys Leu Lys His Gly Leu Lys Val Lys Lys
145                 150                 155                 160
Ser Phe Ile Gly Gln Asn Lys Ser Phe Phe Gly Pro Leu Glu Leu Val
                165                 170                 175
Glu Lys Leu Cys Pro Glu Ala Ser Asp Ile Ala Thr Ser Val Arg Asn
            180                 185                 190
Leu Pro Glu Leu Lys Thr Ala Val Gly Arg Gly Arg Ala Trp Leu Tyr
        195                 200                 205
Leu Ala Leu Met Gln Lys Lys Leu Ala Asp Tyr Leu Lys Val Leu Ile
    210                 215                 220
Asp Asn Lys His Leu Leu Ser Glu Phe Tyr Glu Pro Glu Ala Leu Met
225                 230                 235                 240
Met Glu Glu Glu Gly Met Val Ile Val Gly Leu Leu Val Gly Leu Asn
                245                 250                 255
Val Leu Asp Ala Asn Leu Cys Leu Lys Gly Glu Asp Leu Asp Ser Gln
            260                 265                 270
Val Gly Val Ile Asp Phe Ser Leu Tyr Leu Lys Asp Val Gln Asp Leu
        275                 280                 285
Asp Gly Gly Lys Glu His Glu Arg Ile Thr Asp Val Leu Asp Gln Lys
    290                 295                 300
Asn Tyr Val Glu Glu Leu Asn Arg His Leu Ser Cys Thr Val Gly Asp
305                 310                 315                 320
Leu Gln Thr Lys Ile Asp Gly Leu Glu Lys Thr Asn Ser Lys Leu Gln
                325                 330                 335
Glu Glu Leu Ser Ala Ala Thr Asp Arg Ile Cys Ser Leu Gln Glu Glu
            340                 345                 350
Gln Gln Gln Leu Arg Glu Gln Asn Glu Leu Ile Arg Glu Arg Ser Glu
        355                 360                 365
Lys Ser Val Glu Ile Thr Lys Gln Asp Thr Lys Val Glu Leu Glu Thr
    370                 375                 380
Tyr Lys Gln Thr Arg Gln Gly Leu Asp Glu Met Tyr Ser Asp Val Trp
385                 390                 395                 400
Lys Gln Leu Lys Glu Glu Lys Lys Val Arg Leu Glu Leu Glu Lys Glu
                405                 410                 415
Leu Glu Leu Gln Ile Gly Met Lys Thr Glu Met Glu Ile Ala Met Lys
            420                 425                 430
Leu Leu Glu Lys Asp Thr His Glu Lys Gln Asp Thr Leu Val Ala Leu
        435                 440                 445
Arg Gln Gln Leu Glu Glu Val Lys Ala Ile Asn Leu Gln Met Phe His
    450                 455                 460
Lys Ala Gln Asn Ala Glu Ser Ser Leu Gln Gln Lys Asn Glu Ala Ile
465                 470                 475                 480
Thr Ser Phe Glu Gly Lys Thr Asn Gln Val Met Ser Ser Met Lys Gln
                485                 490                 495
Met Glu Glu Arg Leu Gln His Ser Glu Arg Ala Arg Gln Gly Ala Glu
            500                 505                 510
Glu Arg Ser His Lys Leu Gln Gln Glu Leu Gly Gly Arg Ile Gly Ala
        515                 520                 525
Leu Gln Leu Gln Leu Ser Gln Leu His Glu Gln Cys Ser Ser Leu Glu
    530                 535                 540
Lys Glu Leu Lys Ser Glu Lys Glu Gln Arg Gln Ala Leu Gln Arg Glu
545                 550                 555                 560
Leu Gln His Glu Lys Asp Thr Ser Ser Leu Leu Arg Met Glu Leu Gln
                565                 570                 575
Gln Val Glu Gly Leu Lys Lys Glu Leu Arg Glu Leu Gln Asp Glu Lys
            580                 585                 590
Ala Glu Leu Gln Lys Ile Cys Glu Glu Gln Glu Gln Ala Leu Gln Glu
        595                 600                 605
```

```
Met Gly Leu His Leu Ser Gln Ser Lys Leu Lys Met Glu Asp Ile Lys
    610                 615                 620
Glu Val Asn Gln Ala Leu Lys Gly His Ala Trp Leu Lys Asp Asp Glu
625                 630                 635                 640
Ala Thr His Cys Arg Gln Cys Glu Lys Glu Phe Ser Ile Ser Arg Arg
                645                 650                 655
Lys His His Cys Arg Asn Cys Gly His Ile Phe Cys Asn Thr Cys Ser
            660                 665                 670
Ser Asn Glu Leu Ala Leu Pro Ser Tyr Pro Lys Pro Val Arg Val Cys
        675                 680                 685
Asp Ser Cys His Thr Leu Leu Leu Gln Arg Cys Ser Ser Thr Ala Ser
    690                 695                 700

      <210> 192
      <211> 331
      <212> PRT
      <213> Homo sapien

      <400> 192
Arg Ala Gly Ala Ser Ala Met Ala Leu Arg Lys Glu Leu Leu Lys Ser
 1               5                  10                  15
Ile Trp Tyr Ala Phe Thr Ala Leu Asp Val Glu Lys Ser Gly Lys Val
            20                  25                  30
Ser Lys Ser Gln Leu Lys Val Leu Ser His Asn Leu Tyr Thr Val Leu
        35                  40                  45
His Ile Pro His Asp Pro Val Ala Leu Glu Glu His Phe Arg Asp Asp
    50                  55                  60
Asp Asp Gly Pro Val Ser Ser Gln Gly Tyr Met Pro Tyr Leu Asn Lys
65                  70                  75                  80
Tyr Ile Leu Asp Lys Val Glu Glu Gly Ala Phe Val Lys Glu His Phe
                85                  90                  95
Asp Glu Leu Cys Trp Thr Leu Thr Ala Lys Lys Asn Tyr Arg Ala Asp
            100                 105                 110
Ser Asn Gly Asn Ser Met Leu Ser Asn Gln Asp Ala Phe Arg Leu Trp
        115                 120                 125
Cys Leu Phe Asn Phe Leu Ser Glu Asp Lys Tyr Pro Leu Ile Met Val
    130                 135                 140
Pro Asp Glu Val Glu Tyr Leu Leu Lys Lys Val Leu Ser Ser Met Ser
145                 150                 155                 160
Leu Glu Val Ser Leu Gly Glu Leu Glu Glu Leu Leu Ala Gln Glu Ala
                165                 170                 175
Gln Val Ala Gln Thr Thr Gly Gly Leu Ser Val Trp Gln Phe Leu Glu
            180                 185                 190
Leu Phe Asn Ser Gly Arg Cys Leu Arg Gly Val Gly Arg Asp Thr Leu
        195                 200                 205
Ser Met Ala Ile His Glu Val Tyr Gln Glu Leu Ile Gln Asp Val Leu
    210                 215                 220
Lys Gln Gly Tyr Leu Trp Lys Arg Gly His Leu Arg Arg Asn Trp Ala
225                 230                 235                 240
Glu Arg Trp Phe Gln Leu Gln Pro Ser Cys Leu Cys Tyr Phe Gly Ser
                245                 250                 255
Glu Glu Cys Lys Glu Lys Arg Gly Ile Ile Pro Leu Asp Ala His Cys
            260                 265                 270
Cys Val Glu Val Leu Pro Asp Arg Asp Gly Lys Arg Cys Met Phe Cys
        275                 280                 285
Val Lys Thr Ala Thr Arg Thr Tyr Glu Met Ser Ala Ser Asp Thr Arg
    290                 295                 300
Gln Arg Gln Glu Trp Thr Ala Ala Ile Gln Met Ala Ile Arg Leu Gln
```

305 310 315 320
Ala Glu Gly Lys Thr Ser Leu His Lys Asp Leu
325 330

<210> 193
<211> 475
<212> PRT
<213> Homo sapien

<400> 193
Lys Asn Ser Pro Leu Leu Ser Val Ser Ser Gln Thr Ile Thr Lys Glu
1 5 10 15
Asn Asn Arg Asn Val His Leu Glu His Ser Glu Gln Asn Pro Gly Ser
20 25 30
Ser Ala Gly Asp Thr Ser Ala Ala His Gln Val Val Leu Gly Glu Asn
35 40 45
Leu Ile Ala Thr Ala Leu Cys Leu Ser Gly Ser Gly Ser Gln Ser Asp
50 55 60
Leu Lys Asp Val Ala Ser Thr Ala Gly Glu Glu Gly Asp Thr Ser Leu
65 70 75 80
Arg Glu Ser Leu His Pro Val Thr Arg Ser Leu Lys Ala Gly Cys His
85 90 95
Thr Lys Gln Leu Ala Ser Arg Asn Cys Ser Glu Glu Lys Ser Pro Gln
100 105 110
Thr Ser Ile Leu Lys Glu Gly Asn Arg Asp Thr Ser Leu Asp Phe Arg
115 120 125
Pro Val Val Ser Pro Ala Asn Gly Val Glu Gly Val Arg Val Asp Gln
130 135 140
Asp Asp Asp Gln Asp Ser Ser Ser Leu Lys Leu Ser Gln Asn Ile Ala
145 150 155 160
Val Gln Thr Asp Phe Lys Thr Ala Asp Ser Glu Val Asn Thr Asp Gln
165 170 175
Asp Ile Glu Lys Asn Leu Asp Lys Met Met Thr Glu Arg Thr Leu Leu
180 185 190
Lys Glu Arg Tyr Gln Glu Val Leu Asp Lys Gln Arg Gln Val Glu Asn
195 200 205
Gln Leu Gln Val Gln Leu Lys Gln Leu Gln Gln Arg Arg Glu Glu Glu
210 215 220
Met Lys Asn His Gln Glu Ile Leu Lys Ala Ile Gln Asp Val Thr Ile
225 230 235 240
Lys Arg Glu Glu Thr Lys Lys Lys Ile Glu Lys Glu Lys Lys Glu Phe
245 250 255
Leu Gln Lys Glu Gln Asp Leu Lys Ala Glu Ile Glu Lys Leu Cys Glu
260 265 270
Lys Gly Arg Arg Glu Val Trp Glu Met Glu Leu Asp Arg Leu Lys Asn
275 280 285
Gln Asp Gly Glu Ile Asn Arg Asn Ile Met Glu Glu Thr Glu Arg Ala
290 295 300
Trp Lys Ala Glu Ile Leu Ser Leu Glu Ser Arg Lys Glu Leu Leu Val
305 310 315 320
Leu Lys Leu Glu Glu Ala Glu Lys Glu Ala Glu Leu His Leu Thr Tyr
325 330 335
Leu Lys Ser Thr Pro Pro Thr Leu Glu Thr Val Arg Ser Lys Gln Glu
340 345 350
Trp Glu Thr Arg Leu Asn Gly Val Arg Ile Met Lys Lys Asn Val Arg
355 360 365
Asp Gln Phe Asn Ser His Ile Gln Leu Val Arg Asn Gly Ala Lys Leu
370 375 380

Ser Ser Leu Pro Gln Ile Pro Thr Pro Thr Leu Pro Pro Pro Pro Ser
385 390 395 400
Glu Thr Asp Phe Met Leu Gln Val Phe Gln Pro Ser Pro Ser Leu Ala
405 410 415
Pro Arg Met Pro Phe Ser Ile Gly Gln Val Thr Met Pro Met Val Met
420 425 430
Pro Ser Ala Asp Pro Arg Ser Leu Ser Phe Pro Ile Leu Asn Pro Ala
435 440 445
Leu Ser Gln Pro Ser Gln Pro Ser Ser Pro Leu Pro Gly Ser His Gly
450 455 460
Arg Asn Ser Pro Gly Leu Gly Ser Leu Val Ser
465 470 475

<210> 194
<211> 241
<212> PRT
<213> Homo sapien

<400> 194
Met Ser Gly Glu Ser Ala Arg Ser Leu Gly Lys Gly Ser Ala Pro Pro
1 5 10 15
Gly Pro Val Pro Glu Gly Ser Ile Arg Ile Tyr Ser Met Arg Phe Cys
20 25 30
Pro Phe Ala Glu Arg Thr Arg Leu Val Leu Lys Ala Lys Gly Ile Arg
35 40 45
His Glu Val Ile Asn Ile Asn Leu Lys Asn Lys Pro Glu Trp Phe Phe
50 55 60
Lys Lys Asn Pro Phe Gly Leu Val Pro Val Leu Glu Asn Ser Gln Gly
65 70 75 80
Gln Leu Ile Tyr Glu Ser Ala Ile Thr Cys Glu Tyr Leu Asp Glu Ala
85 90 95
Tyr Pro Gly Lys Lys Leu Leu Pro Asp Asp Pro Tyr Glu Lys Ala Cys
100 105 110
Gln Lys Met Ile Leu Glu Leu Phe Ser Lys Val Pro Ser Leu Val Gly
115 120 125
Ser Phe Ile Arg Ser Gln Asn Lys Glu Asp Tyr Ala Gly Leu Lys Glu
130 135 140
Glu Phe Arg Lys Glu Phe Thr Lys Leu Glu Glu Val Leu Thr Asn Lys
145 150 155 160
Lys Thr Thr Phe Phe Gly Gly Asn Ser Ile Ser Met Ile Asp Tyr Leu
165 170 175
Ile Trp Pro Trp Phe Glu Arg Leu Glu Ala Met Lys Leu Asn Glu Cys
180 185 190
Val Asp His Thr Pro Lys Leu Lys Leu Trp Met Ala Ala Met Lys Glu
195 200 205
Asp Pro Thr Val Ser Ala Leu Leu Thr Ser Glu Lys Asp Trp Gln Gly
210 215 220
Phe Leu Glu Leu Tyr Leu Gln Asn Ser Pro Glu Ala Cys Asp Tyr Gly
225 230 235 240
Leu

<210> 195
<211> 138
<212> PRT
<213> Homo sapien

<400> 195

```
Gln Thr Lys Ile Leu Glu Glu Asp Leu Glu Gln Ile Lys Leu Ser Leu
 1               5                  10                  15
Arg Glu Arg Gly Arg Glu Leu Thr Thr Gln Arg Gln Leu Met Gln Glu
            20                  25                  30
Arg Ala Glu Glu Gly Lys Gly Pro Ser Lys Ala Gln Arg Gly Ser Leu
        35                  40                  45
Glu His Met Lys Leu Ile Leu Arg Asp Lys Glu Lys Glu Val Glu Cys
    50                  55                  60
Gln Gln Glu His Ile His Glu Leu Gln Glu Leu Lys Asp Gln Leu Glu
65                  70                  75                  80
Gln Gln Leu Gln Gly Leu His Arg Lys Val Gly Glu Thr Ser Leu Leu
                85                  90                  95
Leu Ser Gln Arg Glu Gln Glu Ile Val Val Leu Gln Gln Gln Leu Gln
            100                 105                 110
Glu Ala Arg Glu Gln Gly Glu Leu Lys Glu Gln Ser Leu Gln Ser Gln
        115                 120                 125
Leu Asp Glu Ala Gln Arg Ala Leu Ala Gln
    130                 135

      <210> 196
      <211> 102
      <212> PRT
      <213> Homo sapien

      <400> 196
Met Ser Lys Arg Lys Ala Pro Gln Glu Thr Leu Asn Gly Gly Ile Thr
 1               5                  10                  15
Asp Met Leu Thr Glu Leu Ala Asn Phe Glu Lys Asn Val Ser Gln Ala
            20                  25                  30
Ile His Lys Tyr Asn Ala Tyr Arg Lys Ala Ala Ser Val Ile Ala Lys
        35                  40                  45
Tyr Pro His Lys Ile Lys Ser Gly Ala Glu Ala Lys Lys Leu Pro Gly
    50                  55                  60
Val Gly Thr Lys Ile Ala Glu Lys Ile Asp Glu Phe Leu Ala Thr Gly
65                  70                  75                  80
Lys Leu Arg Lys Leu Glu Lys Ile Arg Gln Asp Asp Thr Ser Ser Ser
                85                  90                  95
Ile Asn Phe Leu Thr Arg
            100

      <210> 197
      <211> 138
      <212> PRT
      <213> Homo sapien

      <400> 197
Glu Ala Asn Glu Val Thr Asp Ser Ala Tyr Met Gly Ser Glu Ser Thr
 1               5                  10                  15
Tyr Ser Glu Cys Glu Thr Phe Thr Asp Glu Asp Thr Ser Thr Leu Val
            20                  25                  30
His Pro Glu Leu Gln Pro Glu Gly Asp Ala Asp Ser Ala Gly Gly Ser
        35                  40                  45
Ala Val Pro Ser Glu Cys Leu Asp Ala Met Glu Glu Pro Asp His Gly
    50                  55                  60
Ala Leu Leu Leu Leu Pro Gly Arg Pro His Pro His Gly Gln Ser Val
65                  70                  75                  80
Ile Thr Val Ile Gly Gly Glu Glu His Phe Glu Asp Tyr Gly Glu Gly
                85                  90                  95
```

Ser Glu Ala Glu Leu Ser Pro Glu Thr Leu Cys Asn Gly Gln Leu Gly
100 105 110
Cys Ser Asp Pro Ala Phe Leu Thr Pro Ser Pro Thr Lys Arg Leu Ser
115 120 125
Ser Lys Lys Val Ala Arg Tyr Leu His Gln
130 135

<210> 198
<211> 100
<212> PRT
<213> Homo sapien

<400> 198
Met Gly Asp Val Lys Asn Phe Leu Tyr Ala Trp Cys Gly Lys Arg Lys
1 5 10 15
Met Thr Pro Ser Tyr Glu Ile Arg Ala Val Gly Asn Lys Asn Arg Gln
20 25 30
Lys Phe Met Cys Glu Val Gln Val Glu Gly Tyr Asn Tyr Thr Gly Met
35 40 45
Gly Asn Ser Thr Asn Lys Lys Asp Ala Gln Ser Asn Ala Ala Arg Asp
50 55 60
Phe Val Asn Tyr Leu Val Arg Ile Asn Glu Ile Lys Ser Glu Glu Val
65 70 75 80
Pro Ala Phe Gly Val Ala Ser Pro Pro Pro Leu Thr Asp Thr Pro Asp
85 90 95
Thr Thr Ala Asn
100

<210> 199
<211> 127
<212> PRT
<213> Homo sapien

<400> 199
Met Val Lys Glu Thr Thr Tyr Tyr Asp Val Leu Gly Val Lys Pro Asn
1 5 10 15
Ala Thr Gln Glu Glu Leu Lys Lys Ala Tyr Arg Lys Leu Ala Leu Lys
20 25 30
Tyr His Pro Asp Lys Asn Pro Asn Glu Gly Glu Lys Phe Lys Gln Ile
35 40 45
Ser Gln Ala Tyr Glu Val Leu Ser Asp Ala Lys Lys Arg Glu Leu Tyr
50 55 60
Asp Lys Gly Gly Glu Gln Ala Ile Lys Glu Gly Gly Ala Gly Gly Gly
65 70 75 80
Phe Gly Ser Pro Met Asp Ile Phe Asp Met Phe Phe Gly Gly Gly Gly
85 90 95
Arg Met Gln Arg Glu Arg Arg Gly Lys Asn Val Val His Gln Leu Ser
100 105 110
Val Thr Leu Glu Asp Leu Tyr Asn Gly Ala Thr Arg Lys Leu Ala
115 120 125

<210> 200
<211> 90
<212> PRT
<213> Homo sapien

<400> 200
Met Ala Cys Pro Leu Asp Gln Ala Ile Gly Leu Leu Val Ala Ile Phe

```
 1               5                   10                  15
His Lys Tyr Ser Gly Arg Glu Gly Asp Lys His Thr Leu Ser Lys Lys
            20                  25                  30
Glu Leu Lys Glu Leu Ile Gln Lys Glu Leu Thr Ile Gly Ser Lys Leu
        35                  40                  45
Gln Asp Ala Glu Ile Ala Arg Leu Met Glu Asp Leu Asp Arg Asn Lys
    50                  55                  60
Asp Gln Glu Val Asn Phe Gln Glu Tyr Val Thr Phe Leu Gly Ala Leu
65                  70                  75                  80
Ala Leu Ile Tyr Asn Glu Ala Leu Lys Gly
                85                  90

      <210> 201
      <211> 120
      <212> PRT
      <213> Homo sapien

      <400> 201
Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala
 1               5                   10                  15
Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
            20                  25                  30
Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
        35                  40                  45
Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
    50                  55                  60
Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
65                  70                  75                  80
Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala
                85                  90                  95
Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu
            100                 105                 110
Phe Lys Glu Leu Lys Ala Arg Asn
        115                 120

      <210> 202
      <211> 177
      <212> PRT
      <213> Homo sapien

      <400> 202
Met Ala Ala Gly Val Glu Ala Ala Ala Glu Val Ala Ala Thr Glu Ile
 1               5                   10                  15
Lys Met Glu Glu Glu Ser Gly Ala Pro Gly Val Pro Ser Gly Asn Gly
            20                  25                  30
Ala Pro Gly Pro Lys Gly Glu Gly Glu Arg Pro Ala Gln Asn Glu Lys
        35                  40                  45
Arg Lys Glu Lys Asn Ile Lys Arg Gly Gly Asn Arg Phe Glu Pro Tyr
    50                  55                  60
Ala Asn Pro Thr Lys Arg Tyr Arg Ala Phe Ile Thr Asn Ile Pro Phe
65                  70                  75                  80
Asp Val Lys Trp Gln Ser Leu Lys Asp Leu Val Lys Glu Lys Val Gly
                85                  90                  95
Glu Val Thr Tyr Val Glu Leu Leu Met Asp Ala Glu Gly Lys Ser Arg
            100                 105                 110
Gly Cys Ala Val Val Glu Phe Lys Met Glu Glu Ser Met Lys Lys Ala
        115                 120                 125
Ala Glu Val Leu Asn Lys His Ser Leu Ser Gly Arg Pro Leu Lys Val
```

```
    130                 135                 140
Lys Glu Asp Pro Asp Gly Glu His Ala Arg Arg Ala Met Gln Lys Ala
145                 150                 155                 160
Gly Arg Leu Gly Ser Thr Val Phe Val Ala Asn Leu Asp Tyr Lys Val
                165                 170                 175
Gly


      <210> 203
      <211> 164
      <212> PRT
      <213> Homo sapien

      <400> 203
Met Arg Leu Ala Val Gly Ala Leu Leu Val Cys Ala Val Leu Gly Leu
 1               5                  10                  15
Cys Leu Ala Val Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu
            20                  25                  30
His Glu Ala Thr Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val
        35                  40                  45
Ile Pro Ser Asp Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr
    50                  55                  60
Leu Asp Cys Ile Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr
65                  70                  75                  80
Leu Asp Ala Gly Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu
                85                  90                  95
Lys Pro Val Val Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr
            100                 105                 110
Phe Tyr Tyr Ala Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met
        115                 120                 125
Asn Gln Leu Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser
    130                 135                 140
Ala Gly Trp Asn Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu
145                 150                 155                 160
Pro Arg Lys Pro


      <210> 204
      <211> 241
      <212> PRT
      <213> Homo sapien

      <400> 204
Met Ser Gly Glu Ser Ala Arg Ser Leu Gly Lys Gly Ser Ala Pro Pro
 1               5                  10                  15
Gly Pro Val Pro Glu Gly Ser Ile Arg Ile Tyr Ser Met Arg Phe Cys
            20                  25                  30
Pro Phe Ala Glu Arg Thr Arg Leu Val Leu Lys Ala Lys Gly Ile Arg
        35                  40                  45
His Glu Val Ile Asn Ile Asn Leu Lys Asn Lys Pro Glu Trp Phe Phe
    50                  55                  60
Lys Lys Asn Pro Phe Gly Leu Val Pro Val Leu Glu Asn Ser Gln Gly
65                  70                  75                  80
Gln Leu Ile Tyr Glu Ser Ala Ile Thr Cys Glu Tyr Leu Asp Glu Ala
                85                  90                  95
Tyr Pro Gly Lys Lys Leu Leu Pro Asp Asp Pro Tyr Glu Lys Ala Cys
            100                 105                 110
Gln Lys Met Ile Leu Glu Leu Phe Ser Lys Val Pro Ser Leu Val Gly
```

```
        115                 120                 125
Ser Phe Ile Arg Ser Gln Asn Lys Glu Asp Tyr Asp Gly Leu Lys Glu
    130                 135                 140
Glu Phe Arg Lys Glu Phe Thr Lys Leu Glu Glu Val Leu Thr Asn Lys
145                 150                 155                 160
Lys Thr Thr Phe Phe Gly Gly Asn Ser Ile Ser Met Ile Asp Tyr Leu
                165                 170                 175
Ile Trp Pro Trp Phe Glu Arg Leu Glu Ala Met Lys Leu Asn Glu Cys
            180                 185                 190
Val Asp His Thr Pro Lys Leu Lys Leu Trp Met Ala Ala Met Lys Glu
        195                 200                 205
Asp Pro Thr Val Ser Ala Leu Leu Thr Ser Glu Lys Asp Trp Gln Gly
    210                 215                 220
Phe Leu Glu Leu Tyr Leu Gln Asn Ser Pro Glu Ala Cys Asp Tyr Gly
225                 230                 235                 240
Leu
```

<210> 205
<211> 160
<212> PRT
<213> Homo sapien

<400> 205

```
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
 1               5                  10                  15
Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
            20                  25                  30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
        35                  40                  45
Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
    50                  55                  60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
65                  70                  75                  80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Pro Ser
                85                  90                  95
Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
            100                 105                 110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
        115                 120                 125
Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
    130                 135                 140
Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu
145                 150                 155                 160
```

<210> 206
<211> 197
<212> PRT
<213> Homo sapien

<400> 206

```
Thr Ser Pro Ser Glu Ala Cys Ala Pro Leu Leu Ile Ser Leu Ser Thr
 1               5                  10                  15
Leu Ile Tyr Asn Gly Ala Leu Pro Cys Gln Cys Asn Pro Gln Gly Ser
            20                  25                  30
Leu Ser Ser Glu Cys Asn Pro His Gly Gly Gln Cys Leu Cys Lys Pro
        35                  40                  45
Gly Val Val Gly Arg Arg Cys Asp Leu Cys Ala Pro Gly Tyr Tyr Gly
```

```
    50                  55                  60
Phe Gly Pro Thr Gly Cys Gln Gly Ala Cys Leu Gly Cys Arg Asp His
65                  70                  75                  80
Thr Gly Gly Glu His Cys Glu Arg Cys Ile Ala Gly Phe His Gly Asp
                85                  90                  95
Pro Arg Leu Pro Tyr Gly Gly Gln Cys Arg Pro Cys Pro Cys Pro Glu
            100                 105                 110
Gly Pro Gly Ser Gln Arg His Phe Ala Thr Ser Cys His Gln Asp Glu
        115                 120                 125
Tyr Ser Gln Gln Ile Val Cys His Cys Arg Ala Gly Tyr Thr Gly Leu
    130                 135                 140
Arg Cys Glu Ala Cys Ala Pro Gly His Phe Gly Asp Pro Ser Arg Pro
145                 150                 155                 160
Gly Gly Arg Cys Gln Leu Cys Glu Cys Ser Gly Asn Ile Asp Pro Met
                165                 170                 175
Asp Pro Asp Ala Cys Asp Pro His Thr Gly Gln Cys Leu Arg Cys Leu
            180                 185                 190
His His Thr Glu Gly
        195

      <210> 207
      <211> 175
      <212> PRT
      <213> Homo sapien

      <400> 207
Ile Ile Arg Gln Gln Gly Leu Ala Ser Tyr Asp Tyr Val Arg Arg Arg
 1               5                  10                  15
Leu Thr Ala Glu Asp Leu Phe Glu Ala Arg Ile Ile Ser Leu Glu Thr
            20                  25                  30
Tyr Asn Leu Leu Arg Glu Gly Thr Arg Ser Leu Arg Glu Ala Leu Glu
        35                  40                  45
Ala Glu Ser Ala Trp Cys Tyr Leu Tyr Gly Thr Gly Ser Val Ala Gly
    50                  55                  60
Val Tyr Leu Pro Gly Ser Arg Gln Thr Leu Ser Ile Tyr Gln Ala Leu
65                  70                  75                  80
Lys Lys Gly Leu Leu Ser Ala Glu Val Ala Arg Leu Leu Leu Glu Ala
                85                  90                  95
Gln Ala Ala Thr Gly Phe Leu Leu Asp Pro Val Lys Gly Glu Arg Leu
            100                 105                 110
Thr Val Asp Glu Ala Val Arg Lys Gly Leu Val Gly Pro Glu Leu His
        115                 120                 125
Asp Arg Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Arg Asp Pro
    130                 135                 140
Tyr Thr Glu Gln Thr Ile Ser Leu Phe Gln Ala Met Lys Lys Glu Leu
145                 150                 155                 160
Ile Pro Thr Glu Glu Ala Leu Arg Leu Trp Met Pro Ser Trp Pro
                165                 170                 175

      <210> 208
      <211> 177
      <212> PRT
      <213> Homo sapien

      <400> 208
Met Ala Ala Gly Val Glu Ala Ala Ala Glu Val Ala Ala Thr Glu Ile
 1               5                  10                  15
Lys Met Glu Glu Glu Ser Gly Ala Pro Gly Val Pro Ser Gly Asn Gly
```

```
        20                  25                  30
Ala Pro Gly Pro Lys Gly Glu Gly Glu Arg Pro Ala Gln Asn Glu Lys
        35                  40                  45
Arg Lys Glu Lys Asn Ile Lys Arg Gly Gly Asn Arg Phe Glu Pro Tyr
    50                  55                  60
Ala Asn Pro Thr Lys Arg Tyr Arg Ala Phe Ile Thr Asn Ile Pro Phe
65                  70                  75                  80
Asp Val Lys Trp Gln Ser Leu Lys Asp Leu Val Lys Glu Lys Val Gly
                85                  90                  95
Glu Val Thr Tyr Val Glu Leu Leu Met Asp Ala Glu Gly Lys Ser Arg
            100                 105                 110
Gly Cys Ala Val Val Glu Phe Lys Met Glu Glu Ser Met Lys Lys Ala
        115                 120                 125
Ala Glu Val Leu Asn Lys His Ser Leu Ser Gly Arg Pro Leu Lys Val
    130                 135                 140
Lys Glu Asp Pro Asp Gly Glu His Ala Arg Arg Ala Met Gln Lys Val
145                 150                 155                 160
Met Ala Thr Thr Gly Gly Met Gly Met Gly Pro Gly Gly Pro Gly Met
                165                 170                 175
Ile


      <210> 209
      <211> 196
      <212> PRT
      <213> Homo sapien

      <400> 209
Asp Leu Gln Asp Met Phe Ile Val His Thr Ile Glu Glu Ile Glu Gly
 1               5                  10                  15
Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp
            20                  25                  30
Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys Glu Ala Gln Arg Ile
        35                  40                  45
Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr
    50                  55                  60
Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln Leu
65                  70                  75                  80
Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln
                85                  90                  95
Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val Val
            100                 105                 110
Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile Ser Ile
        115                 120                 125
Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser His Leu Lys Gln Tyr
    130                 135                 140
Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu Asp Leu Leu Glu Gln
145                 150                 155                 160
Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys His Thr
                165                 170                 175
Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu Leu Thr
            180                 185                 190
Thr Ile Ala Arg
        195

      <210> 210
      <211> 156
      <212> PRT
```

<213> Homo sapien

<400> 210
Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly Lys Glu
1   5   10   15
Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn Arg Ile Gly Tyr Ser
            20   25   30
Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser Leu Ile Val Gly Tyr
        35   40   45
Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser Gly Arg
    50   55   60
Glu Thr Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Val Thr Gln
65   70   75   80
Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile Lys Ser Asp Leu Val
                85   90   95
Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr Pro Glu Leu Pro Lys
            100   105   110
Pro Ser Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys Asp Ala
        115   120   125
Val Ala Phe Thr Cys Glu Pro Glu Val Gln Asn Thr Thr Tyr Leu Trp
    130   135   140
Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro Lys
145   150   155

<210> 211
<211> 92
<212> PRT
<213> Homo sapien

<400> 211
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
1   5   10   15
Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
            20   25   30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
        35   40   45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
    50   55   60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65   70   75   80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly
                85   90

<210> 212
<211> 142
<212> PRT
<213> Homo sapien

<400> 212
Glu Lys Gln Lys Asn Lys Glu Phe Ser Gln Thr Leu Glu Asn Glu Lys
1   5   10   15
Asn Thr Leu Leu Ser Gln Ile Ser Thr Lys Asp Gly Glu Leu Lys Met
            20   25   30
Leu Gln Glu Glu Val Thr Lys Met Asn Leu Leu Asn Gln Gln Ile Gln
        35   40   45
Glu Glu Leu Ser Arg Val Thr Lys Leu Lys Glu Thr Ala Glu Glu Glu
    50   55   60
Lys Asp Asp Leu Glu Glu Arg Leu Met Asn Gln Leu Ala Glu Leu Asn

```
65                  70                  75                  80
Gly Ser Ile Gly Asn Tyr Cys Gln Asp Val Thr Asp Ala Gln Ile Lys
                85                  90                  95
Asn Glu Leu Leu Glu Ser Glu Met Lys Asn Leu Lys Lys Cys Val Ser
            100                 105                 110
Glu Leu Glu Glu Glu Lys Gln Gln Leu Val Lys Glu Lys Thr Lys Val
        115                 120                 125
Glu Ser Glu Ile Arg Lys Glu Tyr Leu Glu Lys Ile Gln Gly
    130                 135                 140

      <210> 213
      <211> 142
      <212> PRT
      <213> Homo sapien

      <400> 213
Gly Gly Tyr Gly Gly Gly Tyr Gly Gly Val Leu Thr Ala Ser Asp Gly
 1               5                  10                  15
Leu Leu Ala Gly Asn Glu Lys Leu Thr Met Gln Asn Leu Asn Asp Arg
            20                  25                  30
Leu Ala Ser Tyr Leu Asp Lys Val Arg Ala Leu Glu Ala Ala Asn Gly
        35                  40                  45
Glu Leu Glu Val Lys Ile Arg Asp Trp Tyr Gln Lys Gln Gly Pro Gly
    50                  55                  60
Pro Ser Arg Asp Tyr Ser His Tyr Tyr Thr Thr Ile Gln Asp Leu Arg
65                  70                  75                  80
Asp Lys Ile Leu Gly Ala Thr Ile Glu Asn Ser Arg Ile Val Leu Gln
                85                  90                  95
Ile Asp Asn Ala Arg Leu Ala Ala Asp Asp Phe Arg Thr Lys Phe Glu
            100                 105                 110
Thr Glu Gln Ala Leu Arg Met Ser Val Glu Ala Asp Ile Asn Gly Leu
        115                 120                 125
Arg Arg Val Leu Asp Glu Leu Thr Leu Ala Arg Thr Asp Leu
    130                 135                 140

      <210> 214
      <211> 129
      <212> PRT
      <213> Homo sapien

      <400> 214
Val Met Arg Val Asp Phe Asn Val Pro Met Lys Asn Asn Gln Ile Thr
 1               5                  10                  15
Asn Asn Gln Arg Ile Lys Ala Ala Val Pro Ser Ile Lys Phe Cys Leu
            20                  25                  30
Asp Asn Gly Ala Lys Ser Val Val Leu Met Ser His Leu Gly Arg Pro
        35                  40                  45
Asp Gly Val Pro Met Pro Asp Lys Tyr Ser Leu Glu Pro Val Ala Val
    50                  55                  60
Glu Leu Arg Ser Leu Leu Gly Lys Asp Val Leu Phe Leu Lys Asp Cys
65                  70                  75                  80
Val Gly Pro Glu Val Glu Lys Ala Cys Ala Asn Pro Ala Ala Gly Ser
                85                  90                  95
Val Ile Leu Leu Glu Asn Leu Arg Phe His Val Glu Glu Glu Gly Lys
            100                 105                 110
Gly Lys Asp Ala Ser Gly Asn Lys Val Lys Ala Glu Pro Ala Lys Ile
        115                 120                 125
Glu
```

<210> 215
<211> 148
<212> PRT
<213> Homo sapien

<400> 215
Met Ala Thr Leu Lys Glu Lys Leu Ile Ala Pro Val Ala Glu Glu Glu
1 5 10 15
Ala Thr Val Pro Asn Asn Lys Ile Thr Val Val Gly Val Gly Gln Val
20 25 30
Gly Met Ala Cys Ala Ile Ser Ile Leu Gly Lys Ser Leu Ala Asp Glu
35 40 45
Leu Ala Leu Val Asp Val Leu Glu Asp Lys Leu Lys Gly Glu Met Met
50 55 60
Asp Leu Gln His Gly Ser Leu Phe Leu Gln Thr Pro Lys Ile Val Ala
65 70 75 80
Asp Lys Asp Tyr Ser Val Thr Ala Asn Ser Lys Ile Val Val Val Thr
85 90 95
Ala Gly Val Arg Gln Gln Glu Gly Glu Ser Arg Leu Asn Leu Val Gln
100 105 110
Arg Asn Val Asn Val Phe Lys Phe Ile Ile Pro Gln Ile Val Lys Tyr
115 120 125
Ser Pro Asp Cys Ile Ile Ile Val Val Ser Asn Pro Val Asp Ile Leu
130 135 140
Thr Tyr Val Thr
145

<210> 216
<211> 527
<212> PRT
<213> Homo sapien

<400> 216
Gln Arg Ala Pro Gly Ile Glu Glu Lys Ala Ala Glu Asn Gly Ala Leu
1 5 10 15
Gly Ser Pro Glu Arg Glu Glu Lys Val Leu Glu Asn Gly Glu Leu Thr
20 25 30
Pro Pro Arg Arg Glu Glu Lys Ala Leu Glu Asn Gly Glu Leu Arg Ser
35 40 45
Pro Glu Ala Gly Glu Lys Val Leu Val Asn Gly Gly Leu Thr Pro Pro
50 55 60
Lys Ser Glu Asp Lys Val Ser Glu Asn Gly Gly Leu Arg Phe Pro Arg
65 70 75 80
Asn Thr Glu Arg Pro Pro Glu Thr Gly Pro Trp Arg Ala Pro Gly Pro
85 90 95
Trp Glu Lys Thr Pro Glu Ser Trp Gly Pro Ala Pro Thr Ile Gly Glu
100 105 110
Pro Ala Pro Glu Thr Ser Leu Glu Arg Ala Pro Ala Pro Ser Ala Val
115 120 125
Val Ser Ser Arg Asn Gly Gly Glu Thr Ala Pro Gly Pro Leu Gly Pro
130 135 140
Ala Pro Lys Asn Gly Thr Leu Glu Pro Gly Thr Glu Arg Arg Ala Pro
145 150 155 160
Glu Thr Gly Gly Ala Pro Arg Ala Pro Gly Ala Gly Arg Leu Asp Leu
165 170 175
Gly Ser Gly Gly Arg Ala Pro Val Gly Thr Gly Thr Ala Pro Gly Gly

```
            180                      185                      190
Gly Pro Gly Ser Gly Val Asp Ala Lys Ala Gly Trp Val Asp Asn Thr
        195                      200                      205
Arg Pro Gln Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Glu Ala Gln
    210                      215                      220
Pro Arg Arg Leu Glu Pro Ala Pro Pro Arg Ala Arg Pro Glu Val Ala
225                      230                      235                      240
Pro Glu Gly Glu Pro Gly Ala Pro Asp Ser Arg Ala Gly Gly Asp Thr
                245                      250                      255
Ala Leu Ser Gly Asp Gly Asp Pro Pro Lys Pro Glu Arg Lys Gly Pro
            260                      265                      270
Glu Met Pro Arg Leu Phe Leu Asp Leu Gly Pro Pro Gln Gly Asn Ser
        275                      280                      285
Glu Gln Ile Lys Ala Arg Leu Ser Arg Leu Ser Leu Ala Leu Pro Pro
    290                      295                      300
Leu Thr Leu Thr Pro Phe Pro Gly Pro Gly Pro Arg Arg Pro Pro Trp
305                      310                      315                      320
Glu Gly Ala Asp Ala Gly Ala Ala Gly Gly Glu Ala Gly Gly Ala Gly
                325                      330                      335
Ala Pro Gly Pro Ala Glu Glu Asp Gly Glu Asp Glu Asp Glu Asp Glu
            340                      345                      350
Glu Glu Asp Glu Glu Ala Ala Ala Pro Gly Ala Ala Ala Gly Pro Arg
        355                      360                      365
Gly Pro Gly Arg Ala Arg Ala Ala Pro Val Pro Val Val Val Ser Ser
    370                      375                      380
Ala Asp Ala Asp Ala Ala Arg Pro Leu Arg Gly Leu Leu Lys Ser Pro
385                      390                      395                      400
Arg Gly Ala Asp Glu Pro Glu Asp Ser Glu Leu Glu Arg Lys Arg Lys
                405                      410                      415
Met Val Ser Phe His Gly Asp Val Thr Val Tyr Leu Phe Asp Gln Glu
            420                      425                      430
Thr Pro Thr Asn Glu Leu Ser Val Gln Ala Pro Pro Glu Gly Asp Thr
        435                      440                      445
Asp Pro Ser Thr Pro Pro Ala Pro Pro Thr Pro Pro His Pro Ala Thr
    450                      455                      460
Pro Gly Asp Gly Phe Pro Ser Asn Asp Ser Gly Phe Gly Gly Ser Phe
465                      470                      475                      480
Glu Trp Ala Glu Asp Phe Pro Leu Leu Pro Pro Pro Gly Pro Pro Leu
                485                      490                      495
Cys Phe Ser Arg Phe Ser Val Ser Pro Ala Leu Glu Thr Pro Gly Pro
            500                      505                      510
Pro Ala Arg Ala Pro Asp Ala Arg Pro Ala Gly Pro Val Glu Asn
        515                      520                      525
```

<210> 217
<211> 466
<212> DNA
<213> Homo sapien

<400> 217

```
gaatggtgcc tgtcctgctg tctctgctgc tgcttctggg tcctgctgtc ccccaggaga      60
accaagatgg tcgttactct ctgacctata tctacactgg gctgtccaag catgttgaag     120
acgtccccgc gtttcaggcc cttggctcac tcaatgacct ccagttcttt agatacaaca     180
gtaaagacag gaagtctcag cccatgggac tctggagaca ggtggaagga atggaggatt     240
ggaagcagga cagccaactt cagaaggcca gggaggacat ctttatggag accctgaaag     300
acatcgtgga gtattacaac gacagtaacg ggtctcacgt attgcaggga aggtttggtt     360
gtgagatcga gaataacaga agcagcggag cattctggaa atattactat gatggaaagg     420
actacattga attcaacaaa gaaatcccag cctgggtccc cttcga                    466
```

<210> 218
<211> 381
<212> DNA
<213> Homo sapien

<400> 218
gagtttcctt cgcaagttca tgtggggtac cttcccaggc tgcctggctg accagctggt 60
tttaaagcgc cggggtaacc agttggagat ctgtgccgtg gtcctgaggc agttgtctcc 120
acacaagtac tacttcctcg tgggctacag tgaaactttg ctgtcctact tttacaaatg 180
tcctgtgcga ctccacctcc aaactgtgcc ctcaaaggtt gtgtataagt acctctagaa 240
caatcccctt ttttccatca agctgtagcc tgcagagaat ggaaacgtgg gaaaggaatg 300
gtatgtgggg gaaatgcatc ccctcagagg actgaggcat agtctctcat ctgctattga 360
ataaagacct tctatcttgt a 381

<210> 219
<211> 1293
<212> DNA
<213> Homo sapien

<400> 219
gaggggaggc gcatggcggg gatggcgctg gcgcgggcct ggaagcagat gtcctggttc 60
tactaccagt acctgctggt cacggcgctc tacatgctgg agccctggga gcggacggtg 120
ttcaattcca tgctggtttc cattgtgggg atggcactat acacaggata cgtcttcatg 180
ccccagcaca tcatggcgat attgcactac tttgaaatcg tacaatgacc aagatgcgac 240
caggatcaga ggttccttgg ggaagaccca ccctacgaag ttggaatgag accatcagat 300
gtgataagaa actcttctag atgtcaacat aaccaacctt ataaagacta aaattcatga 360
gtagaacagg aaaatcatcc tgactcatgt gttgtgttct ttatttttaa ttttcaaaga 420
ggctcttgta tagcagtttt tgtctatttt aacattgtag tcatttgtac tttgatatca 480
gtattttctt aacctttgtg actgtttcaa tattaccccc gtgaaagctt ttcttaatgt 540
aactttgagt acattttaat tgccttctat ttttaaaact caaaatcatt agttgggctt 600
tactgttctt gctattgtat ggcatataca tctgcctgga tatatttcta ctcttgacca 660
aagttttgta aagaacaata taagatttcg ggtaggggta tggggaggga agatatttta 720
ttgagaacta cttaacaaaa gatttatctg taagcttgaa ctcaggagta cagttttagc 780
tatctagact ctaacagctt ttgctttaaa attattaaag tgtttcttaa tgaaaaagaa 840
aagatcttgc taaagttaaa ataaggaaca tttcaccttt taaatattta attcttatgt 900
ggacttattt ccagaaaact ttggtgataa ttcttgagac aaaaggtggt taagtagcat 960
tattatgtaa tgcttatata ccatagagtt tttaatagaa gagaaatcca tttcctccga 1020
gggtcactat taacaatgta cttccttaaa tttagtttaa tgattgtaat gggtgctgca 1080
tttgcacatt gcattaagtt atgatgagac gaattgttgt taaaaattat agcaaaaaga 1140
aatgtaaact tggttaaaat cctttcactc tttgtattgt ttttttaag gtttttattc 1200
cttaaatgta aaatgactac ctaatttttt gatgtaaata cattaaattc aaagagaaaa 1260
aaaatcaaaa aaaaaaaaaa aaaaaaactc gag 1293

<210> 220
<211> 983
<212> DNA
<213> Homo sapien

<400> 220
caggttattc tgatcctgcc gcctgtcttc cctgtaagag tggagcctcg aggtgtacct 60
taaagtgacc ggaatgttag agatgcaatt tgcagagctg gggcaaggaa gggctccttg 120
tcactgtagt tactttcctt gcagtggcca aatgcccaat aagaaggaat acatgaccac 180
tgctgtgggg agtcagcagg tgcgtgatgc agctggccac actccatcca cggccatgac 240
ataaaacaga caagaagtaa ggctggactg taacacctca aggcctgctc cagtgaccca 300
ctttcttcag agaggctcta ccacacacac aaccaccttc caaatttaca ctcagatcac 360
tacaccatgt ctcccaagtt aaaacatgta tccacctaga ctttaaatgt gctttgtaac 420
tgttgatggc actgtacaga gggccaaagt atttcccatc agatagcatt tttctgaacc 480

catgcctctt gggacgagat cacaggactt gacccatcat caaataggac caggtgacct 540
acagagacat cacaatgatg gcttcctaca gtcaagtcca tttccaataa tgctctcatc 600
taagagaacc catgaacctt atttgaatcc tggttcaaac aaaaacctta aattatttat 660
gagacaatta taaacttgat agattttgat gtgtgaaggt atttatgaat atttttagtc 720
agtgatggta tactgttaag gaaaaggttc atattttagg gacaaaggct gaaacattta 780
tggacagagt gatatgatat ctgggatttg ttttaggatg aagtgggagg gaggaaatga 840
atggaaatag tgttgaaaca gtattggcca cgagtcagct attgtgtgct aagacgctcc 900
tcacaccagt ctactctgta tgtgtttgaa tatctctgta ataaacttaa caaggaaaaa 960
aaaaaaaaaa aaaaaaactc gag 983

<210> 221
<211> 373
<212> DNA
<213> Homo sapien

<400> 221
cattttatgg gttaattttt tattaaatag caataagata cttttataac tcaataaaat 60
tattcaatga tacattcgga aaataaatgt ataaaatatg aaaaagtact aaaaagcatt 120
tttcagtact tttaggtaag attaatccaa ctaaacacta gcatatgtta tacagtaata 180
ataaggggaa aatacaataa tgttgagaaa gcaaactcaa agcatagatc aatgaaaaaa 240
ttgagaaatg gacataaatg atttagtatt tttaaagaga gtgaaaaatc attattttat 300
gcttttgtgt agcgttagat gaattaaata acatatgcac atatagcttt gcgatacaaa 360
tttccagacc ata 373

<210> 222
<211> 544
<212> DNA
<213> Homo sapien

<400> 222
cagagatgct gctgctacaa aggatcggtg taagcagtta acccaggaaa tgatgacaga 60
gaaagaaaga agcaatgtgg ttataacaag gatgaaagat cgaattggaa cattagaaaa 120
ggaacataat gtatttcaaa acaaaataca tgtcagttat caagagactc aacagatgca 180
gatgaagttt cagcaagttc gtgagcagat ggaggcagag atagctcact tgaagcagga 240
aaatggtata ctgagagatg cagtcagcaa cactacaaat caactggaaa gcaagcagtc 300
tgcagaacta aataaactac gccaggatta tgctaggttg gtgaatgagc tgactgagaa 360
aacaggaaag ctacagcaag aggaagtcca aaagaagaat gctgagcaag cagctactca 420
gttgaaggtt caactacaag aagctgagag aaggtgggaa gaagttcaga gctacatcag 480
gaagagaaca gcggaacatg aggcagcaca gctagattta cagagtaaat ttgtggccaa 540
agaa 544

<210> 223
<211> 316
<212> DNA
<213> Homo sapien

<400> 223
gaggcaaggg atatgcttta gtgcctatta tagttaattc ttcaactcca aagtctaaaa 60
cagttgaatc tgctgaagga aaatctgaag aagtaaatga aacattagtt atacccactg 120
aggaagcaga aatggaagaa agtggacgaa gtgcaactcc tgttaactgt gaacagcctg 180
atatcttggt ttcttctaca ccaataaatg aaggacagac tgtgttagac aaggtggctg 240
agcagtgtga acctgctgaa agtcagccag aagcacttct gagaggaaga tgtttgcaag 300
gtaactctaa cagttg 316

<210> 224
<211> 1583
<212> DNA
<213> Homo sapien

<400> 224
cagaccacgt ctgccctcgc cgctctagcc ctgcgcccca gcccggccgc ggcacctccg 60
cctcgccgcc gctaggtcgg ccggctccgc ccggctgccg cctaggatga atatcatgga 120
cttcaacgtg aagaagctgg cggccgacgc aggcaccttc ctcagtcgcg ccgtgcagtt 180
cacagaagaa aagcttggcc aggctgagaa gacagaattg gatgctcact tagagaacct 240
ccttagcaaa gctgaatgta ccaaaatatg gacagaaaaa ataatgaaac aaactgaagt 300
gttattgcag ccaaatccaa atgccaggat agaagaattt gtttatgaga aactggatag 360
aaaagctcca agtcgtataa acaacccaga acttttggga caatatatga ttgatgcagg 420
gactgagttt ggcccaggaa cagcttatgg taatgccctt attaaatgtg gagaaaccca 480
aaaaagaatt ggaacagcag acagagaact gattcaaacg tcagccttaa attttcttac 540
tcctttaaga aactttatag aaggagatta caaaacaatt gctaaagaaa ggaaactatt 600
gcaaaataag agactggatt tggatgctgc aaaaacgaga ctaaaaaagg caaaagctgc 660
agaaactaga aattcatctg aacaggaatt aagaataact caaagtgaat ttgatcgtca 720
agcagagatt accagacttc tgctagaggg aatcagcagt acacatgccc atcaccttcg 780
ctgtctgaat gactttgtag aagcccagat gacttactat gcacagtgtt accagtatat 840
gttggacctc cagaaacaac tgggaagttt tccatccaat tatcttagta acaacaatca 900
gacttctgtg acacctgtac catcagtttt accaaatgcg attggttctt ctgccatggc 960
ttcaacaagt ggcctagtaa tcacctctcc ttccaacctc agtgacctta aggagtgtag 1020
tggcagcaga aaggccaggg ttctctatga ttatgatgca gcaaacagta ctgaattatc 1080
acttctggca gatgaggtga tcactgtgtt cagtgttgtt ggaatggatt cagactggct 1140
aatgggggaa aggggaaacc agaagggcaa ggtgccaatt acctacttag aactgctcaa 1200
ttaagtaggt ggactatgga aaggttgccc atcatgactt tgtatttata tacaattaac 1260
tctaaataaa gcaggttaag tatcttccat gttaatgtgt taagagactg aaaataccag 1320
ccatcagaaa ctggcctttt tgccaataaa gttgcatggt aaatatttca ttacagaatt 1380
tatgttagag ctttcatgcc aagaatgttt tcttacaaaa ttctcttttt attgaggttt 1440
cactaataag cagcttctac ttttgagcct caacttaaag cagaactgtt ttttactgga 1500
tttttcatta acagcaagct ttttttttta tgtaaaataa atctattgtg aattgaaaaa 1560
aaaaaaaaaa aaaaaaactc gag 1583

<210> 225
<211> 491
<212> DNA
<213> Homo sapien

<400> 225
gaacaacatc atcttgaatc actagataga ctcttgacgg aaagcaaagg ggaaatgaaa 60
aaggaaaata tgaagaaaga tgaagcttta aaagcattac agaaccaagt atctgaagaa 120
acaatcaagg ttaggcaact agattcagca ttggaaattt gtaaggaaga acttgtcttg 180
catttgaatc aattggaagg aaataaggaa aagtttgaaa aacagttaaa gaagaaatct 240
gaagaggtat attgtttaca gaaagagcta aagataaaaa atcacagtct tcaagagact 300
tctgagcaaa acgttattct acagcatact cttcagcaac agcagcaaat gttacaacaa 360
gagacaatta gaaatggaga gctagaagat actcaaacta aacttgaaaa acaggtgtca 420
aaactggaac aagaacttca aaaacaaagg gaaagttcag ctgaaaagtt gagaaaaatg 480
gaggagaaat g 491

<210> 226
<211> 483
<212> DNA
<213> Homo sapien

<400> 226
cagccgcacg ccgcggagca ggggctcgga ggtcccggga ttacggtgct cgagcacgct 60
ggtgggaaag gacccgggac ttgaacagtg ttgtgcggcg ccatgcaggt ctccagcctc 120
aatgaggtga agatttacag cctcagctgc ggcaagtccc ttcctgagtg gctttctgat 180
aggaagaaga gagcgctaca gaagaaagat gtagatgtcc gtaggagaat tgaacttatt 240
caggactttg aaatgcctac tgtgtgtacc actattaagg tgtcaaaaga tggacagtac 300
attttagcaa ctggaacata taaacctcgg gttcgatgtt atgacaccta tcaattatcc 360

ttgaagtttg aaaggtgttt agattcagaa gttgtcacct ttgaaatttt gtctgatgac 420
tactcaaaga ttgtcttctt acataatgat agatacattg aatttcattc gcaatcaggt 480
ttt 483

<210> 227
<211> 486
<212> DNA
<213> Homo sapien

<400> 227
gagcctcgct aagctccgac tctgggcggc accgggcgtc ccacgatgcc gaagaacaag 60
aagcggaaca ctccccaccg cggtagcagt gctggcggcg gcgggtcagg agcagccgca 120
gcgacggcgg cgacagcagg tggccagcat cgaaatgttc agccttttag tgatgaagat 180
gcatcaattg aaacagtgag ccattgcagt ggttatagcg atccttccag ttttgctgaa 240
gatggaccag aagtccttga tgaggaagga actcaagaag acctagagta caagttgaag 300
ggattaattg acctaaccct ggataagagt gcgaagacaa ggcaagcagc tcttgaaggt 360
attaaaaatg cactggcttc aaaaatgctg tatgaattta ttctggaaag gagaatgact 420
ttaactgata gcattgaacg ctgcctgaaa aaaggtaaga gtgatgagca acgtgcagct 480
gcagcg 486

<210> 228
<211> 494
<212> DNA
<213> Homo sapien

<400> 228
gaggccagga ctccgggaat gcgagcaggc cccttattct cccagtggcc tcggtctgtc 60
cccacagcgg cccggtcagg gttgcccgag ccccaaggcg gggggcggca ccggggtgct 120
gaaagggaca gaatgctttg acctccaagc tgttttaaat ctagtagata agccagatcc 180
tgtgttgcca taagcccttg gcccacattt aagtgggaat gcagctagct tggatgtctg 240
aaactttgta agcgccttct gtctgaatcc tgaacacagg caccaagact actgaagaag 300
ctcgtcattc ttgtgcaggg atagccacac aagcaaacat gtttgcaaaa cttgaaagaa 360
agaaaattgc agaaagaaga cttgctgttc ttaagaggcc caggaaggtg ctacttagga 420
atcccaccgg cttgtgaagc aagggaatca agtttgcctt caatggggaa cttgacttca 480
ggaaaatgaa cttt 494

<210> 229
<211> 465
<212> DNA
<213> Homo sapien

<400> 229
gtcagagagc tggtataacc tcctgttgga catgcagaac cgactcaata aggtcatcaa 60
aagcgtgggc aagattgagc actccttctg gagatccttt cacactgagc gaaagacaga 120
accagccaca ggcttcatcg atggtgatct gattgaaagt ttcctagata tcagccgccc 180
taagatgcag gaggttgtgg caaacttgca gtatgatgat ggcagtggta tgaagcggga 240
ggcaactgca gatgacctca tcaaagtcgt ggaggaacta actcggatcc attagccaag 300
gacaggatct cttttcctga ccctcctaaa ggcgttgccc tcctatcctc ccttccttgc 360
ccacccttgg tttctttggc atgggaaggt tttccttaac cacttgccct agagccacca 420
gtgaccttgt gtggaaacag ggtttttttt acttaaaaca gttca 465

<210> 230
<211> 495
<212> DNA
<213> Homo sapien

<400> 230
caggggaaag ggtgtttggc cttgaccagc cactgctgac ctcaatctca gacctacaga 60

tggtgaatat ctccctgcga gtgttgtctc gacccaatgc tcaggagctt cctagcatgt 120
accagcgcct agggctggac tacgaggaac gagtgttgcc gtccattgtc aacgaggtgc 180
tcaagagtgt ggtggccaag ttcaatgcct cacagctgat cacccagcgg gcccaggtat 240
ccctgttgat ccgccgggag ctgacagaaa gggccaaagg acttcagcct catcctggat 300
gatgtggcca tcacagactt gagctttagc cgagaagtac acaagctgcc tgtaagaaac 360
ccaaccaagt ggggtgaatt ccaaaaaccc gtgggggtga agggcttctt aagaatgcaa 420
ggaaggagga aaagaattcc atgggggggg ggttccttaa cccaggaaca ggggtttccc 480
ttgaattttt ttcca 495

<210> 231
<211> 498
<212> DNA
<213> Homo sapien

<400> 231
ggcagcttct gagaccaggg ttgctccgtc cgtgctccgc ctcgccatga cttcctacag 60
ctatcgccag tcgtcggcca cgtcgtcctt cggaggcctg ggcggcggct ccgtgcgttt 120
tgggccgggg gtcgcttttc gcgcgcccag cattcacggg ggctccggcg gccgcggcgt 180
atccgtgtcc tccgcccgct ttgtgtcctc gtcctcctcg gggggctacg gcggcggcta 240
cggcggcgtc ctgaccgcgt ccgacgggct gctggcgggc aacgagaagc taaccatgca 300
gaacctcaac gaccgcctgc ctcctacctg gacaaagtgc gcgccctgga agcgggcaac 360
ggcgaactta gaggtgaaag aatcccgcga actggtacca aaaacaaggg gcctggggcc 420
ttccgcgact tacagccaac ttactacacc gaacattcaa gaacttgcgg gaacaaaaat 480
ttttggtgcc acccattt 498

<210> 232
<211> 465
<212> DNA
<213> Homo sapien

<400> 232
caggccggcc gagtaggaaa gctggaggcg cgggtgggga acatgtctga gtcggagctc 60
ggcaggaagt gggaccggtg tctggcggat gcggtcgtga agataggtac tggttttgga 120
ttaggaattg ttttctcact taccttcttt aaaagaagaa tgtggccatt agccttcggt 180
tctggcatgg gattaggaat ggcttattcc aactgtcagc atgatttcca ggctccatat 240
cttctacatg gaaaatatgt caaagagcag gagcagtgac ttcacctgag aacatcccag 300
cgggaggaca agagaaaatc atgtttattc ctcaggaata cttgaagtgc cctggagtaa 360
actgccattc ttctgtaaca atggtatcag taatgcttta aactccagca cctggttatg 420
catttgaaac ccaagtctgg ttcttggttt ggattttctc tctgg 465

<210> 233
<211> 366
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(366)
<223> n = A,T,C or G

<400> 233
cagtaaaaaa ggttatgttt tattaattgc tggacaaccg tgggaaaaca aataagcaat 60
tgacaccacc aaattcttat tacattcaan ataaaanatt tattcacacc acaaaaagat 120
aatcacaaca aaatatacac taacttaaaa aacaaaagat tatagtgaca taaaatgtta 180
tattctcttt ttaagtgggt aaaagtattt tgtttgcttc tacataaatt tctattcatg 240
ananaataac aaatattaaa atacagtgat agtttgcatt tcttctatag aatgaacata 300
gacataaccc tgaagctttt agtttacagg gagtttccat gaagccacaa actaaactaa 360
ttatca 366

<210> 234
<211> 379
<212> DNA
<213> Homo sapien

<400> 234
gagggcagcc ctcctacctg cgcacgtggt gccgccgctg ctgcctcccg ctcgccctga 60
acccagtgcc tgcagccatg gctcccggcc agctcgcctt atttagtgtc tctgacaaaa 120
ccggccttgt ggaatttgca agaaacctga ccgctcttgg tttgaatctg gtcgcttccg 180
gagggactgc aaaagctctc agggatgctg gtctggcagt cacagatgtc tctgagttga 240
cgggatttct gaaatgttgg ggggacgtgt gaaaactttg catcctgcac gatcccatgc 300
tggaatccta gctcctaata ttcagaagat aatgcttgac atgcgccaca cttgattcaa 360
tcttataaca attgttgcc 379

<210> 235
<211> 406
<212> DNA
<213> Homo sapien

<400> 235
caggctgcac catgtacccc accttcagtt taaaagaaaa aaaaaatccc cttcactcct 60
actgggaggt gggacccctt tcattttcag ttttgctcat ctagggaaaa taaggctttg 120
gtttccagtt taattgtttt tgaccttcta aaatgttttt atgttagcac tgatagttgg 180
cattactgtt gttaagcact gtgttccaga ccgtgtctga cttagtgtaa cctaggagat 240
tttatagttt tattttaatg aaaccctgat tgacgcacag cagtggggag aacagcgtct 300
tttacctgtc accgaagcca ggaagccccg tttgtaagcg tgtgttgtgg tgctttattg 360
tacatcctcc agtggcgttc tttttactct aatgttcttt tggttt 406

<210> 236
<211> 278
<212> DNA
<213> Homo sapien

<400> 236
gagattagca cctgtgaaca atgcgttctc tgatgacact ctgagcatgg accaacgcct 60
tcttaagcta attctgcaaa atcacatatt gaaagtaaaa gttggcctta gcgacctcta 120
caatggacag atactggaaa ccattggagg caaacaactc cgagtctttg tgtatcggac 180
ggctatctgc atagaaaact catgcatggt gagaggaagc aagcagggaa ggaacggtgc 240
cattcacata ttccgagaga tcatccaacc agcagaat 278

<210> 237
<211> 322
<212> DNA
<213> Homo sapien

<400> 237
cagggccgtg gcggaggagg agcgctgcac ggtggagcgt cgggccgacc tcacctacgc 60
ggagttcgtg cagcagtacg tgcgcccctg atcgcggagg tcgcgtcctg ttcaccggcc 120
cgtctgcccc gaccgcccaa ggccgccttc ccctgacctc gcgcgcacgc gtggggctgg 180
ggcggcgagg ctggcggtcc ggcctggccg cgactctgcc cttctttcca gaggttccgg 240
gccctgtgct cccgcgacag gttgctggct tcgtttgggg acagagtggt ccggtgagca 300
ccgccaacac ctactcctac ct 322

<210> 238
<211> 613
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (399)
<223> n=A,T,C or G

<400> 238
gaattcggca ccagccttct tggatcagga ccagtctcca ccccgtttct acagtggaga 60
tcagcctcct tcttatcttg gtgcaagtgt ggataaactc catcaccctt tagaatttgc 120
agacaaatct cccacacctc ctaatttacc tagcgataaa atctaccctc cttctgggtc 180
ccccgaagag aataccagca cagccaccat gacttacatg acaactactc cagcaacagc 240
ccaaatgagc accaaggaag ccagctggga tgtggctgaa caacccacca ctgctgattt 300
tgctgctgcc acacttcagc gcacgcacag aactaatcgt ccccttcccc ctccgccttc 360
ccagagatct gcagagcagc caccagttgt ggggcaggna caagcagcaa ccaatatagg 420
attaaataat tcccacaagg ttcaaggagt agttccagtt ccagagaggc cacctgaacc 480
tcgagccatg gatgaccctg cgtctgcctt catcagtgac agtggtgctg ctgctgctca 540
gtgtcccatg gctacagctg tccagccagg cctgcctgag aaagtgcggg acggtgcccg 600
ggtcccgctg ctg 613

<210> 239
<211> 613
<212> DNA
<213> Homo sapiens

<400> 239
gaattcggca ccaggggaca ctggtgctga gctggatgat gatcagcact ggtctgacag 60
cccgtcggat gctgacagag agctgcgttt gccgtgccca gctgaggggg aagcagagct 120
ggagctgagg gtgtcggaag atgaggagaa gctgcccgcc tcaccgaagc accaagagag 180
aggtccctcc caagccacca gccccatccg gtctccccag gaatcagctc ttctgttcat 240
tccagtccac agcccctcaa cagaggggcc ccaactccca cctgtccctg ccgccaccca 300
ggagaaatca cctgaggagc gccttttccc tgagcctttg ctccccaaag agaagcccaa 360
agctgatgcc ccctcggatc tgaaagctgt gcactctccc atccgatcac agccagtgac 420
cctgccagaa gctaggactc ctgtctcacc agggagcccg cagccccagc cacccgtggc 480
ggcctccacg cccccaccca gcgaggtctc cagagccttc tctctcctgt gcaaaatggc 540
aactcttaag gaaaaactca ttgcaccagt tgcggaagaa gaggcaacag ttccaaacaa 600
taagatcact gta 613

<210> 240
<211> 585
<212> DNA
<213> Homo sapiens

<400> 240
gaattcggca cgaggtgaga tctacgatga actttaagat tggaggtgtg acagaacgca 60
tgccaacccc agttattaaa gcttttggca tcttgaagcg agcggccgct gaagtaaacc 120
aggattatgg tcttgatcca aagattgcta atgcaataat gaaggcagca gatgaggtag 180
ctgaaggtaa attaaatgat cattttcctc tcgtggtatg gcagactgga tcaggaactc 240
agacaaatat gaatgtaaat gaagtcatta gcaatagagc aattgaaatg ttaggaggtg 300
aacttggcag caagatacct gtgcatccca acgatcatgt taataaaagc cagagctcaa 360
atgatacttt tcccacagca atgcacattg ctgctgcaat agaagttcat gaagtactgt 420
taccaggact acagaagtta catgatgctc ttgatgcaaa atccaaagag tttgcacaga 480
tcatcaagat tggacgtact catactcagg atgctgttcc acttactctt gggcaggaat 540
ttagtggtta tgttcaacaa gtaaaatatg caatgacaag aataa 585

<210> 241
<211> 566
<212> DNA

<213> Homo sapiens

<400> 241
gaattcggca ccaggcgagc tgcacctcga ggtgaaggcc tcactgatga acgatgactt 60
cgagaagatc aagaactggc agaaggaagc ctttcacaag cagatgatgg gcggcttcaa 120
ggagaccaag gaagctgagg acggctttcg gaaggcacag aagccctggg ccaagaagct 180
gaaagaggta gaagcagcaa agaaagccca ccatgcagcg tgcaaagagg agaagctggc 240
tatctcacga gaagccaaca gcaaggcaga cccatccctc aaccctgaac agctcaagaa 300
attgcaagac aaaatagaaa agtgcaagca agatgttctt aagaccaaag agaagtatga 360
gaagtccctg aaggaactcg accagggcac accccagtac atggagaaca tggagcaggt 420
gtttgagcag tgccagcagt tcgaggagaa acgccttcgc ttcttccggg aggttctgct 480
ggaggttcag aagcacctag acctgtccaa tgtggctggc tacaaagcca tttaccatga 540
cctggagcag agcatcagag cagctg 566

<210> 242
<211> 556
<212> DNA
<213> Homo sapiens

<400> 242
gaattcggca cgagcaaagg tgaagcagga catgcctccg cccgggggct atgggcccat 60
cgactacaaa cggaacttgc cgcgtcgagg actgtcgggc tacagcatgc tggccatagg 120
gattggaacc ctgatctacg ggcactggag cataatgaag tggaaccgtg agcgcaggcg 180
cctacaaatc gaggacttcg aggctcgcat cgcgctgttg ccactgttac aggcagaaac 240
cgaccggagg accttgcaga tgcttcggga gaacctggag gaggaggcca tcatcatgaa 300
ggacgtgccc gactggaagg tgggggagtc tgtgttccac acaacccgct gggtgccccc 360
cttgatcggg gagctgtacg ggctgcgcac cacagaggag gctctccatg ccagccacgg 420
cttcatgtgg tacacgtagg ccctgtgccc tccggccacc tggatccctg cccctcccca 480
ctgggacgga ataaatgctc tgcagacctg gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 540
aaaaaaaaaa ctcgag 556

<210> 243
<211> 591
<212> DNA
<213> Homo sapiens

<400> 243
gtctatgttt gcagaaatac agatccaaga caaagacagg atgggcactg ctggaaaagt 60
tattaaatgc aaagcagctg tgctttggga gcagaagcaa cccttctcca ttgaggaaat 120
agaagttgcc ccaccaaaga ctaaagaagt tcgcattaag attttggcca caggaatctg 180
tcgcacagat gaccatgtga taaaaggaac aatggtgtcc aagtttccag tgattgtggg 240
acatgaggca actgggattg tagagagcat tggagaagga gtgactacag tgaaaccagg 300
tgacaaagtc atccctctct ttctgccaca atgtagagaa tgcaatgctt gtcgcaaccc 360
agatggcaac ctttgcatta ggagcgatat tactggtcgt ggagtactgg ctgatggcac 420
caccagattt acatgcaagg gcaaaccagt ccaccacttc atgaacacca gtacatttac 480
cgagtacaca gtggtggatg aatcttctgt tgctaagatt gatgatgcag ctcctcctga 540
gaaagtctgt ttaattggct gtgggttttc cactggatat ggcgctgctg t 591

<210> 244
<211> 594
<212> DNA
<213> Homo sapiens

<400> 244
gaattcggca cgagaacaga gtgaactgag catcagtcag aaaaagtcta tgtttgcaga 60
aatacagatc caagacaaag acaggatggg cactgctgga aaagttatta aatgcaaagc 120
agctgtgctt tgggagcaga agcaaccctt ctccattgag gaaatagaag ttgccccacc 180
aaagactaaa gaagttcgca ttaagatttt ggccacagga atctgtcgca cagatgacca 240

```
tgtgataaaa ggaacaatgg tgtccaagtt tccagtgatt gtgggacatg aggcaactgg 300
gattgtagag agcattggag aaggagtgac tacagtgaaa ccaggtgaca aagtcatccc 360
tctctttctg ccacaatgta gagaatgcaa tgcttgtcgc aacccagatg gcaacctttg 420
cattaggagc gatattactg gtcgtggagt actggctgat ggcaccacca gatttacatg 480
caagggcaaa ccagtccacc acttcatgaa caccagtaca tttaccgagt acacagtggt 540
ggatgaatct tctgttgcta agattgatga tgcagctcct cctgagaaag tctg       594

<210> 245
<211> 615
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (105)
<223> n=A,T,C or G

<400> 245
gtccctttcc tctgctgccg ctcggtcacg cttgtgcccg aaggaggaaa cagtgacaga 60
cctggagact gcagttctct atccttccac agctctttca ccatnctgga tcacttcctt 120
tgaatgcaga agcttgctgg ccaaaagatg tgggaattgt tgcccttgag atctattttc 180
cttctcaata tgttgatcaa gcagagttgg aaaaatatga tggtgtagat gctggaaagt 240
ataccattgg cttgggccag gccaagatgg gcttctgcac agatagagaa gatattaact 300
ctctttgcat gactgtggtt cagaatctta tggagagaaa taacctttcc tatgattgca 360
ttgggcggct ggaagttgga acagagacaa tcatcgacaa atcaaagtct gtgaagacta 420
atttgatgca gctgtttgaa gagtctggga atacagatat agaaggaatc gacacaacta 480
atgcatgcta tggaggcaca gctgctgtct tcaatgcttg ttaactggat tgagtccagc 540
tcttgggatg gacggtatgc cctggtaagt tgcaggagat attgctgtat atgccacagg 600
aaatgctaga cctac                                                  615

<210> 246
<211> 546
<212> DNA
<213> Homo sapiens

<400> 246
gaattcggca ccaggctgcc tcccgctcgc cctgaaccca gtgcctgcag ccatggctcc 60
cggccagctc gccttattta gtgtctctgc aaaaccggcc ttgtgaattt gcaagaaacc 120
tgaccgctct tggtttgaat ctggtcgctt ccggagggac tgcaaaagct ctcagggatg 180
ctggtctggc agtcagagat gtctctgagt tgacgggatt tcctgaaatg ttgggggggac 240
gtgtgaaaac tttgcatcct gcagtccatg ctggaatcct agctcgtaat attccagaag 300
ataatgctga catggccaga cttgatttca atcttataag agttgttgcc tgcaatctct 360
atccctttgt aaagacagtg gcttctccag gtgtaactgt tgaggaggct gtggagcaaa 420
ttgacattgg tggagtaacc ttactgagag ctgcagccaa aaaccacgct cgagtgacag 480
tggtgtgtga accagaggac tatgtgggtg ggtgtccacg gagatgcaga gctccgagag 540
taagga                                                            546

<210> 247
<211> 564
<212> DNA
<213> Homo sapiens

<400> 247
gaattcggca ccagagatca cgtgcagtga gatgcagcaa aaagttgaac ttctgagata 60
tgaatctgaa aagcttcaac aggaaaattc tattttgaga aatgaaatta ctactttaaa 120
tgaagaagat agcatttcta acctgaaatt agggacatta aatggatctc aggaagaaat 180
gtggcaaaaa acggaaactg taaaacaaga aaatgctgca gttcagaaga tggttgaaaa 300
tttaaagaaa cagatttcag aattaaaaat caaaaaccaa caattggatt tggaaaatac 300
```

agaacttagc caaaagaact ctcaaaacca ggaaaaactg caagaactta atcaacgtct 360
aacagaaatg ctatgccaga aggaaaaaga gccaggaaac agtgcattgg aggaacggga 420
acaagagaag tttaatctga aagaagaact ggaacgttgt aaagtgcagt cctccacttt 480
agtgtcttct ctggaggcgg agctctctga agttaaaata cagacccata ttgtgcaaca 540
ggaaaaccac cttctcaaag atga 564

<210> 248
<211> 434
<212> DNA
<213> Homo sapiens

<400> 248
gttcttgttt gtggatcgct gtgatcgtca cttgacaatg cagatcttcg tgaagactct 60
gactggtaag accatcaccc tcgaggttga gcccagtgac accatcgaga atgtcaaggc 120
aaagatccaa gataaggaag gcatccctcc tgaccagcag aggctgatct ttgctggaaa 180
acagctggaa gatgggcgca ccctgtctga ctacaacatc cagaaagagt ccaccctgca 240
cctggtgctc cgtctcagag gtgggatgca aatcttcgtg aagacactca ctggcaagac 300
catcaccctt gaggtggagc ccagtgacac catcgagaac gtcaaagcaa agatccagga 360
caaggaaggc attcctcctg accagcagag gttgatcttt gccggaaagc cagcctggga 420
agatggggcc gcca 434

<210> 249
<211> 416
<212> DNA
<213> Homo sapiens

<400> 249
gcgggcccag gaggcggcgg cggcggcggc ggacgggccc cccgcggcag acggcgagga 60
cggacaggac ccgcacagca agcacctgta cacggccgac atgttcacgc acgggatcca 120
gagcgccgcg cacttcgtca tgttcttcgc gccctggtgt ggacactgcc agcggctgca 180
gccgacttgg aatgacctgg gagacaaata caacagcatg gaagatgcca aagtctatgt 240
ggctaaagtg gactgcacgg cccactccga cgtgtgctcc gcccaggggg tgcgaggata 300
ccccaccttа aagcttttca agccaggcca agaagctgtg aagtaccagg gtcctcggga 360
cttccagaca ctggaaaact ggatgctgca gacactgaac gaggagccag tgacac 416

<210> 250
<211> 504
<212> DNA
<213> Homo sapiens

<400> 250
gaattcggca cgaggcgggt aacgttatag tatttgtcag aagttggggt ctccgtgggc 60
attgtgatcc gtcccaggca gtggattagg aggccagaag gagatccctt ccacggtgct 120
aggctgagat ggatcctctc agggcccaac agctggctgc ggagctggag gtggagatga 180
tggccgatat gtacaacaga atgaccagtg cctgccaccg gaagtgtgtg cctcctcact 240
acaaggaagc agagctctcc aagggcgagt ctgtgtgcct ggaccgatgt gtctctaagt 300
acctggacat ccatgagcgg atgggcaaaa agttgacaga gttgtctatg caggatgaag 360
agctgatgaa gagggtgcag cagagctctg ggcctgcatg aggtccctgt cagtatacac 420
cctggggtgt accccacccc ttcccacttt aataaacgtg ctccctgttg ggtgtcatct 480
gtgaagactg ccaggcctag ctct 504

<210> 251
<211> 607
<212> DNA
<213> Homo sapiens

<400> 251
gatgaaaata cacaatttta ctagcaaatg cctctactgt aatcgctatt tacccacaga 60

tactctgctc aaccatatgt taattcatgg tctgtcttgt ccatattgcc gttcaacttt 120
caatgatgtg gaaaagatgg ccgcacacat gcggatggtt cacattgatg aagagatggg 180
acctaaaaca gattctactt tgagttttga tttgacattg cagcagggta gtcacactaa 240
catccatctc ctggtaacta catacaatct gagggatgcc ccagctgaat ctgttgctta 300
ccatgcccaa aataatcctc cagttcctcc aaagccacag ccaaaggttc aggaaaaggc 360
agatatccct gtaaaaagtt cacctcaagc tgcagtgccc tataaaaaag atgttgggaa 420
aacccttttgt cctctttgct tttcaatcct aaaaggaccc atatctgatg cacttgcaca 480
tcacttacga gagaggcacc aagttattca gacggttcat ccagttgaga aaaagctcac 540
ctacaaatgt atccattgcc ttggtgtgta taccagcaac atgaccgcct caactatcac 600
tctgcat 607

<210> 252
<211> 618
<212> DNA
<213> Homo sapiens

<400> 252
gaattcgcac caggggtcct gctggtcttc gcctttcttc tccgcttcta ccccgtcggc 60
cgctgccact ggggtccctg gccccaccga catggcggcg gtgttgagca agtcctggag 120
cgcacggagc tgaacaagct gcccaagtct gtccagaaca aacttgaaaa gttccttgct 180
gatcagcaat ccgagatcga tggcctgaag ggcggcatgg agaaatttaa ggtggagagc 240
gaacaacagt attttgaaat agaaaagagg ttgtcccaca gtcaggagag acttgtgaat 300
gaaacccgag agtgtcaaag cttgcggctt gagctagaga aactcaacaa tcaactgaag 360
gcactaactg agaaaaacaa agaacttgaa attgctcagg atcgcaatat tgccattcag 420
agccaattta caagaacaaa ggaagaatta gaagctgaga aaagagactt aattagaacc 480
aatgagagac tatctcaaga acttgaatac ttaacagagg atgttaaacg tctgaatgaa 540
aaacttaaag aaagcaatac aacaaagggt gaacttcagt taaaattgga tgaacttcaa 600
gcttctgatg tttctgtt 618

<210> 253
<211> 1201
<212> DNA
<213> Homo sapiens

<400> 253
gaattcggca ccagggtggc gagcgcggct gctgtgctgg ggcgagcagc ggggaccgtg 60
tgtgagtttg gcatgatttg gtcccctggg attctgcctt agcaagaaag aagttggaaa 120
tacttcctgg aagaaaacta aaacaataca aaagccacag cttattgatt gcatgtcagc 180
ccccttacaa atatggacac atttcctagc ctatttccac ctggaggaga tagtaggctg 240
aatcctgagc ctgagttcca aaatatgtta attgatgaaa gggtacgctg tgaacatcat 300
aaacataatt atcaggctct gaaaattgaa cacaaaaggt tgcaggaaga atatgtaaaa 360
tcacaaaatg aacttaaacg tgtattaatt gaaaagcaag caagccagga aaaattccaa 420
ctgctccttg aagacttaag gggagaatta gtagagaaag ctagagacat agaaaaaatg 480
aaactgcagg tactaacacc acaaaaattg gaattggtaa aagcccaact acaacaagaa 540
ttagaagctc caatgcgaga acgttttcgg actcttgatg aagaagtgga aaggtacaga 600
gctgagtata acaagctgcg ctacgagtat acatttctca agtcagagtt tgaacaccag 660
aaagaagagt ttactcgggt ttcagaagaa gagaaaatga aatacaagtc agaggttgca 720
cgactggaga aggacaaaga ggagctacat aaccagctgc ttagtgttga tcccacgaga 780
gacagcaaac gaatggagca acttgttcga gaaaaaaccc atttgcttca gaaattgaaa 840
agtttagagg ctgaagtagc agaattaagg gctgagaaag aaaattctgg tgctcaggta 900
gaaaatgtcc aaagaataca ggtgaggcag ttggctgaga tgcaggctac actcagatcc 960
ttggaggctg aaaagcagtc agctaaacta caagctgagc gtttagaaaa agaactacaa 1020
tcaagcaatg aacagaatac ctgcttaatc agcaaactgc atagagctga ccgagaaatc 1080
agcacactgg ccagtgaagt gaaagagctt aaacatgcaa acaaactaga aataactgac 1140
atcaaactgg aggcagcaag agctaagagt gagctcgaaa gagaaaggaa taagatccaa 1200
a 1201

<210> 254

<211> 560
<212> DNA
<213> Homo sapiens

<400> 254
gaattcggca ccagtttggg gggtgaggtt taattggaaa tggtctctgg ggactgaaaa 60
ctgatgtttt tgcagattac ctcagggaaa cggaggtttg ttgagttaca gacacattaa 120
accaaaggcc gtgggaaaac ccctctccag ctccagggga ttggtcagga ccacccacta 180
accagtgcct tccttcttaa cattcacttt tagcagcttg tgtttatttt acatgggcag 240
ttttgatggg aaattgccat gaccacaggg gtttggagtt ctgctttttt tttttcttct 300
tctttttcgg gggactgggg gactcctccc aagatcacat tttagcatct ttctctccta 360
ctccatttag aaaaataagt aacaggtgaa atgtggtctc agtgttaacg ggataattct 420
gctaccggct cctccctgat gattctgaaa tacactactg aacgagctct ggctggtcct 480
ttctatcctg gatgtggttc ttctgtgtag caattccttg atgtccagtt tggaaagatg 540
tactcttctc aacaagaaaa 560

<210> 255
<211> 612
<212> DNA
<213> Homo sapiens

<400> 255
gaattcggca ccaggcgggg cagcagggcc gcggccatgg ggagcttgaa ggaggagctg 60
ctcaaagcca tctggcacgc cttcaccgac tcgaccagga ccacagggca aggtctccaa 120
gtcccagctc aaggtccttt cccataacct gtgcacggtg ctgaaggttc ctcatgaccc 180
agttgccctt gaagagcact tcagggatga tgatgagggt ccagtgtcca accagggcta 240
catgccttat ttaaacaggt tcattttgga aaaggtccaa gacaactttg acaagattga 300
attcaatagg atgtgttgga ccctctgtgt caaaaaaaaa cctcacaaag aatcccctgc 360
tcattacaga agaagatgca tttaaaatat gggttatttt caacttttta tctgaggaca 420
agtatccatt aattattgtg tcagaagaga ttgaatacct gcttaagaag cttacagaag 480
ctatgggagg aggttggcag caagaacaat ttgaacatta taaaatcaac tttgatgaca 540
gtaaaaatgg cctttctgca tgggaactta ttgagcttat tggaaatgga cagtttagca 600
aaggcatgga cc 612

<210> 256
<211> 1132
<212> DNA
<213> Homo sapiens

<400> 256
gaattcggca cgaggtctgg gagaggcctc tggagcagga ggcccagtgg ctcttctgac 60
ccaaggcccc gccgtccagc ttctaagtgc cagatgatgg aggagcgtgc caacctgatg 120
cacatgatga aactcagcat caaggtgttg ctccagtcgg ctctgagcct gggccgcagc 180
ctggatgcgg accatgcccc cttgcagcag ttctttgtag tgatggagca ctgcctcaaa 240
catgggctga aagttaagaa gagttttatt ggccaaaata aatcattctt tggtcctttg 300
gagctggtgg agaaactttg tccagaagca tcagatatag cgactagtgt cagaaatctt 360
ccagaattaa agacagctgt gggaagaggc cgagcgtggc tttatcttgc actcatgcaa 420
aagaaactgg cagattatct gaaagtgctt atagacaata aacatctctt aagcgagttc 480
tatgagcctg aggctttaat gatggaggaa gaagggatgg tgattgttgg tctgctggtg 540
ggactcaatg ttctcgatgc caatctctgc ttgaaaggag aagacttgga ttctcaggtt 600
ggagtaatag atttttccct ctaccttaag gatgtgcagg atcttgatgg tggcaaggag 660
catgaaagaa ttactgatgt ccttgatcaa aaaaattatg tggaagaact taaccggcac 720
ttgagctgca cagttgggga tcttcaaacc aagatagatg gcttggaaaa gactaactca 780
aagcttcaag aagagctttc agctgcaaca gaccgaattt gctcacttca agaagaacag 840
cagcagttaa gagaacaaaa tgaattaatt cgagaaagaa gtgaaaagag tgtagagata 900
acaaaacagg ataccaaagt tgagctggag acttacaagc aaactcggca aggtctggat 960
gaaatgtaca gtgatgtgtg gaagcagcta aaagaggaga agaaagtccg gttggaactg 1020
gaaaaagaac tggagttaca aattggaatg aaaaccgaaa tggaaattgc aatgaagtta 1080

ctggaaaagg acacccacga gaagcaggac acactagttg ccctccgcca gc 1132

<210> 257
<211> 519
<212> DNA
<213> Homo sapiens

<400> 257
gaattcgtga cacgaggtgc tcgagatgaa ccccagcgcc cccagctacc ccatggcctc 60
tctgtacgtg gggggacctgc accccgacgt gaccgaggcg atgctctacg agaagttcag 120
cccggccggg cccatcctct ccatccgggt ctgcagggac atgatcaccc gccgctcctt 180
gggctacgcg tacgtgaact tccagcagcc ggcggacgcg gaacgtgctt tggacaccat 240
gaattttgat gttataaagg gcaagccagt acgcatcatg tggtctcagc gtgatccatc 300
acttcgcaaa agtggagtag gcaacatatt cattaaaaat ttggacaaat ccatcgacaa 360
taaagcacta tatgatacgt tttctgcgtt tggtaacatc ctttcatgta aggtggtttg 420
tgatgaaaat ggctccaagg gctatggatt tgtacacttt gaaacacagg aagcagctga 480
aagagctatt gaaaaaatga atgggatgct tctaaatga 519

<210> 258
<211> 596
<212> DNA
<213> Homo sapiens

<400> 258
gctttgccaa agacttagaa gctaagcaga aaatgagctt aacatcctgg tttttggtga 60
gcagtggagg cactcgccac aggctgccac gagaaatgat ttttgttgga agagatgact 120
gtgagctcat gttgcagtct cgtagtgtgg ataagcaaca cgctgtcatc aactatgatg 180
cgtctacgga tgagcattta gtgaaggatt tgggcagcct caatgggact tttgtgaatg 240
atgtaaggat tccggaacag acttatatca ccttgaaact tgaagataag ctgagatttg 300
gatatgatac aaatcttttc actgtagtac aaggagaaat gagggtccct gaagaagctc 360
ttaagcatga gaagtttacc attcagcttc agttgtccca aaaatcttca gaatcagaat 420
tatccaaatc tgcaagtgcc aaaagcatag attcaaaggt agcagacgct gctactgaag 480
tgcagcacaa aactactgaa gcactgaaat ccgaggaaaa agccatggat atttctgcta 540
tgccccgtgg tactccatta tatgggcagc cgtcatggtg gggggatgat gaggtg 596

<210> 259
<211> 595
<212> DNA
<213> Homo sapiens

<400> 259
gaattcggca ccagagaaaa agcttcaagg tatattgagt cagagtcaag ataaatcact 60
tcggagaatt tcagaattaa gagaggagct gcaaatggac cagcaagcaa agaaacatct 120
tcaggacgag tttgatgcat gtttggagga gaaagatcag tatatcagtg ttctccagac 180
tcaggtttct cttctaaagc agcgattaca gaatggccca atgaatgttg atgctcccaa 240
acccctccct cccggggagc tccaggcaga agtgcacggt gacacggaga agatggaggg 300
cgtcggggaa ccagtgggag gtgggacttc cgctaaaacc ctggaaatgc tccagcaaag 360
agtgaaacgt caggagaatc tgcttcagcg ctgtaaggag acaattgggt cccacaagga 420
gcagtgcgca ctgctgctga gtgagaagga ggcactgcag gagcagttgg atgaaaggct 480
gcaggagctg gaaaagatga aggggatggt aataaccgag acgaagcggc aaatgcttga 540
gaccctggaa ctgaaagaag atgaaattgc tcagcttcgt agtcatatca aacag 595

<210> 260
<211> 994
<212> DNA
<213> Homo sapiens

<400> 260

gaattcggca cgaggcgttg cctgccttct tgctgtctat cagcctttct tgcctcttcc 60
ttttcgcctt ccctgttctt ccctttctca aacaaacaag acatggcaaa ccgcagtcta 120
acccagccct ttgaaattat ccatagtttt acagacagct ccaggccatg agccacaatg 180
tccaaaatta ttcttgagca ctgatataaa ttacttagac cttctttgag ggcagaactc 240
agctgttgct ctcatgatgg gcagtgctgg aaagggttct ggtatgtctt caaaatgagt 300
ccacgagttt actgagtgct tacaggtaaa ggaatgaata taagatgtct ttctgatcag 360
aacaggtgtc ccttcacatg agctttacta gactctggga gggaaaagta gccaagtact 420
tctgaaccat tttttaatac ttgttttgtc atggtgaaat tatagcagtt atcccaaaat 480
gttttaatta tcaaaatact gtcttttaaa aaaaaaaaaa agtaacacct tttaaagcat 540
tagatttcac ttgggtttct tttccaaaaa atgctaggta gacaaggcat tgtaaacatg 600
agtttccttt aagaaccatc agaatataaa tttaacatga agaaaactgc tatatctagt 660
agaaataata tctaaagttt aacaactaaa gtaccctcac agaatagcaa ataccettct 720
gttctggaca tgggttcaaa tttgaatatg gaaataattt ccttggaagt ccctagaggc 780
aggtcagagg aagtatgcat taagagggaa aggagagaat ggaaataaaa gtcactataa 840
tgcagattta tgccttattt tttagcattt tttaaatgtt gggtctttca aggtgttttt 900
tgctttttat tagatctata taaataagtt aactagcaat ttagttttgt atttaagcta 960
cacttaatct ttttctttgg tgatatttat ttct 994

<210> 261
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (538)
<223> n=A,T,C or G

<400> 261
gaattcggca ccagtggaga tccagctgaa ccatgccaac cgccaggctg cggaggcaat 60
caggaacctt cggaacaccc agggaatgct gaaggacaca cagctgcacc tggacgatgc 120
tctcagaggc caggacgacc tgaaagagca gctggccatg gttgagcgca gagccaacct 180
gatgcaggct gagatcgagg agctcagggc atccctggaa cagacagaga ggagcaggag 240
agtggccgag caagagctac tggatgccag tgagcgcgtg cagctcctcc acacccagaa 300
caccagcctc atcaacacca agaagaagct ggagacagac atttcccaaa tccagggaga 360
gatggaagac atcgtccagg aagcccgcaa cgcagaagag aaggccaaga aagccatcac 420
tgatgccgcc atgatggcgg aggagctgaa gaaggagcag gacaccagcg cccacctgga 480
gcggatgaag aagaacatgg agcagaccgt gaaggacctg cagcaccgtc tggacgangc 540
tgagcagctt ggcgctgaag ggcgggcaag aagcagatcc agaaactgga ggct 594

<210> 262
<211> 594
<212> DNA
<213> Homo sapiens

<400> 262
gaaaaggtgg ctggagccaa aggcatagtc agggttaatg ctcctttttc tttatcccaa 60
atcagatagt gtttaggctt tttcatcaaa tataaaaacc cagcccagtt catggctcat 120
tcggcagcaa ccctgagacg ctttacagct ctagacccta aaaggtcaaa aggccgtctt 180
atgctcaata tacattttat tacccaatct gccccggaca ttaaataaaa ctccaaaaat 240
taaatccggc cctcaaaccc cacaacagga cttaattgac ctcaccttca aggtgtagaa 300
taataaaaaa aaaaagttgc aattccttgc ctccgctgtg agacaaaccc cagccacatc 360
tccagcacac aagaacttcc aaacgcctga accacagcag ccaggcgttc ctccagaacc 420
tcctccccca ggagcttgct acatgtgccg gaaatctggc cactaggcca aggaatgcct 480
gcagccccgg attcctccta agccgtgtcc catctgtgcg ggaccccact gaaaatcgga 540
ctgttcaact cacctggcag ccactctcag agaccctgga actctggccc aagg 594

<210> 263

<211> 506
<212> DNA
<213> Homo sapiens

<400> 263
gaattcggca cgagcggaaa cttaggggcc acgtgagcca cggccacggc cgcataggca 60
agcaccggaa gcaccccggc ggccgcggta atgctggtgg tctgcatcac caccggatca 120
acttcgacaa ataccaccca ggctactttg ggaaagttgg tatgaagcat taccacttaa 180
agaggaacca gagcttctgc ccaactgtca accttgacaa attgtggact ttggtcagtg 240
aacagacacg ggtgaatgct gctaaaaaca agactggggc tgctcccatc attgatgtgg 300
tgcgatcggg ctactataaa gttctgggaa agggaaagct cccaaagcag cctgtcatcg 360
tgaaggccaa attcttcagc agaagagctg aggagaagat taagagtgtt gggggggcct 420
gtgtcctggt ggcttgaagc cacatggagg gagtttcatt aaatgctaac tactttttaa 480
aaaaaaaaaa aaaaaaaaaa ctcgag 506

<210> 264
<211> 600
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (32)
<223> n=A,T,C or G

<400> 264
ggctcgtgaa cacacactga cagctatagg gnaggcggcg gcaccgtccc cgcttcccct 60
cggcggcggg gtgtcccgtc ggcggccctg aagtgaccca taaacatgtc ttgtgagagg 120
aaaggcctct cggagctgcg atcggagctc tacttcctca tcgccccggtt cctggaagat 180
ggaccctgtc agcaggcggc tcaggtgctg atccgcgagg tggccgagaa ggagctgctg 240
ccccggcgca ccgactggac cgggaaggag catcccagga cctaccagaa tctggtgaag 300
tattacagac acttagcacc tgatcacttg ctgcaaatat gtcatcgact aggacctctt 360
cttgaacaag aaattcctca aagtgttcct ggagtacaaa ctttattagg agctggaaga 420
cagtctttac tacgcacaaa taaaagctgc aagcatgttg tgtggaaagg atctgctctg 480
gctgcgttgc actgtggaag accacctgag tcaccagtta actatggtag cccacccagc 540
attgcggata ctctgttttc aaggaagctg aatgggaaat acagacttga gcgacttgtt 600

<210> 265
<211> 534
<212> DNA
<213> Homo sapiens

<400> 265
gaattcggca cgagtgagga gcccatcatg gcgacgcccc ctaagcggcg ggcggtggag 60
gccacggggg agaaagtgct gcgctacgag accttcatca gtgacgtgct gcagcgggac 120
ttgcgaaagg tgctggacca tcgagacaag gtatatgagc agctggccaa ataccttcaa 180
ctgagaaatg tcattgagcg actccaggaa gctaagcact cggagttata tatgcaggtg 240
gatttgggct gtaacttctt cgttgacaca gtggtcccag atacttcacg catctatgtg 300
gccctgggat atggtttttt cctggagttg acactggcag aagctctcaa gttcattgat 360
cgtaagagct ctctcctcac agagctcagc aacagcctca ccaaggactc catgaatatc 420
aaagcccata tccacatgtt gctagagggg cttagagaac tacaaggcct gcagaatttc 480
ccagagaagc ctcaccattg acttcttccc cccatcctca gacattaaag agcc 534

<210> 266
<211> 552
<212> DNA
<213> Homo sapiens

<400> 266
gaattcggca ccagggcacc tccgcctcgc cgccgctagg tcggccggct ccgcccggct 60
gccgcctagg atgaatatca tggacttcaa cgtgaagaag ctggcggccg acgcaggcac 120
cttcctcagt cgcgccgtgc agttcacaga agaaaagctt ggccaggctg agaagacaga 180
attggatgct cacttagaga acctccttag caaagctgaa tgtaccaaaa tatggacaga 240
aaaaataatg aaacaaactg aagtgttatt gcagccaaat ccaaatgcca ggatagaaga 300
atttgtttat gagaaactgg atagaaaagc tccaagtcgt ataaacaacc cagaactttt 360
gggacaatat atgattgatg cagggactga gtttggccca ggaacagctt atggtaatgc 420
ccttattaaa tgtggagaaa cccaaaaaag aattggaaca gcagacagag aactgattca 480
aacgtcagcc ttaaattttc ttactccttt aagaaacttt atagaaggag attacaaaac 540
aattgctaaa ga 552

<210> 267
<211> 551
<212> DNA
<213> Homo sapiens

<400> 267
gaagcctacc agccaggtgc cggccccccc acccccggcc cagccccctc ctgcagcggt 60
ggaagcggct cggcagatcg agcgtgaggc ccagcagcag cagcacctgt accgggtgaa 120
catcaacaac agcatgcccc caggacgcac gggcatgggg accccgggga gccagatggc 180
cccgtgagc ctgaatgtgc cccgacccaa ccaggtgagc gggcccgtca tgcccagcat 240
gcctcccggg cagtggcagc aggcgcccct tccccagcag cagcccatgc caggcttgcc 300
caggcctgtg atatccatgc aggcccaggc ggccgtggct gggccccgga tgcccagcgt 360
gcagccaccc aggagcatct cacccagcgc tctgcaagac ctgctgcgga ccctgaagtc 420
gcccagctcc cctcagcagc aacagcaggt gctgaacatt ctcaaatcaa acccgcagct 480
aatggcagct ttcatcaaac agcgcacagc caagtacgtg gccaatcagc ccggcatgca 540
gccccagcct g 551

<210> 268
<211> 573
<212> DNA
<213> Homo sapiens

<400> 268
gaattcggca ccagggttcc ttgtgggcta gaagaatcct gcaaaaatgt ctctctatcc 60
atctctcgaa gacttgaagg tagacaaagt aattcaggct caaactgctt tttctgcaaa 120
ccctgccaat ccagcaattt tgtcagaagc ttctgctcct atccctcacg atggaaatct 180
ctatcccaga ctgtatccag agctctctca atacatgggg ctgagtttaa atgaagaaga 240
aatacgtgca aatgtggccg tggtttctgg tgcaccactt caggggcagt tggtagcaag 300
accttccagt ataaactata tggtggctcc tgtaactggt aatgatgttg gaattcgtag 360
agcagaaatt aagcaaggga ttcgtgaagt cattttgtgt aaggatcaag atggaaaaat 420
tggactcagg cttaaatcaa tagataatgg tatatttgtt cagctagtcc aggctaattc 480
tccagcctca ttggttggtc tgagatttgg ggaccaagta cttcagatca atggtgaaaa 540
ctgtgcagga tggagctctg ataaagcgca caa 573

<210> 269
<211> 500
<212> DNA
<213> Homo sapiens

<400> 269
gaatcggcac caggaaacct ttattagcag agatagctgg cttggatcag attacgggga 60
atgtggggga gccatgaaga aactaactaa aggggagcct ttggggacca gggggagaca 120
agtcactatt ttgagggaga aagctctgga ttgattctga caggacactt gagtgtgaac 180
tgtccaagct aagcctctgg gtgtgtagag agagccctta cagatagata gcacctttgc 240
tttcagagtg gaaggactag ccactaagga ccagaccaag atgcatgtag gtcactgaca 300
agcacctgat gaagaggagg ggtctcctcc aagtttgtgt ttggaactcc tcctgtgttc 360

aatttcctaa aagccataat ccagcaagct gaactcatga gaaggtctgc ttcatgttga 420
gcatggaaga cagaacacag acggaaactg cagtgatggt gtgaagacac cacggatagg 480
ttaggggcag tgaggaggaa 500

<210> 270
<211> 224
<212> DNA
<213> Homo sapiens

<400> 270
gaattcggca cgagaagact acaatctcca gggaaacctg gggcgtctcg cgcaaacgtc 60
cataactgaa agtagctaag gcaccccagc cggaggaagt gagctctcct ggggcgtggt 120
tgttcgtgat ccttgcatct gttacttagg gtcaaggctt gggtcttgcc ccgcagaccc 180
ttgggacgac ccggccccag cgcagctatg aacctggagc gagt 224

<210> 271
<211> 447
<212> DNA
<213> Homo sapiens

<400> 271
gaattcggca cgaggctggg ccgggcccga gcggatcgcg ggctcgggct gcggggctcc 60
ggctgcgggc gctgggccgc gaggcgcgga gcttgggagc ggagcccagg ccgtgccgcg 120
cggcgccatg aagggcaagg aggagaagga gggcggcgca cggctgggcg ctggcggcgg 180
aagccccgag aagagcccga gcgcgcagga gctcaaggag cagggcaatc gtctgttcgt 240
gggccgaaag tacccggagg cggcggcctg ctacggccgc gcgatcaccc ggaacccgct 300
ggtggccgtg tattacacca accgggcctt gtgctacctg aagatgcagc agcacgagca 360
ggccctggcc gactgccggc gcgccctgga gctggacggg cagtctgtga aggcgcactt 420
cttcctgggg cagtgccagc tggagat 447

<210> 272
<211> 606
<212> DNA
<213> Homo sapiens

<400> 272
gcaactactt atattccttt gatggataat gctgactcaa gtcctgtggt agataagaga 60
gaggttattg atttgcttaa acctgaccaa gtagaaggga tccagaaatc tgggactaaa 120
aaactgaaga ccgaaactga caaagaaaat gctgaagtga agtttaaaga ttttcttctg 180
tccttgaaga ctatgatgtt ttctgaagat gaggctcttt gtgttgtaga cttgctaaag 240
gagaagtctg gtgtaataca agatgcttta aagaagtcaa gtaaggga ga attgactacg 300
cttatacatc agcttcaaga aaaggacaag ttactcgctg ctgtgaagga agatgctgct 360
gctacaaagg atcggtgtaa gcagttaacc caggaaatga tgacagagaa agaaagaagc 420
aatgtggtta taacaaggat gaaagatcga attggaacat tagaaaagga acataatgta 480
tttcaaaaca aaatacatgt cagttatcaa gagactcaac agatgcagat gaagtttcag 540
caagttcgtg agcagatgga ggcagagata gctcacttga agcaggaaaa tgggtatact 600
ggagaa 606

<210> 273
<211> 598
<212> DNA
<213> Homo sapiens

<400> 273
gaattcggca ccaggcccgg tcccgcggtc gcagctccag ccgcctcctc cgcgcagccg 60
ccgcctcagc tgctcgctct gtgggtcggt cctctccggc acttgggctc cagtcgcgcc 120
ctccaagccc ttcaggccgc cccagtgtcc tcctccttct ccggccagac ccagccccgc 180
gaagatggtg gaccgcgagc aactggtgca gaaagcccgg ctggccgagc aggcggagcg 240

ctacgacgac atggccgcgg ccatgaagaa cgtgacagag ctgaatgagc cactgtcgaa 300
tgaggaacga aaccttctgt ctgtggccta caagaacgtt gtgggggcac gccgctcttc 360
ctggagggtc atcagtagca ttgagcagaa gacatctgca gacggcaatg agaagaagat 420
tgagatggtc cgtgcgtacc gggagaagat agagaaggag ttggaggctg tgtgccagga 480
tgtgctgagc ctgctggata actacctgat caagaattgc agcgagaccc agtacgagag 540
caaagtgttc tacctgaaga tgaaagggga ctactaccgc tacctggctg aagtggcc 598

<210> 274
<211> 536
<212> DNA
<213> *Homo sapiens*

<400> 274
gcaccaagag actaaacaag aaagtggatc agggaagaag aaagcttcat caaagaaaca 60
aaagacagaa aatgtcttcg tagatgaacc ccttattcat gcaactactt atattccttt 120
gatggataat gctgactcaa gtcctgtggt agataagaga gaggttattg atttgcttaa 180
acctgaccaa gtagaaggga tccagaaatc tgggactaaa aaactgaaga ccgaaactga 240
caaagaaaat gctgaagtga agtttaaaga ttttcttctg tccttgaaga ctatgatgtt 300
ttctgaagat gaggctcttt gtgttgtaga cttgctaaag gagaagtctg gtgtaataca 360
agatgcttta aagaagtcaa gtaaggagaa attgactacg cttatacatc agcttcaaga 420
aaaggacaag ttactcgctg ctgtgaagga agatgctgct gctacaaagg atcggtgtaa 480
gcagttaacc caggaaatga tgacagagaa agaaagaagc aatgtggtta taacaa 536

<210> 275
<211> 494
<212> DNA
<213> *Homo sapiens*

<220>
<221> misc_feature
<222> (379)
<223> n=A,T,C or G

<400> 275
gaattcggca ccagggtcgc ggttcttgtt tgtggatcgc tgtgatcgtc acttgacaat 60
gcagatcttc gtgaagactc tgactggtaa gaccatcacc ctcgaggttg agcccagtga 120
caccatcgag aatgtcaagg caaagatcca agataaggaa ggcatccctc ctgaccagca 180
gaggctgatc tttgctggaa aacagctgga agatgggcgc accctgtctg actacaacat 240
ccagaaagag tccaccctgc acctggtgct ccgtctcaga ggtgggatgc aaatcttcgt 300
gaagacactc actggcaaga ccatcaccct tgaggtggag cccagtgaca ccatcgagaa 360
cgtcaaagca aagatccang acaaggaagg cattcctcct gaccagcaga ggttgatctt 420
tgccggaaag cagctggaag atgggcgcac cctgtctgac tacaacatcc agaaagagtc 480
taccctgcac ctgg 494

<210> 276
<211> 484
<212> DNA
<213> *Homo sapiens*

<400> 276
ggcttttaac cagaagtcaa acctgttcag acagaaggca gtcacagcag aaaaatcttc 60
agacaaaagg cagtcacagg tgtgcaggga gtgtgggcga ggctttagca ggaagtcaca 120
gctcatcata caccagagga cacacacagg agaaaagcct tatgtctgcg gagagtgtgg 180
gcgaggcttt atagttgagt cagtcctccg caaccacctg agtacacact ccggggagaa 240
accttatgtg tgcagccatt gtgggcgagg ctttagctgc aagccatacc tcatcagaca 300
tcagaggaca cacacaaggg agaaatcgtt tatgtgcaca gtgtgtgggc gaggctttcg 360
tgaaaagtca gagctcatta agcaccagag aattcacacg ggggataagc cttatgtgtg 420
cagagattga ggccgaggct ttgtaaagga gatcatgtct caacacacac cagaggatta 480

catt 484

<210> 277
<211> 513
<212> DNA
<213> Homo sapiens

<400> 277
gcttgaggct gccaatcaga gcttggcaga gctgagagat cagcggcagg gggagcgcct 60
ggaacatgca gcagctttgc gggccctaca agatcaggta tccatccaga gtgcagatgc 120
acaggaacaa gtggaagggc ttttggctga gaacaatgcc ttgaggacta gcctggctgc 180
cctggagcag atccaaacag caaagaccca agaactgaat atgctccggg aacagaccac 240
tgggctggca gctgagttgc agcagcagca ggctgagtac gaggacctta tgggacagaa 300
agatgacctc aactcccagc tccaggagtc attacgggcc aatagtcgac tgctggaaca 360
acttcaagaa atagggcagg agaaggagca gttgacccag gaattacagg aggctcggaa 420
gagtgcggag aagcggaagg ccatgcttgg atgagctagc aatggaaacg ctgcaagaga 480
agtcccacac aaggaagagc ttgggagcag ttc 513

<210> 278
<211> 471
<212> DNA
<213> Homo sapiens

<400> 278
gaattcggca ccagccaagg ccctgtccct ggctcgggcc cttgaagagg ccttggaagc 60
caaagaggaa ctcgagcgga ccaacaaaat gctcaaagcc gaaatggaag acctggtcag 120
ctccaaggat gacgtgggca agaacgtcca tgagctggag aagtccaagc gggccctgga 180
gacccagatg gaggagatga agacgcagct ggaagagctg gaggacgagc tgcaagccac 240
ggaggacgcc aaactgcggc tggaagtcaa catgcaggcg ctcaagggcc agttcgaaag 300
ggatctccaa gcccgggacg agcagaatga ggagaagagg aggcaactgc agagacagct 360
tcacgagtat gagacggaac tggaagacga gcgaaagcaa cgtgccctgg cagctgcagc 420
aaagaagaag ctggaagggg acctgaaaga cctggagctt caggccgact t 471

<210> 279
<211> 497
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (457)
<223> n=A,T,C or G
<221> misc_feature
<222> (471)
<223> n=A,T,C or G

<400> 279
gaattcggca cgaggccaca gaggcggcgg agagatggcc ttcagcggtt cccaggctcc 60
ctacctgagt ccagctgtcc ccttttctgg gactattcaa ggaggtctcc aggacggact 120
tcagatcact gtcaatggga ccgttctcag ctccagtgga accaggtttg ctgtgaactt 180
tcagactggc ttcagtggaa atgacattgc cttccacttc aaccctcggt ttgaagatgg 240
agggtacgtg gtgtgcaaca cgaggcagaa cggaagctgg gggcccgagg agaggaagac 300
acacatgcct ttccagaagg ggatgccctt tgacctctgc ttcctggtgc agagctcaga 360
tttcaaggtg atggtgaacg ggatcctctt cgtgcagtac ttccaccgcg tgcccttcca 420
ccgtgtggac accatctccg tcaatggctc tgtgcanctg tcctacatca ncttccagac 480
ccagacagtc atccaca 497

<210> 280

<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (451)
<223> n=A,T,C or G

<400> 280
gaattcggca ccagaatagg aacagctccg gtctacagct cccagcgtga gcgacgcaga 60
agacgggtga tttctgcatt tccatctgag gtaccgggtt catctcacta gggagtgcca 120
gacagtgggc gcaggccagt gtgtgtgcgc accgtgcgcg agccgaagca gggcgaggca 180
ttgcctcacc tgggaagcac aaggggtcag ggagttccct ttccgagtca aagaaagggg 240
tgacggacgc acctggaaaa tcgggtcact cccacccgaa tattgtgctt ttcagaccgg 300
cttaagaaac ggcgcaccac gagactatat cccacacctg gctcagaggg tcctacgccc 360
acggaatctc gctgattgct agcacagcag tcttagatca aactgcaagg ggggcaacga 420
ggctggggga ggggcgcccg ccattgccca ngcttgctta ggtaaacaaa gcagccggga 480
agcttgaact gggtggagcc caccacagct caaggaggcc tgcctgcctc tgtagctcca 540
cctc 544

<210> 281
<211> 527
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (456)
<223> n=A,T,C or G

<400> 281
gaattcggca cgaggcctcg ctcagctcca acatggcaaa aatctccagc cctacagaga 60
ctgagcggtg catcgagtcc ctgattgctg tcttccagaa gtatgctgga aaggatggtt 120
ataactacac tctctccaag acagagttcc taagcttcat gaatacagaa ctagctgcct 180
tcacaaagaa ccagaaggac cctggtgtcc ttgaccgcat gatgaagaaa ctggacacca 240
acagtgatgg tcagctagat ttctcagaat ttcttaatct gattggtggc ctagctatgg 300
cttgccatga ctccttcctc aaggctgtcc cttcccagaa gcggacctga ggaccccttg 360
gccctggcct tcaaacccac cccctttcct tccagccttt ctgtcatcat ctccacagcc 420
cacccatccc ctgagcacac taaccacctc atgcanggcc cccctgccaa tagtaataaa 480
gcaatgtcct tttttaaaac atgaaaaaaa aaaaaaaaaa actcgag 527

<210> 282
<211> 514
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (494)
<223> n=A,T,C or G

<400> 282
ggaagactgg agcctttgcg gcggcgctgc ccctcccctg gtccccgcga gctcggaggg 60
cccggctggt gctgcggggg ccccgggagg ttgaaaacta agcatgggga agagctgcaa 120
ggtggtcgtg tgtggccagg cgtctgtggg caaaacttca atcctggagc agcttctgta 180
tgggaaccat gtagtgggtt cggagatgat cgagacgcag gaggacatct acgtgggctc 240
cattgagaca gaccgggggg tgcgagagca ggtgcgtttc tatgacaccc gggggctccg 300

agatggggcc gaactgcccc gacactgctt ctcttgcact gatggctacg tcctggtcta 360
tagcacagat agcagagagt cttttcagcg tgtggagctg ctcaagaagg agattgacaa 420
atccaaggac aagaaggagg tcaccatcgt ggtccttggc aacaagtgtg acttacagga 480
gcagcggcgt gtanacccaa atgtggctca acac 514

<210> 283
<211> 484
<212> DNA
<213> Homo sapiens

<400> 283
gggcgggcgg tggacagtca tggcggcccg gcgcggggct ctcatagtgc tggagggcgt 60
ggaccgcgcc gggaagagca cgcagagccg caagctggtg gaagcgctgt gcgccgcggg 120
ccaccgcgcc gaactgctcc ggttcccgga aagatcaact gaaatcggca aacttctgag 180
ttcctacttg caaaagaaaa gtgacgtgga ggatcactcg gtgcacctgc ttttttctgc 240
aaatcgctgg gaacaagtgc cgttaattaa ggaaaagttg agccagggcg tgaccctcgt 300
cgtggacaga tacgcatttt ctggtgtggc cttcaccggt gccaaggaga atttttccct 360
agactggtgt aaacagccag acgtgggcct tcccaaaccc gacctggtcc tgttcctcca 420
gttacagctg gcggatgctg ccaagcgggg agcgtttggc catgagcgct atgagaacgg 480
ggct 484

<210> 284
<211> 514
<212> DNA
<213> Homo sapiens

<400> 284
gaattcggca cgaggcggag gccgcggagg ctcctcggtc cttcagcacc cctcggcccg 60
acgcacccac gcccctcacc ccccgagagc cgaaaatgga cccaagtggg gtcaaagtgc 120
tggaaacagc agaggacatc caggagaggc ggcagcaggt cctagaccga taccaccgct 180
tcaaggaact ctcaaccctt aggcgtcaga agctggaaga ttcctatcga ttccagttct 240
ttcaaagaga tgctgaagag ctggagaaat ggatacagga aaaacttcag attgcatctg 300
atgagaatta taaagaccca accaacttgc agggaaagct tcagaagcat caagcatttg 360
aagctgaagt gcaggccaac tcaggagcca ttgttaagct ggatgaaact ggaaacctga 420
tgatctcaga agggcatttt gcatctgaaa ccatacggac ccgtttgatg gagctgcacc 480
gccagtggga attacttttg gagaagatgc gaga 514

<210> 285
<211> 383
<212> DNA
<213> Homo sapiens

<400> 285
gaattcggca cgaggccggg ctccaccgcg catcctgctc cactctggcg accgccccccg 60
gggcccccgc cgcgggcgcg gcgcccgcca tgggcgagga ggactactat ctggagctgt 120
gcgagcggcc ggtgcagttc gagaaggcga accctgtcaa ctgcgtcttc ttcgatgagg 180
ccaacaagca ggtttttgct gttcgatctg gtggagctac tggcgtggta gttaaaggcc 240
cagatgatag gaatcccatc tcatttagaa tggatgacaa aggagaagtg aagtgcatta 300
agttttcctt agaaaataag atattggctg ttcagaggac ctcaaagact gtggattttt 360
gtaattttat ccctgataat tcc 383

<210> 286
<211> 943
<212> DNA
<213> Homo sapiens

<400> 286
gaattcggca ccagggccgt ggcggaggag gagcgctgca cggtggagcg tcgggccgac 60

ctcacctacg cggagttcgt gcagcagtac gtgcgcccct gatcgcggag gtcgcgtcct 120
gttcaccggc ccgtctgccc cgaccgccca aggccgcctt cccctgacct cgcgcgcacg 180
cgtggggctg gggcggcgag gctggcggtc cggcctggcc gcgactctgc ccttctttcc 240
agaggttccg ggccctgtgc tcccgcgaca ggttgctggc ttcgtttggg gacagagtgg 300
tccggctgag caccgccaac acctactcct accacaaagt ggacttgccc ttccaggagt 360
atgtggagca gctgctgcac ccccaggacc ccacctccct gggcaatggt gaggcagccc 420
taggcggcgg taggggtgg ggacgcttgg agtctccagg tgccaggatc cctgtccccg 480
ccgtctctgt tggcagacac cctgtacttc ttcggggaca acaacttcac cgagtgggcc 540
tctctctttc ggcactactc cccaccccca tttggcctgc tgggaaccgc tccagcttac 600
agctttggaa tcgcaggagc tggctcgggg gtgcccttcc actggcatgg acccgggtac 660
tcagaagtga tctacggtcg taagcgctgg ttcctttacc cacctgagaa gacgccagag 720
ttccacccca acaagaccac actggcctgg ctccgggaca catacccagc cctgccaccg 780
tctgcacggc ccctggagtg taccatccgg gctggtgagg tgctgtactt ccccgaccgc 840
tggtggcatg ctacgctcaa ccttgacacc agcgtcttca tctccacctt cctcggctag 900
ccaaaacagc tggcaggact gccggtcaca caccagcacg tcc 943

<210> 287
<211> 1143
<212> DNA
<213> Homo sapiens

<400> 287
gaattcggca cgagggaaga acagctgttg gaacaacaag aatatttaga aaaagaaatg 60
gaggaagcaa agaaaatgat atcaggacta caggccttac tgctcaatgg atccttacct 120
gaagatgaac aggagaggcc cttggccctc tgtgaaccag gtgtcaatcc cgaggaacaa 180
ctgattataa tccaaagtcg tctggatcag agtatggagg agaatcagga cttaaagaag 240
gaactgctga aatgtaaaca agaagccaga aacttacagg ggataaagga tgccttgcag 300
cagagattga ctcagcagga cacatctgtt cttcagctca aacaagagct actgagggca 360
aatatggaca aagatgagct gcacaaccag aatgtggatc tgcagaggaa gctagatgag 420
aggaaccggc tcttgggaga atataaaaaa gagctggggc agaaggatcg ccttcttcag 480
cagcaccagg ccaagttaga agaagcactc cggaaactct ctgatgtcag ttaccaccag 540
gtggatctag agcgagagct agaacacaaa gatgtcctct tggctcactg tatgaaaaga 600
gaggcagatg aggcgaccaa ctacaacagt cacaactctc aaagcaatgg ttttctcctt 660
ccaacggcag gaaaaggagc tacttcagtc agcaacagag ggaccagcga cctgcagctt 720
gttcgagatg ctctccgcag cctgcgcaac agcttcagtg gccacgatcc tcagcaccac 780
actattgaca gcttggagca gggcatttct agcctcatgg agcgcctgca tgttatggag 840
acgcagaaga aacaagaaag aaaggttcgg gtcaagtcac ccagaactca agtaggtagt 900
gaataccggg agtcctggcc ccctaactca aagttgcctc actcacagag ctctccaact 960
gtcagcagca cctgtactaa agtgctctat ttcactgacc ggtcacttac gcccttcatg 1020
gtcaatatac caaagaggtt ggaggaggtg acgttaaagg attttaaagc agctattgat 1080
cgggaaggaa atcaccggta tcacttcaaa gcactggatc ctgagtttgg cactgtcaaa 1140
gag 1143

<210> 288
<211> 881
<212> DNA
<213> Homo sapiens

<400> 288
gtgagagcgg gccgaggaga ttggcgacgg tgtcgcccgt gttttcgttg gcgggtgcct 60
gggctggtgg gaacagccgc ccgaaggaag caccatgatt tcggccgcgc agttgttgga 120
tgagttaatg ggccgggacc gaaacctagc cccggacgag aagcgcagca acgtgcggtg 180
ggaccacgag agcgtttgta aatattatct ctgtggtttt tgtcctgcgg aattgttcac 240
aaatacacgt tctgatcttg gtccgtgtga aaaaattcat gatgaaaatc tacgaaaaca 300
gtatgagaag agctctcgtt tcatgaaagt tggctatgag agagattttt tgcgatactt 360
acagagctta cttgcagaag tagaacgtag gatcagacga ggccatgctc gtttggcatt 420
atctcaaaac cagcagtctt ctggggccgc tggcccaaca ggcaaaaatg aagaaaaaat 480
tcaggttcta acagacaaaa ttgatgtact tctgcaacag attgaagaat tagggtctga 540

aggaaaagta gaagaagccc aggggatgat gaaattagtt gagcaattaa aagaagagag 600
agaactgcta aggtccacaa cgtcgacaat tgaaagcttt gctgcacaag aaaaacaaat 660
ggaagtttgt gaagtatgtg gagccttttt aatagtagga gatgcccagt cccgggtaga 720
tgaccatttg atgggaaaac aacacatggg ctatgccaaa attaaagcta ctgtagaaga 780
attaaaagaa aagttaagga aaagaaccga agaacctgat cgtgatgagc gtctaaaaaa 840
ggagaagcaa gaaagagaaa aaaaaaaaaa aaaaactcga g 881

<210> 289
<211> 987
<212> DNA
<213> Homo sapiens

<400> 289
gaattcggca cgagggactg tggtttccag gaatggtggc gtctcacgct tcttgtgctt 60
tttcctttgg ggcctccgag cggctggggt tgggggactg ggcaggaggc tccctgtaaa 120
catttggact tgggctgggg caggggctgg tgttgggcaa agctgggggt ccaggctgga 180
gaagcagggg cccctccaga cgcagccttg ggagactcag catgtgcccc cctcccctca 240
tcacagaaca agacaatggt taaaaaccag aacagatgcc cagaaggggg taccatggcc 300
attaccagca tctcagacaa gggcaggctt caaacaggga ggcctgtggc aacccctccc 360
ctacgtctgg agctgagggg acagggggag ctgagaacaa agagaggaaa gaggagaaaa 420
gcggcggggg aacaggcggg gagcgtgatc ttcttgcccc catcttcctc aggggttggg 480
gggtacaaag tcggcggtgg cccatcccgc caggccccgc tgcccctcag aagaggccgc 540
agtccttcag gttgttcttg atgatgacat cggtgacggc gtcaaacacg aactgcacgt 600
tcttggtgtc ggtggcgcac gtgaagtgcg tgtagatctc cttggtgtct ttgcgcttat 660
tcaggtcctc aaacttactc tggatgtagc tggctgcctc atcatatttg ttggcccctg 720
tatactcagg gaagcagatg gtcaggggac tgtgtgtgat cttctcctca aacaggtcct 780
tcttgttgag gaagaggatg atggacgtgt ctgtgaacca cttgttgttg cagatgctat 840
cgaatagctt catgctctca tgcatgcggt tcatctcctc gtcctcagct agcaccaagt 900
cataggcgct caaggctacg cagaagatga tggctgtgac gccctcaaag cagtggatcc 960
acttcttccg ctcagaccgc tgaccac 987

<210> 290
<211> 300
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(300)
<223> n = A,T,C or G

<400> 290
gattcaagat gtaccccatt gactttgaga aggatgatga cagcaacttt catatggatt 60
tcatcgtggc tgcatccaac ctccgggcag aaaactatga cattccttct gcagaccggc 120
acaagagcaa gctgattgca gggaagatca tcccagccat tgccacgacc acagcagccg 180
tggttggcct tgtgtgtctg gagctgtaca aggttgtgca ggggcaccga cancttgact 240
cctacangaa tgggtgcctc aacttgagcc ctgcctttct ttggtttctc tgaacccctt 300

<210> 291
<211> 352
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(352)
<223> n = A,T,C or G

<400> 291
aaccaagctg ccaccggggg tggatcggat gcggcttgag aggcatctgt ctgccgagga 60
cttctcaagg gtatttgcca tgtcccctga agagtttggc aagctggctc tgtggaagcg 120
gaatgagctc aagaagaagg cctctctctt ctgatggccc ccacctgctc cgggacggcc 180
cccttacccc tgctgcttca gggtttttcc ccggcgggtt gggaggggca ggaggtgggg 240
tggaaatngg gtgggcncct ttcctcaggt agagnggggg gccaaaacct ctgcngtccc 300
cggagngagc tatggacttt cttccccctc acaaggntgg gggcctcctg ct 352

<210> 292
<211> 511
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 292
cgcggtggct gcgcactcng cctgagaaac tcggcaagcg cgcagtgtcg actccccggt 60
ctatgccagg cgcatctcag ctaatccaaa agtaaatgag aaacttagaa aaagattgcc 120
aattccaaat caacatattt agagaaaatt ggaaaaggag aagcttacta cagctttatt 180
tgaggacttt ttaaagaacg ctgggttcta tctgtgagct gcaaatcttg gagcaaaaac 240
cagagacatt gccagagcaa acaagaacag aaatacaaat ggagaactgg tcaaaagaca 300
taacccacag ttatcttgaa caagaaacta cggggataaa taaaagtacg canccagatg 360
agcaactgac tatgaattct gagaaaagta tgcatcggaa atccactgaa ttagntaatg 420
aaataacatg ngagaacaca gaatggccag gggcagagat caacgaattt tcanatcatc 480
agttcttatc cagatgatga gtctgtttac t 511

<210> 293
<211> 526
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(526)
<223> n = A,T,C or G

<400> 293
gataaaaaga actttaatgg aaggcactgt tgtccaaaat cacataaagg gtaagagccc 60
acacggtacc accctgctct cctacttctc aaacccacat ccaccaccca gacaggaggg 120
tgcanacccc acaggaaatt acctcccgga gcactgactg atatttttcc ttaaaacaaa 180
aaaatggctg tctcagacta ataacagaac atcttaagag ctataccagc tattacagcc 240
tggtaatana agcagctttc taanaattcc caagtttata anaggcccaa naaatgcatt 300
tattctgttg tctattaagc ctccatgaca aggagaaagt tatgagtaaa tccttggttc 360
atcaggagtt aagagctgtg ngcctcatga ggagttaana gctgtgtgca taagcaggtt 420
caagaaacaa actcctgttt gtttgcctct ttgatggttc aaaaacattc agctgctttc 480
acctctanga caaaatgctt aaagaattta ctctcatcac cttggg 526

<210> 294
<211> 601
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature

<222> (1)...(601)
<223> n = A,T,C or G

<400> 294
actttaaaag ccaaatatat ttttaaaaga tcatgcttat aataagtaaa ttacncatta 60
aggaaacatc aaaataaagt agatgaataa aaaggcacac tcgaaaaatt tgagcgcaga 120
aaggacagtt ctttttgttt tgtttctaat gtcggaagaa aaagaaagag atatattaaa 180
atcattgttt tcaagtgaag gtttctgtca gttgaagtag ttagcaatgg cttcttttct 240
cccgtgtcca aagcaggctc ttcctgcgct gacttctgag gaggngttca gtcctctgcc 300
atgtataggc gatacatcaa ggcgacggcc actgcagaga tggcagggat cacccagttg 360
gtccaccaac tggaactaga atcaatagta gtgataagag tttccggagg cttgtttaac 420
tttggtctgt catctggatg gagctcccca atgatgaatg ttttggacat ttccctggca 480
tctgtagant gcccgacatc ctcaaagttc tcagtagcng tcacctccac ttgttccctt 540
aaaacttctt ccccaccagg atgctcttcc agaaatttgg gncaaatcgn acaccttgtg 600
g 601

<210> 295
<211> 262
<212> DNA
<213> Homo sapien

<400> 295
cccttagccc caagggccct gggggcagcc accctcccgc ctgtcggccc gtagatttat 60
caagggtgtt atgggcccag ctttgggggg ccagtcccga tgcactttga ggggtgttgg 120
agaggggact cccccactcg cacttaactc aacggctctc gggccctggg gctgttttta 180
ccatgtttgt ttttgaagct caggtgtctc acgtctgggc tgcaccaggc gaagagagaa 240
attaaagatt tgaggttttt cc 262

<210> 296
<211> 598
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(598)
<223> n = A,T,C or G

<400> 296
gttagaacaa ctcagcaaaa taaaattcct gtttattgtt ggacaacatt gtttcacaca 60
tacatcaaac aggccaaaaa aaataaacag caacttcata gacaaaaaag gaaaaaaaaa 120
gaaacctttt atctttggcc tttttaacca tctcatacaa accaactact tatagtacag 180
ctaagtacat acacaaaaaa gttactggaa tgctcggaat aagattgttt ttctgttgtc 240
atttttgctt tttttacaag gntttttttc tcctttgaga ttataatgaa catggncaca 300
ccacaagtaa agtcagaagt aggacagana acgctccgaa ggctggtttg gtcatccgan 360
atcattaaaa atggctgacc ctaacaatat gtacaaaaat ataaaatgta aataaaaaat 420
acaaacaaat ttccttttta aagtactttt aagaaaaaaa gcagggcctt ggaagttttg 480
gttctttttt cctcccctgt tgcaaattct catggtttgg gttgggtggn gganancccg 540
tgtcatctgc gggtggcact gccccggngg gcgggcgggc ctctctctcg aangngac 598

<210> 297
<211> 509
<212> DNA
<213> Homo sapien

<400> 297
agaacacagg tgtcgtgaaa actacccctа aaagccaaaa tgggaaagga aaagactcat 60
atcaacattg tcgtcattgg acacgtagat tcgggcaagt ccaccactac tggccatctg 120

```
atctataaat gcggtggcat cgacaaaaga accattgaaa aatttgagaa ggaggctgct     180
gagatgggaa agggctcctt caagtatgcc tgggtcttgg ataaactgaa agctgagcgt     240
gaacgtggta tcaccattga tatctccttg tggaaatttg agaccagcaa gtactatgtg     300
actatcattg atgccccagg acacagagac tttatcaaaa acatgattac agggacatct     360
caggctgact gtgctgtcct gattgttgct gctggtgttg gtgaatttga agctggtatc     420
tccaagaatg ggcaggaccc gagagcatgc ccttctggct tacacactgg gtgtgaaaca     480
actaattgtc ggtgttaaca aaatggatt                                       509

      <210> 298
      <211> 267
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
      <222> (1)...(267)
      <223> n = A,T,C or G

      <400> 298
gggacggggg aaaggagacg cttcttcctc ttgctgctct tctcgttccc gagatcagcg      60
gcggcggtga ccgcgagtgg gtcggcaccg tctccggctc cgggngcnaa caatgctgac     120
tgatagcgga ggcggnggca cctccttnna ggaggacctg gactctgtgg ctccgcgatc     180
cgccccagct ggggcctcgg agccgcctcc gccgggaggg gtcggtctgg ggatccncac     240
cgngaggctn tttggggagg gcgggcc                                         267

      <210> 299
      <211> 121
      <212> DNA
      <213> Homo sapien

      <400> 299
ggcacgaggg ccctcggagc tcgtttccag atcgaggtaa gagggacttt cttaaaggcc      60
tagtctatgg gatggggcgg cggagggaat tttttgagaa ataaaatgaa gctgcagtgt     120
a                                                                     121

      <210> 300
      <211> 533
      <212> DNA
      <213> Homo sapien

      <400> 300
aaggtgcaca gtatttgatg caggctgctg gtcttggtcg tatgaagcca aacacacttg      60
tccttggatt taagaaagat tggttgcaag cagatatgag ggatgtggat atgtatataa     120
acttatttca tgatgctttt gacatacaat atggagtagt ggttattcgc ctaaaagaag     180
gtctggatat atctcatctt caaggacaag aagaattatt gtcatcacaa gagaaatctc     240
ctggcaccaa ggatgtggta gtaagtgtgg aatatagtaa aaagtccgat ttagatactt     300
ccaaaccact cagtgaaaaa ccaattacac acaaagttga ggaagaggat ggcaagactg     360
caactcaacc actgttgaaa aaagaatcca aaggccctat tgtgccttta aatgtagctg     420
accaaaagct tcttgaagct agtacacagt ttcagaaaaa acaaggaaag aatactattg     480
atgtctggtg gctttttgat gatggaggtt tgaccttatt gataccttac ctt            533

      <210> 301
      <211> 560
      <212> DNA
      <213> Homo sapien

      <220>
      <221> misc_feature
```

<222> (1)...(560)
<223> n = A,T,C or G

<400> 301
ataaatgatc ccttttattg taagtaatgc gcaacactgg cctggctttg cactgcaagc 60
cctcggtcaa gatatagtca aataactatg gctgcaggtt ccacagttcc acaataacca 120
tggctgcacg atccacaatt cagacacaga catagagctg gggtgggtgg aaggggcagg 180
agggtggcag agtgcggact gtccccagcc ctggcctctc catgcanagt tggcccaggc 240
agacacaccc catggaatga tgagaaagtg acggcacggc cccttcccac agcaagcctg 300
gggctgccag gaactgccct tcanaacctt tgggcccagg tcnccctgaa nccccacaac 360
tttttatctg gaataagtat taaaaaacaa taaattaagc aaacaacntg gnccttgaag 420
gatgttgacc nacatggtcc acagtttttg gcncaaaaaa ataagggctg gtttgctttt 480
tttggaaggc agggtttgtg gnttggcttt caaatnattt tcaaaccatt ccccagggag 540
gganaacccc cgggggggaa 560

<210> 302
<211> 599
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(599)
<223> n = A,T,C or G

<400> 302
gcaaagttac aaatttattg gtctggaaat aaatacaaat atctcattaa naaactcctc 60
tggaaagact tgtgcacaat agtttcccat ccgtactcag cctctcttgc cccgatcccc 120
gacttttcta ctcaaggcca gggaaggcct ccaaggngat gggcggcagg taacgagtca 180
ttgcctctca cgccacctgg aaggctggac tacttcctcc tcccaactgc ggggtcccan 240
aaatcctcgg gtcccagngg ctgacttaca atattcaatt cactctgacc aaacttccta 300
tganaaaatc cacggngagc caaaatgaaa agtacaaggc agtagtacag gaacctggca 360
gccgcactgg ccgcccanaa acgtcagtgg ngctgcccca ttcggcgaaa ggttagggag 420
caggaaaaga ggaagcagga gagggaagga aagtcccatg gaatatgtat tccanaatcc 480
ttacattttc tcagccaccg ctccccacgt gagttcccac ccccaccccg acaagaagca 540
aagagttctg aggatccaag aacgtgaccg ggtcanacan gttcagctac tgagttcac 599

<210> 303
<211> 591
<212> DNA
<213> Homo sapien

<400> 303
cggagttgta acgctccact gactgataga gcgaccggcc gaccatggcg cccggagtgg 60
cccgcgggcc gacgccgtac tggaggttgc gcctcggtgg cgccgcgctg ctcctgctgc 120
tcatcccggt ggccgccgcg caggagcctc ccggagctgc ttgttctcag aacacaaaca 180
aaacctgtga agagtgcctg aagaacgtct cctgtctttg gtgcaacact aacaaggctt 240
gtctggacta cccagttaca agcgtcttgc caccggcttc cctttgtaaa ttgagctctg 300
cacgctgggg agtttgttgg gtgaactttg aggcgctgat catcaccatg tcggtagtcg 360
ggggaacccct cctcctgggc attgccatct gctgctgctg ctgctgcagg aggaagagga 420
gccggaagcc ggacaggagt gaggagaagg ccatgcgtga gcgggaggag aggcggatac 480
ggcaggagga acggagagca gagatgaaga caagacatga tgaaatcaga aaaaaatatg 540
gcctgtttaa agaagaaaac ccgtatgcta gatttgaaaa caactaaagc g 591

<210> 304
<211> 441
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(441)
<223> n = A,T,C or G

<400> 304
gctggacgga gacctgctgg aggaggagga gctggaggaa gcagaggagg aggaccggtc 60
gtcgctgctg ctgctgtcgc cgcccgcggc caccgcctct cagacccagc agatcccagg 120
cgggtccctg ggtctgtgc tgctgccagc cgccaggttc gatgcccggg aggcggcggc 180
ggcggcgggg gtgctgtacg gaggggacga tgcccagggc atgatggcgg cgatgctgtc 240
ccacgcctac ggccccggcg gttgtggggc ggcggcggcc gccctgaacg gggagcaggc 300
ggccctgctc cggagaaaga gcgtcaacac caccgagtgc gtcccggtgc ccagctccga 360
gcacgtcgcc gagatcgtcg gccgccaggg ttgtaaaatt aaagcactga nagccaagac 420
aaacacgtat atcaagactc c 441

<210> 305
<211> 491
<212> DNA
<213> Homo sapien

<400> 305
tcgccatgcc cccttcttag cactgcaccg ccaggtccat gctgctgcca ccccagacct 60
gggctttgcc tgccacctct gtgggcagag cttccgaggc tgggtggccc tggttctgca 120
tctgcgggcc cattcagctg caaagcggcc catcgcttgt cccaaatgcg agagacgctt 180
ctggcgacga aagcagcttc gagctcatct gcggcggtgc caccctcccg ccccggaggc 240
ccggcccttc atatgcggca actgtggccg gagctttgcc cagtgggacc agctagttgc 300
ccacaagcgg gtgcacgtag ctgaggccct ggaggaggcc gcagccaagg ctctggggcc 360
ccggcccagg ggccgccccg cggtgaccgc cccccggccc ggtggagatg ccgtcgaccg 420
ccccttccag tgtgcctgtt gtggcaagcg cttccggcac aagcccaact tgatcgctca 480
cccgcgcgtg c 491

<210> 306
<211> 547
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(547)
<223> n = A,T,C or G

<400> 306
tctctttctt ttaagacagg aatgtaagcc acaacattta caaatacaat gttttaactc 60
tctacatgta ggaagccaac ctgctccttt ttgatcttct tctttggcac aacctcagtg 120
gatttctctg attcagaacg agttctaatt gatcttctct gttgcttctt ttctactgag 180
cctgtagaac cagatgttgc ttcaggagat gatacactct gcgttggctt ttcatttctc 240
tggtttggtg tagaaattat aagcctgtct tgccccctga cacttatttc tgttttgtta 300
ccaattccct ttgttgaata aacaaattga tcgataaatt tcccatcccc tgtagcattc 360
tgaagagcaa acacttgttc aattttcaca actggagaca tgttacactt ctgcaaatcc 420
aggctccctt tgtgcatccg taatggaagc tggtaaggat ttccttgctg ccgcagtttt 480
ccaggctatt ttaacaggcg gnggctcttc ctctttccgc acttgtgtgc cgcctctggc 540
tatgtct 547

<210> 307
<211> 571
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(571)
<223> n = A,T,C or G

<400> 307
cgctgcatgt gataatgtca tcatttattt ttaaatggtt ctaaattgca natttaagtt 60
gatttcaaat caaccctatt tttaaattac ttttaatagg aanaaatgaa gcaaggacat 120
acataatcta ctatatttga aggactcaaa caaatacatg tttggctgtg aattctgtac 180
tctcaccaaa acagagataa aaatccacct aaaatacact ttccttcatt tagtgcttgt 240
ggganaaggt caagtattgc actttaaaat tactttcatc taacatttgc cccaactttc 300
cccctgaatt cactatatgt tttcagcaaa catgatttta taaattttaa gtataaaagc 360
aactaggttt tctaattcaa ctttggaagg tttactttac tctacanagc tatttttgta 420
aaacggcata tttacttaca aaattganag ataggggcat ccagctgagg tacatttcct 480
cccttggcgt tgagtttctg gacttgggtc gggggcacag gcttgtgtga ctgccccgtg 540
gcccgataca tggcctggac cccaggatgc g 571

<210> 308
<211> 591
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(591)
<223> n = A,T,C or G

<400> 308
ctccttatgt gtctgcctac ttcattcttc ggcatttcct gcttatccaa gttcaccatt 60
tcaggtcacc actggatatc agttgcctgt atataattat caggcatttc ctgcttatcc 120
aagttcacca tttcaggtca ccactggata tcagttgcct gtatataatt atcaggcatt 180
tcctgcttat ccaagttcac catttcaggt caccactgga tatcagttgc ctgtatataa 240
ttatcaggca tttcctgctt atccaagttc accatttcag gtcaccactg gatatcagtt 300
gcctgtatat aattatcagg catttcctgc ttatccaagt tcaccatttc aggtcaccac 360
tggatatcag ttgcctgtat ataattatca ggcatttcct gcttatccaa gttcaccatt 420
tcaggtcacc actggatatc agttgcctgt atataattat caggcatttc ctgcttatcc 480
aaattcagca gttcaggtca ccactggata tcagttccat gtatacaatt accagatgcc 540
accgcagtgc cctgttgggg gagcaaagga gaaatntgtg gaccgaagca t 591

<210> 309
<211> 591
<212> DNA
<213> Homo sapien

<400> 309
agggggtgca cgtactccca actgtggtcg cgctctcacc ccttctgctg ctctcgtggc 60
cccctcgcga tggcgggcat cctgtttgag gatattttcg atgtgaagga tattgacccg 120
gagggcaaga agtttgaccg aggtaagtaa gtgtctcgac tgcattgtga gagtgaatct 180
ttcaagatgg atctaatctt agatgtaaac attcaaattt accctgtaga cttgggtgac 240
aagtttcggt tggtcatagc tagtaccttg tatgaagatg gtaccctgga tgatggtgaa 300
tacaacccca ctgatgatag gccttccagg gctgaccagt ttgagtatgt aatgtatgga 360
aaagtgtaca ggattgaggg agatgaaact tctactgaag cagcaacacg cctgctgaga 420
ttgagagctg ctgagtggca gtgctccaga atcacgggat ggggccttct gtttcagctc 480
tgcgtacgtg tcctatgggg gcctgctcat gaggctgcag gggatgcca acaacctgca 540
tggattcgag gtggactcca gagtttatct cctgatgaag aagctagcct t 591

<210> 310

<211> 488
<212> DNA
<213> Homo sapien

<400> 310
tggtctcaag cctgaagagg ctccgcccac aagctggccc atgaagttag caatgcctgt 60
ggcttcagtc aattgtcttg agactgtgaa gaggctgaaa gacaccttcc cgggtggaag 120
aaggagttca ctgaaaactt atcttaaact gacccttccc tttgagtgag tcttcattcc 180
tctcccatgt gggaacccag cctccgatgc cccggggact aggggaaaca gttggaggtc 240
cgtgccgtcc ccagcctgcc acgggtgcga ggacagccaa gtcctgagtg actcaagatg 300
cttcacttac atggaagaaa cttctaaaac tctaccgagt ggtttttgta tatactaaag 360
ttctatttag agcttttctg ttttgggcaa gttcgctgct ccttctattt gggcactttg 420
gtttttgtac tgtcttttgt gacggcattg attgaacatt ttttactagt agtcttatga 480
cttttgta 488

<210> 311
<211> 511
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 311
cccgtttntg nagcaaaana gggggaagat ttataggtag aggcgacaaa cctaccgagc 60
ctggtgatag ctggttgtcc aagatagaat cttagttcaa ctttaaattt gcccacagaa 120
ccctctaaat ccccttgtaa atttaactgt tagtccaaag aggaacagct ctttggacac 180
taggaaaaaa ccttgtagag agagtaaaaa atttaacacc catagtaggc ctaaaagcag 240
ccaccaatta agaaagcgtt caagctcaac acccactacc taaaaaatcc caaacatata 300
actgaactcc tcacacccaa ttggaccaat ctatcaccct atagaagaac taatgttagt 360
ataagtaaca tgaaaacatt ctcctccgca taagcctgcg tcagattaaa acactgaact 420
gacaattaac agcccaatat ctacaatcaa ccaacaagtc attattaccc tcactgtcaa 480
cccaacacag gcatgctcat aaggaaaggt t 511

<210> 312
<211> 591
<212> DNA
<213> Homo sapien

<400> 312
gaacttgcgt tgaaggaagc agaaactgat gaaataaaaa ttttgctgga agaaagcaga 60
gcccagcaga aggagacctt gaaatctctt cttgaacaag agacagaaaa tttgagaaca 120
gaaattagta aactcaacca aaagattcag gataataatg aaaattatca ggtgggctta 180
gcagagctaa gaactttaat gacaattgaa aaagatcagt gtatttccga gttaattagt 240
agacatgaag aagaatctaa tatacttaaa gctgaattaa acaaagtaac atctttgcat 300
aaccaagcat ttgaaataga aaaaaaccta aaagaacaaa taattgaact gcagagtaaa 360
ttggattcag aattgagtgc tcttgaaaga caaaaagatg aaaaaattac ccaacaagaa 420
gagaaatacg aagctattat ccagaacctt gagaaagaca gacaaaaatt ggtcagcagc 480
caggagcaag acagagaaca gttaattcag aagcttaatt gtgaaaaaga tgaagctatt 540
cagactgccc taaaagaatt taaattggag agagaagttg ttgagaaaga g 591

<210> 313
<211> 373
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(373)
<223> n = A,T,C or G

<400> 313
```
ttgattttta ttctgnattt tattactgaa atangttgtc ctantnatcc caccccacaa      60
taaaaatntn acccangccc cccntttctt tncctnatnc cctnttccac cacaccatcc     120
cggaacaagt gctccaggat tccctgccca ctggccattt tggagtgtgn ccattgggta     180
gcaatgtgga aaccaccaag gcctttgtgg anaaaatgga gggggttgag ggagncccan     240
gaggggctna tttgagggcc tttgccactt gctcataggc gagctcnatc tcctcntnat     300
ctgnacangt ggaagcaaat tcttcccggg cgtnggnant gctnaagnac cgatgcactc     360
cccggaaggn ctn                                                        373
```

<210> 314
<211> 591
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(591)
<223> n = A,T,C or G

<400> 314
```
cccgtgccgc cgccgcctcc tgggaagaga ggaagcggga gaggagccca cgtcgcctgt      60
cacccaatat ctccagccgc gcagtcccga agagtgtaag atgttcgcct gcgccaagct     120
cgcctgcacc ccctctctga tccgagctgg atccagagtt gcatacagac caatttctgc     180
atcagtgtta tctcgaccag aggctagtag gactggagag ggctctacgg tatttaatgg     240
ggcccagaat ggtgtgtctc agctaatcca aagggagttt cagaccagtg caatcagcag     300
agacattgat actgctgcca aatttattgg tgcaggtgct gcaacagtag gagtggctgg     360
ttctggtgct ggtattggaa cagtctttgg cagccttatc attggttatg ccagaaaccc     420
ttcgctgaag cagcagctgt tctcatatgc tatcctggga tttgccttgt ctgaagctat     480
gggtctcttt tgtttgatgg ttgctttctt gattttgttt gccatgtaac aaattactgc     540
ttgacatgtt ggcattcata ttaattacng atgtaattct gtgtatctta c              591
```

<210> 315
<211> 591
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(591)
<223> n = A,T,C or G

<400> 315
```
aagcccttca ccaacaaaga tgcctatact tgtgcaaatt gcagtgcttt tgtccacaaa      60
ggctgccgag aaagtctagc ctcctgtgca aaggtcaaaa tgaagcagcc caaagggagc     120
cttcaggcac atgacacatc atcactgccc acggtcatta tgagaaacaa gccctcacag     180
cccaaggagc gtcctcggtc cgcagtcctc ctggtggatg aaaccgctac caccccaata     240
tttgccaata gacgatccca gcagagtgtc tcgctctcca aaagtgtctc catacagaac     300
attactggag ttggcaatga tgagaacatg tcaaacacct ggaaattcct gtctcattca     360
acagactcac taaataaaat cagcaaggtc aatgagtcaa cagaatcact tactgatgag     420
ggtacagaca tgaatgaagg acaactactg ggagactttg agattgagtc caaacagctg     480
gaagcagagt cttggagtcg gataatagac agcaagtttc taaaacagcc aaaagaaaga     540
tgtgggtcaa acngcgagaa gtaatatatg agttggatgc agacagagtt t              591
```

<210> 316
<211> 591
<212> DNA
<213> Homo sapien

<400> 316
gtttttataa gaataaaatt ccattcaagc cagatggtgt ttacattgaa gaagttctaa 60
gtaaatggaa aggagattat gaaaaactgg agcacaacca cacttacatt caatggcttt 120
tccccctgag agaacaaggc ttgaacttct atgccaaaga actaactaca tatgaaattg 180
aggaattcaa aaaaacaaaa gaagcaatta gaagattcct cctggcttat aaaatgatgc 240
tagaattttt tggaataaaa ctgactgata aaactggaaa tgttgctcgg gctgttaact 300
ggcaggaaag atttcagcat ctgaatgagt cccagcacaa ctatttaaga atcactcgta 360
ttcttaaaag ccttggtgag cttggatatg aaagttttaa atctcctctt gtaaaattta 420
ttcttcatga agctcttgtg gagaatacta ttcccaatat taagcagagt gctctagagt 480
attttgttta tacaattaga gacagaagag aaaggagaaa gctcctgcgg ttcgcccaga 540
aacactacac gccttcagag aactttatct ggggacccgc ctcgaaaaga a 591

<210> 317
<211> 323
<212> DNA
<213> Homo sapien

<400> 317
ccaagctacg gaagcaagtg gaagagattt ttaatttgaa atttgctcaa gctcttggac 60
tcaccgaggc agtaaaagta ccatatcctg tgtttgaatc aaacccggag ttcttctatg 120
tggaaggctt gccagagggg attcccttcc gaagccctac ctggtttgga attccacgac 180
ttgaaaggat cgtccacggg agtaataaaa tcaagttcgt tgttaaaaaa cctgaactag 240
ttatttccta cttgcctcct gggatggcta gtaaaataaa cactaaagct ttgcagtccc 300
ccaaaagacc acgaagtcct ggg 323

<210> 318
<211> 591
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(591)
<223> n = A,T,C or G

<400> 318
gatggcgtac ttggcttgga gactggcgcg gcgttcgtgt ccgagttctc tgcaggtcac 60
tagtttcccg gtagttcagc tgcacatgaa tagaacagca atgagagcca gtcagaagga 120
ctttgaaaat tcaatgaatc aagtgaaact cttgaaaaag gatccaggaa acgaagtgaa 180
gctaaaactc tacgcgctat ataagcaggc cactgaagga ccttgtaaca tgcccaaacc 240
aggtgtattt gacttgatca acaaggccaa atgggacgca tggaatgccc ttggcagcct 300
gcccaaggaa gctgccaggc agaactatgt ggatttggtg tccagtttga gtccttcatt 360
ggaatcctct agtcaggtgg agcctggaac agacaggaaa tcaactgggt ttgaaactct 420
ggtggtgacc tccgaagatg gcatcacaaa gatcatgttc aaccggccca aaaagaaaaa 480
tgccataaac actgagatgt atcatgaaat tatgcgtgca cttaaagctg ccagcaanga 540
tgactcaatc atcacttgtt ttaacaggaa atggtgacta ttacagtagn g 591

<210> 319
<211> 591
<212> DNA
<213> Homo sapien

<400> 319

gaattcggca cgaggttgct gctaagcgaa cgccctttgg agcttacgga ggccttctga 60
aagacttcac tgctactgac ttgtctgaat ttgctgccaa ggctgccttg tctgctggca 120
aagtctcacc tgaaacagtt gacagtgtga ttatgggcaa tgtcctgcag agttcttcag 180
atgctatata tttggcaagg catgttggtt tgcgtgtggg aatcccaaag gagaccccag 240
ctctcacgat taataggctc tgtggttctg gttttcagtc cattgtgaat ggatgtcagg 300
aaatttgtgt taaagaagct gaagttgttt tatgtggagg aaccgaaagc atgagccaag 360
ctccctactg tgtcagaaat gtgcgttttg gaaccaagct tggatcagat atcaagctgg 420
aagattcttt atgggtatca ttaacagatc agcatgtcca gctccccatg gcaatgactg 480
cagagaatct tgctgtaaaa cacaaaataa gcagagaaga atgtgacaaa tatgccctgc 540
agtcacagca gagatggaaa gctgctaatg atgctggcta ctttaatgat g 591

<210> 320
<211> 591
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(591)
<223> n = A,T,C or G

<400> 320
ggctccggcg tctgcagggg tcgccgagct aacccgtggc taggcgagtg gggcggggcg 60
gccggcacca tgtcgaggca ggcgaaccgt ggcaccgaga gcaagaaaat gagctctgag 120
ctcttcaccc tgacctatgg tgccctggtc acccagctat gtaaggacta tgaaaatgat 180
gaagatgtga ataaacagct ggacaaaatg ggctttaaca ttggagtccg gctgattgaa 240
gatttcttgg ctcggtcaaa tgttgggagg tgccatgact ttcgggaaac tgcggatgtc 300
attgccaagg tggcgttcaa gatgtacttg ggcatcactc caagcattac taattggagc 360
ccagctggtg atgaattctc cctcatttg gaaaataacc ccttggtgga ctttgtggaa 420
cttcctgata accactcatc ccttatttat tccaatctct tgtgtggggt gttgcgggga 480
gctttggaga tggtccagat ggctngngga ggcccaagtt tgtccaggac accctnaaag 540
gagacgggng tgacagaaat ccggatgaga ttcatcaggc ggattganga c 591

<210> 321
<211> 260
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(260)
<223> n = A,T,C or G

<400> 321
ctgcttggct ccacacgtgg gccgccgtag gtattccgac cggtaattcc tcctattggt 60
gtgcagcagc cacattgaag gatagagtgg cagcagaggc caaggatcgt gagttgatgg 120
agtttgctgc tgaaaatgaa gggaagtctg ggggaggtct ccacagcgta gctgaggggg 180
tgcggctaag tccagagcct ggcagggagg gagtaaggga cttagcaggg gcggaggagt 240
tctgcggngg anaggagggg 260

<210> 322
<211> 559
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(559)

<223> n = A,T,C or G

<400> 322
ttccacatga catggagtgt gaagctggat gagcacatca ttccactggg aagcatggca 60
nttaacagca tctcaaaact gactnanctc acccagtctt ccatgtattc acttcctaat 120
gcacccactc tggcanacct gnaggacnat acacatgaag ncantgatga tcagccagan 180
aancctcact ttgactctcg canngtgata tttgagctgg attcatgcaa tggnagtggg 240
aaagtttgcc ttgtctacaa aagtgggaaa ccagnattag cagaanacac tgagatctgg 300
ttcctgnaca nancgttata ctggcatttt ctcacanaca cctttactgc ctattaccgc 360
ctgctcatca cccacctggg cctgccccag tggcaatatg ccttcccagc tatggcatta 420
gcccacaggc caagcaatgg ttcagcatgt ataaacctat cacctacaac acaaacctgc 480
tcacagaaga naccgactcc tttgtgaata agctagatcc canctnagtg tttaagagca 540
agaacaagat cgttatccc 559

<210> 323
<211> 492
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(492)
<223> n = A,T,C or G

<400> 323
cctgtctccc agccgtacca gcgagggctc ggccggcagc gccgggctgg ggggcggcgg 60
cgccggcgcc ggagccgggg tgggtgcagg cggcggcggg ggcagcggcg cgagcagcgg 120
cggcggggcc ggggggctgc aacccagcag ccgcgctggc ggcggccggc cctccagccc 180
cagccccgtcg gtggtgagcg agaaggagaa ggaagagttg gagcggctgc agaaagagga 240
ggaggagagg aagaagaggc tgcagctgta tgtgttcgtg atgcgctgca tcgcctaccc 300
ctttaatgcc aagcagccca ccgacatggc tcgccggcag cagaagatca gcaaacagca 360
gctgcagaca gtcaaggacc ggtttcaggc tttcctcaat ggggaaaccc anatcatggc 420
tgacgaagcc ttcatgaacc gctgtngcag agttactatg aggtgttcct gaagaccacc 480
cgtgtggccg ca 492

<210> 324
<211> 474
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(474)
<223> n = A,T,C or G

<400> 324
aatttcagca acatacttct caatttcttc aggatttaaa atcttgaggg attgatctcg 60
cctcatgaca gcaagttcaa tgtttttgcc acctgactga accacttcca ggagtgcctt 120
gatcaccagc ttaatggtca natcatctgt ttcaatggct tcgtcagtat agttcttctc 180
cagnaactca cgcactgact tggcaccccg gcctatggca ttggccttcc aggcatggta 240
tgtgcccgag ggtcagtct gatagagcct aggagtgcca tcaaagtcga aacccacgat 300
gagggcagag atgccaaacg gcctgcgccc attgctctgc gtataacgct gcttcanact 360
ggcgatgtag cgggtgatgt actccacagt gaccgggtcc tccacagtca gccggtggct 420
ctggcactcc acccgggccc tgttgatgac tatccttgca tcggcggtga ggcc 474

<210> 325
<211> 532
<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(532)
<223> n = A,T,C or G

<400> 325
```
gaggagacag gacagagcgt ctggagaggc aggaggacac cgagttcccc gtgttggcct     60
ccaggtcctg tgcttgcgga gccgtccggc ggctgggatc gagccccgac aatgggcaac    120
gcgcaggagc ggccgtcaga gactatcgac cgcgagcgga aacgcctggt cgagacgctg    180
caggcggact cgggactgct gttggacgcg ctgctggcgc ggggcgtgct caccgggcca    240
gagtacgagg cattggatgc actgcctgat gccgagcgca gggtgcgccg cctactgctg    300
ctggtgcagg gcaagggcga ggccgcctgc caggagctgc tacgctgtgc ccagcgtacc    360
gcgggcgcgc cggaccccgc ttgggactgg cagcacgtgg gtccgggcta ccgggaccgc    420
agctatgacc ctccatgccc aggccactgg acgccggagg cacccggctc ggggaccaca    480
tgccccgggt tgcccagact tcagaccctg acgaggncgg gggccctgag gg            532
```

<210> 326
<211> 322
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(322)
<223> n = A,T,C or G

<400> 326
```
caaaattaac atttttatta aatcaagtta aaaaaaatgt tcagtgtana aaagtcaaca     60
agggttttaa caaaaccaaa atataccttt ttatacaata tatgtatata ttagcagcaa    120
actacttctg anattctctt tcttttatgt tcttctagtt attttaaaga aagcataaac    180
aatgtatatt agtatggaat gtcagcaaat ccactcttag tcctttattc tgtgatttgg    240
gccttctaca aaatactttg tgattctcac taatgaatat taagaacata cccaatttta    300
actaaaaagt agtgaaacag tg                                             322
```

<210> 327
<211> 387
<212> DNA
<213> Homo sapien

<400> 327
```
aaaaccgtgt actattagcc atggtcaacc ccaccgtgtt cttcgacatt gccgtcgacg     60
gcgagccctt gggccgcgtc tcctttgagc tgtttgcaga caaggtccca aagacagcag    120
aaaattttcg tgctctgagc actggagaga aaggatttgg ttataagggt tcctgctttc    180
acagaattat tccagggttt atgtgtcagg gtggtgactt cacacgccat aatggcactg    240
gtggcaagtc catctatggg gagaaatttg aagatgagaa cttcatccta aagcatacgg    300
gtcctggcat cttgtccatg gcaaatgctg gacccaacac aaatggttcc cagtttttca    360
tctgcactgc caagactgag tggttgg                                        387
```

<210> 328
<211> 502
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(502)

<223> n = A,T,C or G

<400> 328
agcagcccgg cgcggccgcc gcgccggcgg gcggcaaggc tccgggccag catgggggct 60
tcgtggtgac tgtcaagcaa gagcgcggcg agggtccacg cgcgggcgag aaggggtccc 120
acgaggagga gccggtgaag aaacgcggct ggcccaaggg caagaagcgg aagaagattc 180
tgccgaatgg gcccaaggca ccggtcacgg gctacgtgcg cttcctgaac gagcggcgcg 240
agcagatccg cacgcgccac ccggatctgc cctttcccga gatcaccaag atgctgggcg 300
ccgagtggag caagctgcag ccaacggaaa agcagcggta cctggatgag gccnagagag 360
agaagcagca gtacatgaag gagctgcggg cgtaccagca gtctgaagcc tataagatgt 420
gcacggagaa gatccaggag aagaagatca agaaagaaga ctcgagctct gggctcatga 480
acactcttct gaatggacac aa 502

<210> 329
<211> 463
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(463)
<223> n = A,T,C or G

<400> 329
caagttgcac attttaattt acaattttta ccaataaaaa ggattagttt acaaaaaggg 60
aagtccttta tacaaaataa ggacaatttg taaaganaat ccactgtcat gttttgcctt 120
gtcaagtcaa aactcaaata gcttgttttg gtaaaattat tccagaaaca taatccagac 180
aaaatcaata acgtcatcag cttcctaacc atgtttaana ggaataactt catgaacatt 240
ttgccctgaa ctgaanagtt ctaaatactt gtaaaccttt aggaaaaaat gactgctcgc 300
aggcagcttg actggtaaga gggtacacca nagactccgg gtcactcact gtcagaatat 360
tcttatacat acaatgagtc tccacgcctg tacaatgagt gtcgtgcaac ataattggag 420
taatggcctc taaaatttta caagtaaact ttattgnggc ccc 463

<210> 330
<211> 500
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(500)
<223> n = A,T,C or G

<400> 330
taattataga tctacaaaat atgaaatgta ttccaagaat gcagaaaaac catctagaag 60
caaaaggact ataaaacaaa aacagagaag aaaattcatg gctaaaccag ctgaagaaca 120
gcttgatgtg ggacagtcta aagatgaaaa catacataca tcacatatta cccaagacga 180
atttcaaaga aattcagaca gaaatatgga agagcatgaa gagatgggaa atgattgtgt 240
ttccaaaaaa acagatgcca cctgtgggaa gcaagaaaag tagcactaga aaagataagg 300
aagaatctaa aaagaagcgc ttttccagtg agtccaagaa caaacttgtn cctgaagaag 360
tgacttcaac tgtcacgaaa agtcgaanaa tttccangcg tccatctgat tggtgggtgg 420
taaaancaga ggagagtcct gtttatagca attcttcagt aagaaatgaa ttaccaantg 480
catcacaatn ntgcccggaa 500

<210> 331
<211> 494
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(494)
<223> n = A,T,C or G

<400> 331
tctctctctc tctcaaaatt acagtgttca ttgtcattga cctcagcagc aaatttgact 60
tgaattcact taggatcgca ggaatcaggg gaaagtgatt ttaaaggtgg tttctccagc 120
acattttaag aaaagggacc aaaagttatt ttagcttcct caatagattg catgttgctt 180
attaggataa taaattaata ttaaatgcaa tatatgtctt gnctttatta tggcatctat 240
ttaggagttg ttcaaatcac tgcagtaggg ctctgcaaat aaaataatgn aacctattat 300
catggatcta atgnactgna actttatcag tgaaaggnaa aatctcaaat aacaagtaca 360
aacattggac aattacctat aaagatttgt aaaaggaaaa tttttccata gatttcattc 420
ttggcatttt gtaaagacga ccctgcagnc ccctgtttgn aacttttttta ataaaataga 480
catctgttta cttg 494

<210> 332
<211> 538
<212> DNA
<213> Homo sapien

<400> 332
aaagaacaaa tggaacgcga tggttgttct gaacaagagt ctcaaccgtg tgcatttatt 60
gggataggaa atagtgacca agaaatgcag cagctaaact tggaaggaaa gaactattgc 120
acagccaaaa cattgtatat atctgactca gacaagcgaa agcacttcat gttgtctgta 180
aagatgttct atggcaacag tgatgacatt ggtgtgttcc tcagcaagcg gataaaagtc 240
atctccaaac cttccaaaaa gaagcagtca ttgaaaaatg ctgacttatg cattgcctca 300
ggaacaaagg tggctctgtt taatcgacta cgatcccaga cagttagtac cagatacttg 360
catgtagaag gaggtaattt tcatgccagt tcacagcagt ggggagcctt ttttattcat 420
ctcttggatg atgatgaatc agaaggagaa gaattcacag tccgagatgg ctacatccat 480
tatggacaaa cagtcaaact tgtgtgctca gttactggca tggcactccc aagattga 538

<210> 333
<211> 499
<212> DNA
<213> Homo sapien

<400> 333
ctcagcctgc gggactgctc ggctcggctt ctaggcggtt ttgatgaaca cctggcttta 60
ttcttgcaat gaagaaaggt tctcaacaaa aaatattctc caaagcaaag ataccatcat 120
catctcactc tcctatccca tcatctatgt ccaatatgag atctaggtca ctttcacctt 180
tgattggatc agagactcta cctttttcatt ctggaggaca gtggtgtgag caagttgaga 240
ttgcagatga aaacaatatg cttttggact atcaagacca taaaggagct gattcacatg 300
caggagttag atatattaca gaggccctca ttaaaaaact tactaaacag gataatttgg 360
ctttgataaa atctctgaac ctttcacttt ctaaagacgg tggcaagaaa tttaagtata 420
ttgagaattt ggaaaaatgt gttaaacttg aagtactgaa tctcagctat aatctaatag 480
ggaagattga aaagtcgga 499

<210> 334
<211> 561
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(561)
<223> n = A,T,C or G

<400> 334
ttcccggtag ttcagctgca catgaataga acagcaatga gagccagtca gaaggacttt 60
gaaaattcaa tgaatcaagt gaaactcttg aaaaaggatc caggaaacga agtgaagcta 120
aaactctacg cgctatataa gcaggccact gaaggacctt gtaacatgcc caaaccaggt 180
gtatttgact tgatcaacaa ggccaaatgg gacgcatgga atgcccttgg cagcctgccc 240
aaggaagctg ccaggcagaa ctatgtggat ttggtgtcca gtttgagtcc ttcattggaa 300
tcctctagtc aggtggagcc tggaacagac aggaaatcaa ctgggtttga aactctggtg 360
gtgacctccg aagatggcat cacaaagatc atgttcaacc cggcccaaaa agaaaaatgc 420
cataaacact gagatgtatc atgaaattat gcgtgcactt aaagctgcca gcaaggatga 480
ctcaatcatc actgttttaa cangaaatgg tgactattac agtagtggga atgatctgac 540
taacttcnct gatattcccc c 561

<210> 335
<211> 551
<212> DNA
<213> Homo sapien

<400> 335
aagctggtca tggctgggga gaccaccaac tcccgcggcc agcggctgcc ccagaaggga 60
gacgtggaga tgctgtgcgg cgggccgccc tgccagggct tcagcggcat gaaccgcttc 120
aattcgcgca cctactccaa gttcaaaaac tctctggtgg tttccttcct cagctactgc 180
gactactacc ggccccggtt cttcctcctg gagaatgtca ggaactttgt ctccttcaag 240
cgctccatgg tcctgaagct caccctccgc tgcctggtcc gcatgggcta tcagtgcacc 300
ttcggcgtgc tgcaggccgg tcagtacggc gtggcccaga ctaggaggcg ggccatcatc 360
ctggccgcgg cccctggaga gaagctccct ctgttcccgg agccactgca cgtgtttgct 420
ccccgggcct gccagctgag cgtggtgggt ggatgacaag aagtttgtga gcaacataac 480
caggttgagc tcgggtcctt tccggaccat acggtgcgag aaacgatgtc cgacctgccg 540
gaagtgcgga a 551

<210> 336
<211> 540
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(540)
<223> n = A,T,C or G

<400> 336
aggtctatgt ctactgaagg caataaacga ggaatgatcc agcttattgt tgcaaggaga 60
ataagcaagt gcaatgagct gaagtcacct gggagccccc ctggacctga gctgcccatt 120
gaaacagcgt tggatgatag agaacgaaga atttcccatt ccctctacag tgggattgag 180
gggcttgatg aatcgcccag cagaaatgct gccctcagta ggataatggg taaataccag 240
ctgtccccta cagtgaatat gccccaagat gacactgtca ttatagaaga tgacaggttg 300
ccagtgcttc ctccacatct ctctgaccag tcctcttcca gctcccatga tgatgtgggg 360
tttgtgacgg cagatgctgg tacttggccc aaggctgcaa tcagtgattc agccgactgc 420
tctttgagtc cagatgttga tccagttctt gcttttcaac gaaaaaggat ttggacgtca 480
gaagtatgtc agaaaaacgc accaaagcaa ttttcanatg ccagtcaatt ggatttcgtt 540

<210> 337
<211> 422
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature

<222> (1)...(422)
<223> n = A,T,C or G

<400> 337
gcagcaggaa cagttacagc agcagcagca acagcagctg ttgcaacagc agcaggaaca 60
attgcagcag caacaactgc agcctcctcc cctggagccc gaggaggagg aagaggtgga 120
gctggagctc atgccggtgg acctggggtc agagcaggag ctggagcagc agcggcagga 180
gttggagcgg cagcaggagc tggaacggca gcaggagcag cggcagctgc agctcaaact 240
gcaggaggag ctgcagcagc tggagcaaca gctggagcag cagcagcagc agctggagca 300
gcaggaggtg cagctggagc tgaccccggt ggagctaggc gcccagcagc aggaggtgca 360
gctggagctg acccccgtgc agccggagct gcagctggaa ctggtgccan cccaggggggc 420
gg 422

<210> 338
<211> 601
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(601)
<223> n = A,T,C or G

<400> 338
catcttacga acgctctatg atgtcttatg agcggtctat gatgtcccct atggctgaac 60
gctctatgat gtcagcctac gagcgctcta tgatgtcagc ctacgagcgc tctatgatgt 120
cccctatggc tgagcgctct atgatgtcag cttatgaacg ctccatgatg tcagcttatg 180
aacgctccat gatgtcccca atggctgatc gatctatgat gtccatgggt gctgaccggt 240
ctatgatgtc gtcatactct gctgctgacc ggtctatgat gtcatcgtac tctgcagctg 300
accgatctat gatgtcatct tatactgctg atcgttcaat gatgtctatg gctgctgatt 360
cttacaccga ttcttacact gacacatata cagaggcata tatggtgcca cctttgcctc 420
ctgaagagcc cccaacaatg ccaccgttgc cacctgagga gccaccaatg acaccaccat 480
tgcctnctga ggaaccaccc agagggtcca gcattgccca cttgagcagt cagcattaac 540
cagcttgaaa atacttggcc ctacanangg tgccatcatt accatctgaa gagctgtatc 600
g 601

<210> 339
<211> 440
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(440)
<223> n = A,T,C or G

<400> 339
agagggagga ggcccaactg gtgatgctgc tgctgctgct gctgccgccg ccgccgcctc 60
tattgctgat actctagtgg ggctggaagg gtggttccta ttcgcaccat cgccaaccag 120
agacagaggg aaaaaaaaaa ccggcagcca ctgctgatgt tgggttcgga ggctgcatcc 180
gactcggtca caaggaaaat ggattcagtt tgcatctctc cctcctttaa acagcttctc 240
cgggtctcag catggtatca aagcttgaaa gagagaagac tcaagaagcg aagaggattc 300
gtgagctgga gcagcgcaag cacacggtgc tggtgacaga actcaaagcc aagctccatg 360
aggagaagat gaaggagctg caggctgtga gggagaacct tatcaagcag cacgacagga 420
aatgtcaang acggtgaagg 440

<210> 340
<211> 450

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(450)
<223> n = A,T,C or G

<400> 340
gatttccagg ggcggatatt gagtgtcgac ccagaggaag aaagggagga gggcccgcct 60
aggattcctc aggccgacca gtggaagtct tcaaacaaga gcctggtgga ggctctgggg 120
ctggaagccg agggtgcagt tcctgagaca cagactttga ccggatggag taaggggttc 180
attggcatgc acagggaaat gcaagtcaac cccatttcaa agcggatggg gcccatgact 240
gtggtcagga tggacgcttc agtccagcca ggcccttttc ggaccctgct ccagtttctt 300
tatacgggac aactggatga aaaggaaaag gatttggtgg gcctggctca gatcgcagag 360
gtcctcgaga tgttcgattt gaggatgatg gtggaaaaca tcatgaacaa ggaagccttc 420
atgaaccagg agattacgaa nncctttcac 450

<210> 341
<211> 451
<212> DNA
<213> Homo sapien

<400> 341
aacagctatt aaaacagaaa atggatgaac ttcataagaa gttgcatcag gtggtggaga 60
catcccatga ggatctgccc gcttcccagg aaaggtccga ggttaatcca gcacgtatgg 120
ggccaagtgt aggctcccag caggaactga gagcgccatg tcttccagta acctatcagc 180
agacaccagt gaacatggaa aagaacccaa gagaggcacc tcctgttgtt cctcctttgg 240
caaatgctat ttctgcagct ttggtgtccc cagccaccag ccagagcatt gctcctcctg 300
ttcctttgaa agcccagaca gtaacagact ccatgtttgc agtggccagc aaagatgctg 360
gatgtgtgaa taagagtact catgaattca agccacagag tggagcagag atcaaagaag 420
ggtgtgaaac acataaggtt gccaacacaa g 451

<210> 342
<211> 498
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(498)
<223> n = A,T,C or G

<400> 342
ctcaagcagg ctattgaaga ggaaggaggc gatccagata atattgaatt aactgtttca 60
actgatactc caaacaagaa accaactaaa ggcaaaggta aaaaacatga agcagatgag 120
ttgagtggag atgcttctgt gggaagatga tgcttttatc aaggactgtg aattggagaa 180
tcaagaggca catgagcaag atggaaatga tgaactaaag gactctgaag aatttggtga 240
aaatgaagaa gaaaatgtgc attccaagga gttactctct gcagaagaaa acaagagagc 300
tcatgaatta atagaggcag aaggaataga agatatagaa aaagaggaca tcgaaagtca 360
ggaaattgaa gctcaagaag gtgaagatga tacctttcta acagcccaag atggtgagga 420
agaagaaaat gagaaagata tagcagggtt ctggtgatgg cncacaagaa gtatntaaac 480
ctcttccttc aaaaaggg 498

<210> 343
<211> 491
<212> DNA
<213> Homo sapien

<400> 343
ccgaccccta ctcggcggcg caactccaca accagtacgg ccccatgaat atgaacatgg 60
gtatgaacat ggcagcagcc gcggcccacc accaccacca ccaccaccac caccccggtg 120
ccttttttccg ctatatgcgg cagcagtgca tcaagcagga gctaatctgc aagtggatcg 180
accccgagca actgagcaat cccaagaaga gctgcaacaa aactttcagc accatgcacg 240
agctggtgac acacgtctcg gtggagcacg tcggcggccc ggagcagagc aaccacgtct 300
gcttctggga ggagtgtccg cgcgagggca agcccttcaa ggccaaatac aaactggtca 360
accacatccg cgtgcacaca ggcgagaaac ccttccctgc ccttccgggt gtggcaaagt 420
cttcgcgcgc tccgagaacc tcaagatcca caaaaggacc acacagggga gaagccgtcc 480
agtggagttg a 491

<210> 344
<211> 412
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(412)
<223> n = A,T,C or G

<400> 344
gtgcgctgtc ttcccgcttg cgtcagggac ctgcccgact cagtggccgc catggcatca 60
gatgaaggca aactttttgt tggagggctg agttttgaca ccaatgagca gtcgctggag 120
caggtcttct caaagtacgg acagatctct gaagtggtgg ttgtgaaaga cagggagacc 180
cagagatctc ggggatttgg gtttgtcacc tttgagaaca ttgacgacgc taaggatgcc 240
atgatggcca tgaatgggaa gtctgtagat ggacggcaga tccgagtaga ccaggcaggc 300
aagtcgtcan acaaccgatc ccgtgggtac cgtggtggct ctgccggggg ccggggcttc 360
ttccgtgggg gcccgangac ggggcccgtg ggttctctaa aagaagaggg ga 412

<210> 345
<211> 498
<212> DNA
<213> Homo sapien

<400> 345
aactagtctc gggccatcct ttctgcgcac ccggtgtcgc tgggctgcac cccgggcggg 60
gacgtccgcc gggcacggga gggggccaag atgccgatca ataaatcaga gaagccagaa 120
agctgcgata atgtgaaggt tgttgttagg tgccggcccc tcaatgagag agagaaatca 180
atgtgctaca aacaggctgt cagtgtggat gagatgaggg gaactatcac tgtacataag 240
actgattctt ccaatgaacc tccaaagaca tttacttttg atactgtttt tggaccagag 300
agtaaacaac ttgatgttta taacttaact gcaagaccta ttattgattc tgtacttgaa 360
ggctacaatg ggactatttt tgcatatgga caaaccggaa caggcaaaac ttttaccatg 420
gaaaggtgtc gagctattcc tgaacttaga ggaataattc cccaatttct ttgctcacaa 480
tatttgggcc atatttgc 498

<210> 346
<211> 427
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(427)
<223> n = A,T,C or G

<400> 346

agatggcggt cgccgtgaga actttgcagg aacagctgga aaaggccaaa gagagtctta 60
agaacgtgga tgagaacatt cgcaagctca ccgggcggga tccgaatgac gtgaggccca 120
tccaagccag attgctggcc ctttctggtc ctggtggagg tagaggacgt ggtagtttat 180
tactgaggcg tggattctca gatagtggag gaggaccccc agccaaacag agagaccttg 240
aaggggcagt cagtaggctg ggcggggagc gtcggaccag aagagaatca cgccaggaaa 300
gcgacccgga ggatgatgat gttaaaaagc cagcattgca gtcttcannt gtagctacct 360
cccaaagagc gccccacgta gagaccttat ccagggatca aaattttgga tgaaaaaggg 420
gaaagcc 427

<210> 347
<211> 280
<212> DNA
<213> Homo sapien

<400> 347
cacagaaagt tctccgctcc cagacatggg tccctcggct tcctgcctcg gaagcgcagc 60
agcaggcatc gtgggaaggt gaagagcttc cctaaggatg acccgtccaa gccggtccac 120
ctcacagcct tcctgggata caaggctggc atgactcaca tcgtgcggga agtcgacagg 180
ccgggatcca aggtgaacaa gaaggaggtg gtggaggctg tgaccattgt agagacacca 240
cccatggtgg ttgtgggcat tgtgggctac gtggaaaccc 280

<210> 348
<211> 411
<212> DNA
<213> Homo sapien

<400> 348
caactatgat gtgcctgaaa aatgggcacg attctatact gcagaagtag ttcttgcatt 60
ggatgcaatc cattccatgg gttttattca cagagatgtg aagcctgata acatgctgct 120
ggataaatct ggacatttga agttagcaga ttttggtact tgtatgaaga tgaataagga 180
aggcatggta cgatgtgata cagcggttgg aacacctgat tatatttccc ctgaagtatt 240
aaaatcccaa ggtggtgatg gttattatgg aagagaatgt gactggtggt cggttggggt 300
atttttatac gaaatgcttg taggtgatac acctttttat gcagattctt tggttggaac 360
ttacagtaaa attatgaacc attaaaaatt cacttacctt tcctgatgat a 411

<210> 349
<211> 408
<212> DNA
<213> Homo sapien

<400> 349
gatgggcatc tctcgggaca actggcacaa gcgccgcaaa accgggggca agagaaagcc 60
ctaccacaag aagcggaagt atgagttggg gcgcccagct gccaacacca agattggccc 120
ccgccgcatc cacacagtcc gtgtgcgggg aggtaacaag aaataccgtg ccctgaggtt 180
ggacgtgggg aatttctcct ggggctcaga gtgttgtact cgtaaaacaa ggatcatcga 240
tgttgtctac aatgcatcta ataacgagct ggttcgtacc aagaccctgg tgaagaattg 300
catcgtgctc atcgacagca caccgtaccg acagtggtac gagtcccact atgcgctgcc 360
cctgggccgc aagaagggag ccaaactgac ttctgaggaa gaagaaaa 408

<210> 350
<211> 409
<212> DNA
<213> Homo sapien

<400> 350
ggttccccca gctctgggta cccggctctg catcgcgtcg ccatgatggg ccatcgtcca 60
gtgctcgtgc tcagccagaa cacaaagcgt gaatccggaa gaaaagttca atctggaaac 120
atcaatgctg ccaagactat tgcagatatc atccgaacat gtttgggacc caagtccatg 180

atgaagatgc ttttggaccc aatgggaggc attgtgatga ccaatgatgg caatgccatt 240
cttcgagaga ttcaagtcca gcatccagcg gccaagtcca tgatcgaaat tagccggacc 300
caggatgaag aggttggaga tgggaccaca tcagtaatta ttcttgcagg ggaaatgctg 360
tctgtagctg agcacttcct ggagcagcag atgcacccaa caggtgggg 409

<210> 351
<211> 226
<212> DNA
<213> Homo sapien

<400> 351
aatcccaaac atataactga actcctcaca cccaattgga ccaatctatc accctataga 60
agaactaatg ttagtataag taacatgaaa acattctcct ccgcataagc ctgcgtcaga 120
ttaaaacact gaactgacaa ttaacagccc aatatctaca atcaaccaac aagtcattat 180
taccctcact gtcaacccaa cacaggcatg ctcataagga aaggtt 226

<210> 352
<211> 410
<212> DNA
<213> Homo sapien

<400> 352
gcggaggggc tggctgggca ggaggggttg gcggggcagc agggccgcgg ccatggggag 60
cttgaaggag gagctgctca aagccatctg gcacgccttc accgcactcg accaggacca 120
cagcggcaag gtctccaagt cccagctcaa ggtcctttcc cataacctgt gcacggtgct 180
gaaggttcct catgacccag ttgcccttga agagcacttc agggatgatg atgagggtcc 240
agtgtccaac cagggctaca tgccttattt aaacaggttc attttggaaa aggtccaaga 300
caactttgac aagattgaat tcaataggat gtgttggacc ctctgtgtca aaaaaaacct 360
cacaaagaat cccctgctca ttacagaaga agatgcattt aaaatatggg 410

<210> 353
<211> 380
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

<400> 353
gagtttattt agaaagtatc atagtgtaaa caaacaaatt gtaccacttt gattttcttg 60
gaatacaaga ctcgtgatgc aaagctgaag ttgtgtgtac aagactcttg acagttgtgc 120
ttctctagga ggntgggttt ttttaaaaaa agaattatct gngaaccata cgtgattaat 180
aaagatttcc tttaaggcan aggctggtcn agatgctgct gttatcttct gcctcagaca 240
gacagtataa gnggtcttgt ttctaagatt cctaccacca gttactttgg gccaagtatc 300
cacatcccct tgcgtatggg aggngggtga anagtgttgg atgcaaagng gttattatgg 360
gaagnagctc natggtaaaa 380

<210> 354
<211> 379
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(379)
<223> n = A,T,C or G

<400> 354
caacacatct ttattaaaca cctgaagtta ctgggaggag gccatgatgc tggacacact 60
gtcaaagtca atcttctcca caatgttctt gggtttaatg ctctcttctt ggctacagan 120
gaanatctgc cccgactngt cggcactcca gccgtatttg ctcatccaca cctttagctg 180
gctgtccgac aganccccga gcatntcggc cagcagccan cggncaatgt gctggtaagt 240
gatacccaca acatggcaga taaactttcg gacanagtct tcaaagccag ttataccttc 300
caagaggtcc atgttttcat ccagggcttg ccanaagcct ggaaatggca ggtctccaac 360
aggtccccca ggtacaaaa 379

<210> 355
<211> 499
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(499)
<223> n = A,T,C or G

<400> 355
gtccagagct gctggtgctc ccgttcccca gaccctaccc ctatccccag tggagccgga 60
gtgcgggcgc gccccaccac cgccctcacc atggtgctgt tggcagcagc ggtctgcaca 120
aaagcaggaa aggctattgt ttctcgacag tttgtggaaa tgacccgaac tcggattgag 180
ggcttattag cagcttttcc aaagctcatg aacactggaa aacaacatac gtttgttgaa 240
acagagagtg taagatatgt ctaccagcct atggagaaac tgtatatggt actgatcact 300
accaaaaaca gcaacatttt agaagatttg gagaccctaa ggctcttctc aagagtgatc 360
cctgaatatt gcgagcctta gaagagaatg aaatatctga gcactgnttt gatttgattt 420
ttgcttttga tgaaaatgtc gcactgggat acccgggang aatgttaact tggcacagat 480
canaaccttt cacagaaaa 499

<210> 356
<211> 511
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 356
gggcttctgc tgaggggcca ggcggagctt gaggaaaccg cagataagtt tttttctctt 60
tgaaagatag agattaatac aactacttaa aaaatatagt caataggtta ctaagatatt 120
gcttagcgtt aagtttttaa cgtaatttta atagcttaag attttaagag aaaatatgaa 180
gacttagaag agtagcatga ggaaggaaaa gataaaaggt ttctaaaaca tgacggaggt 240
tgagatgaag cttcttcatg gagtaaaaaa tgtatttaaa agaaaattga gagaaaggac 300
tacagagccc cgaattaata ccaatagaag ggcaatgctt ttagattaaa atgaaggtga 360
cttaaacagc ttaaagttta ntttaaaagt tgtaggtgat taaaataatt tgaaggcgat 420
cttttaaaaa gagattaaac ccgaaggtga ttaaaagacc ttgaaatcca tgacgccagg 480
gagaattgcc gtcatttaaa gcctagttaa c 511

<210> 357
<211> 511
<212> DNA
<213> Homo sapien

<220>

<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 357
gatacttcac atttccctag ggacgggagc ccgaggggtc cgttcggccc tcttcctctc 60
gctgggccga caccccgctg taggaccgta acccttagtc ccaatgcctc cgtaagcgga 120
gttgagtggg tgcctgtggt tggagctgtg gaggtgtccc cggtggcgag cgcggccaga 180
actgcggtca cttaagtttt ccgtgtgcgg gttgcaagga gcgtgcgtgc gtctggtata 240
atttggcttc ctgagattct gcttacaaga aaggagtggg aaataccctt ggaaagaaaa 300
ctaaaacagt aagaaaacca aaacttattt ttacatggnt gtcagcacat ttaccgatat 360
ggacactttt cccaataatt tcctcctggt ggagacagtg gattgacagg ttctcagtcg 420
gaattccaga aaaatgttaa ttgatgaaaa gggtacnatg tgagcatcat aaagntaatt 480
attaanacac tgaaggctga acacacaagg g 511

<210> 358
<211> 401
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 358
acggatgaag atgatgacct tcaagaaaat gaagacaata aacaacataa agaaagcttg 60
aaaagagtga cctttgcttt accagatgat gcggaaactg aagatacagg tgttttaaat 120
gtaaagaaaa attctgatga agttaaatcc tcctttgaaa aaagacagga aaagatgaat 180
gaaaaaattg catctttaga aaaagagttg ttagaaaaaa agcccgtggc agcttcaggg 240
ggaagtgaca gcacagaaga ggccagagaa cacctcctgg aggagaccct acctttgcca 300
tctgccccgat ggccctgtga ttacagagga accccttca ctggagattt ctttaacnga 360
ngatagagat cngnttggga tatgtntcct taagaaaacc t 401

<210> 359
<211> 511
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 359
gcgatgcccg cgcgcccagg acgcctcctc ccgctgctgg cccggccggc ggccctgact 60
gcgctgctgc tgctgctgct gggccatggc ggcggcgggc gctggggcgc ccgggcccag 120
gaggcggcgg cggcggcggc ggacgggccc cccgcggcag acggcgagga cggacaggac 180
ccgcacagca agcacctgta cacggccgac atgttcacgc acgggatcca gagcgcccgc 240
gcacttcgtc atgttcttcg cgccctggtg tggacacttg ccagcggctt gcagccgant 300
ttggaatgac cttggganga acaaatacaa cagcatggaa agaatgccaa aagtctatgt 360
ggnttaaagt ggacttgcac nggccacttc gactngtgct cccccaaggg gngggaagat 420
acccacctta aaacttttca accaagccaa aaactttgaa aaccaggtct cggattcaaa 480
atggaaaact gatgttcaac ctgaacaaga a 511

<210> 360
<211> 511
<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 360
tactgggaga ctttgagatt gagtccaaac agctggaagc agagtcttgg agtcggataa 60
tagacagcaa gtttctaaaa cagcaaaaga aagatgtggt caaacggcaa gaagtaatat 120
atgagttgat gcagacagag tttcatcatg tcccgactct caagatcatg agtggtgtgt 180
cnagccnggg gatgatggcg gatctgnttt ttgagcanca gatggtagaa aaagctggtt 240
ccctgtttgg atgagcttga tcagtatccc atacccattc tttccagagg attcttggag 300
ccggaaagaa nggagtcttc ttggtgggat aaaaagtgaa aaagaacttt ctcttcaana 360
aggatagggg gatgtgcttt gtaaaatcan tttttcaggg ngganaatgc cnnaaccgtt 420
ttaaagaaaa acatnttggg naagtttttg tgggccaaca ttacccggtc ttgtaaacct 480
accttcaaag aaccttttttg cccagggtta a 511

<210> 361
<211> 411
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(411)
<223> n = A,T,C or G

<400> 361
gctcagcggc ccgatcccac ggaagcgcgc tcggaggggt gggacccggc cggaccggag 60
atggcgccgc cagcgggcgg ggcggcggcg gcggcctcgg acttgggctc cgccgcagtg 120
ctcttggctg tgcacgccgc ggtgaggccg ctgggcgccg ggccagacgc cgaagcacaa 180
cttgcggagg ctgcagctta acgcggaccc tgagaagcct ggcgcttncn gctggaactt 240
cttggcgcgg gacctggggc ggtaatttga gtggccctga gtcatttcta caccatccag 300
gcccaccaca cgactaagct cacaagaagg ctgaactnnc tgattctnaa cctagaanta 360
cgtgcatcta tcagtgccng aagaaatgac aacataccac tggcaactct g 411

<210> 362
<211> 511
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 362
cgggggaccg ggctgccttg gcccctcagc gctcgcgtct tttccggcag ttggaacgct 60
tcctgttgtc ctcacccgta accgcctgtt gccccctgtc tcagagtccc tcacgcgtcc 120
cctcccgtct ttggctcgtt ggctgccgcc gccggggctt cgccagcctt caagtcgaga 180
ctactggccg aaggggcgtc tgcggctctc cgccgtcccc agccctgcct ctccctgggc 240
tctgccatgg caatgacagg ctcaacacct tgctcatcca tgagtaacca cacaaaggaa 300
agggtgacaa tgaccaaaag tgacactgga gaatttttat agcaacctta tcgctcacat 360
gaagaacgag aaatgagaca aaagaagtta gaaaaagggg atggaagaag aaggcctaaa 420
aaaatgaagg agaaaaccaa cttccgaaga tcaaccacat tgcttcggaa anggaaacaa 480
aantttcttt cgtttgaaan aaaaacaaan a 511

<210> 363
<211> 401
<212> DNA
<213> Homo sapien

<400> 363
caggatctgg ggagaaagag ccccatccct tctctctctg ccaccatttc ggacaccccg 60
cagggactcg ttttgggatt cgcactgact tcaaggaagg acgcgaaccc ttctctgacc 120
ccagctcggg cggccacctg tctttgccgc ggtgaccctt ctctcatgac cctgcggtgc 180
cttgagccct ccgggaatgg cggggaaggg acgcggagcc agtgggggac cgcggggtcg 240
gcggaggagc catccccgca ggcggcgcgt ctggcgaagg ccctgcggga gctcggtcag 300
acaggatggt actggggaag tatgactgtt aatgaagcca aagagaaatt aaaagaggca 360
ccagaaggaa ctttcttgat tagagatagc tcgcattcag a 401

<210> 364
<211> 401
<212> DNA
<213> Homo sapien

<400> 364
agtcaaaggt ttcttttccc tttttaccat ggtttctaca aaaataacct tcaggaaaaa 60
gaaaatcagg aaaaaaattt tttttcaata atcttattcc ctatattaaa ttagatttga 120
agaggattaa cgttgtttta gtttgggtcc agatcagcct tatacaacat ttctaaactc 180
atttgtactt ttaaaaaatt taaacacaga cttctaaaat tacttgatgt aagtaattta 240
aatcacttat gaccaagtta ttaaccttat gaatcagaag tctgaccctt gtaggaaatt 300
atattcacat ataaagtaca tcagatcttt gccatatatt gatggttatt atgcataaac 360
acattgagtt gtgttggaag cagatttata aacctgcatg t 401

<210> 365
<211> 361
<212> DNA
<213> Homo sapien

<400> 365
atctggagtt gcacaaatag ttctttagaa cataaaacta aatggattta tacataacag 60
ttacattcag catttaagag aggcagtaca aaaatgtgtt ctgcttttat ctgatataaa 120
ttgcatgtaa taccatgatt taaacaatat cagttatatt aactaatgcc atgagatata 180
tcttactcag aacgtctgat gtttcccata atagacagaa aaaatgcagt tgtatgagca 240
actgagtttc ttttcatctt caaattcatt tgtgatggtg ggaagatcta aggacaatcc 300
ttccattgaa gaagtaggaa aaacagttca gcactgttct gaactcatca aaaatgaaat 360
t 361

<210> 366
<211> 401
<212> DNA
<213> Homo sapien

<400> 366
cgggagcagc agaggtctag cagccgggcg ccgcgggccg ggggcctgag gaggccacag 60
gacgggcgtc ttcccggcta gtggagcccg gcgcggggcc cgctgcggcc gcaccgtgag 120
gggaggaggc cgaggaggac gcagcgccgg ctgccggcgg gaggaagcgc tccaccaggg 180
cccccgacgg cactcgttta accacatccg cgcctctgct ggaaacgctt gctggcgcct 240
gtcaccggtt ccctccattt tgaaagggaa aaaggctctc cccacccatt cccctgcccc 300
taggagctgg agccggagga gccgcgctca tggcgttcag cccgtggcag atcctgtccc 360
ccgtgcagtg ggcgaaatgg acgtggtctg cggtacgcgg c 401

<210> 367

<211> 401
<212> DNA
<213> Homo sapien

<400> 367
catggagtcg ggcaagatgg cgcctcccaa gaacgctccg agagatgcct tggtgatggc 60
acagatcctg aaggatatgg gaatcacaga gtatgaacca agggttataa atcaaatgtt 120
ggaatttgct ttccgttatg tgactacaat tctggatgat gcaaaaattt attcgagcca 180
tgctaagaaa cctaatgttg atgcagatga tgtgagactg gcaatccagt gtcgtgctga 240
ccaatctttt acctctcctc ccccaagaga ttttttactg gatatcgcaa ggcagaaaaa 300
tcaaacccct ttgccactga ttaagccata tgcaggacct agactgccac ctgatagata 360
ctgcttaaca gctccaaact ataggctgaa gtccttaatt a 401

<210> 368
<211> 401
<212> DNA
<213> Homo sapien

<400> 368
cggagcggta ggagcagcaa tttatccgtg tgcagcccca aactggaaag aagatgctaa 60
ttaaagtgaa gacgctgacc ggaaaggaga ttgagattga cattgaacct acagacaagg 120
tggagcgaat caaggagcgt gtggaggaga aagagggaat ccccccacaa cagcagaggc 180
tcatctacag tggcaagcag atgaatgatg agaagacagc agctgattac aagattttag 240
gtggttcagt ccttcacctg gtgttggctc tgagaggagg aggtggtctt aggcagtgat 300
ggaccctcca ttttacctct ttaccctgtc gctcataatg aggcatcata tatcctctca 360
ctctctggga caccatagcc ctgccccctc ccctggatgc c 401

<210> 369
<211> 174
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(174)
<223> n = A,T,C or G

<400> 369
gcgagnnggg cgccaagcgc ggggccggag cggccttccc ggagtccttt gcgcggcacc 60
tggcgacaaa atggctgccc gagggagacg ggcggagcct cagggccggg aggctccggg 120
ccccgcgggc ggtggcggtg gcgggagccg ttgggctgag tcgggatcgg ggac 174

<210> 370
<211> 375
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(375)
<223> n = A,T,C or G

<400> 370
tgcttttcca actttattta gaaaaacaaa tccaggtccc agtgccccct gtaccctccc 60
cgaccccagc cataatttaa ataacttana gacagagttg gagggagggg acagganagg 120
ttggggtcac ggtggaagga ggaaganagc ccactacagc cgccgcagcg cccgcttctt 180
gtccgtcttt ttcttggccg ccagcttctt atcgcgctcg ccagcatgct tnttggccat 240
gggaccctca gcccctcccg ggccccctgg ggccccaggg tcggtggagg aagcttcagt 300

gccactggcc agggcccgac cggcttcggc cctgccgctg ggcccgccgg cgcccccgtg 360
gatctctgtg agcag 375

<210> 371
<211> 375
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(375)
<223> n = A,T,C or G

<400> 371
taaattctaa aaaatatttt aatacttgaa aacttctaaa acaaaaggta aggtaacatg 60
ttctttcaaa agtgaatttc acatgcaaac cattaattat atttatttta ctgngagata 120
aaagcaaaac ataacattcg gagaaagaga ccagtaactg acctatttat tttatattat 180
attaatgnga atcctcatta gaaatgtgat aacgttattg cacaaacaaa accgtgggca 240
gaaacatccc agcaatgcag gggcgcccat accgggttac aagggatgtc cagcatgtgt 300
ttccctggaa cactcanagt ctgcactttt cctgcaaatg ggaccatgtc tgattattta 360
ttatgaaaga acact 375

<210> 372
<211> 164
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(164)
<223> n = A,T,C or G

<400> 372
cgctctgtnt cctcaacctc tacctggcgg aggttatatg taaagtcaga tgtgccactg 60
aacttgacag acacaaaatt ctactgcatt tgggctttat aatggcaagc ctgctctttt 120
tagtggtgaa cttgacttgc gcaatgctag ttcatggaga tgtc 164

<210> 373
<211> 401
<212> DNA
<213> Homo sapien

<400> 373
gcgctgttcg cctttgccta cctgcagctg tggcggctgc tcctgtaccg cgagcggcgg 60
ctgagttacc agagcctctg cctcttcctc tgtctcctgt gggcagcgct caggaccacc 120
ctcttctccg ccgccttctc gctcagcggc tccctgccct tgctccggcc gcccgctcac 180
ctgcacttct tccccactg gctgctctac tgcttcccct cctgtctcca gttctccacg 240
ctctgtctcc tcaacctcta cctggcggag gttatatgta aagtcagatg tgccactgaa 300
cttgacagac acaaaattct actgcatttg ggctttataa tggcaagcct gctcttttta 360
gtggtgaact tgacttgcgc aatgctagtt catggagatg t 401

<210> 374
<211> 401
<212> DNA
<213> Homo sapien

<400> 374
ggaatgatac cattcagatt gatttggaga ctggcaagat tactgatttc atcaagttcg 60

acactggtaa cctgtgtatg gtgactggag gtgctaacct aggaagaatt ggtgtgatca 120
ccaacagaga gaggcaccct ggatcttttg acgtggttca cgtgaaagat gccaatggca 180
acagctttgc cactcgactt tccaacattt ttgttattgg caagggcaac aaaccatgga 240
tttctcttcc ccgaggaaag ggtatccgcc tcaccattgc tgaagagaga gacaaaagac 300
tggcggccaa acagagcagt gggtgaaatg ggtccctggg tgacatgtca gatctttgta 360
cgtaattaaa aatattgtgg caggattaat agcaaaaaaa a 401

<210> 375
<211> 401
<212> DNA
<213> Homo sapien

<400> 375
gagcggagtc cgctggctga cccgagcgct ggtctccgcc gggaaccctg gggcatggag 60
aggtctgagt acctcggccg cggcgcacgc tgcatcgcgg agccaggccg aggacgtgag 120
ggtggagggc tcctttcccg tgaccatgct tccgggagac ggtgtggggc ctgagctgat 180
gcacgccgtc aaggaggtgt tcaaggctgc cgctgtccca gtggagttcc aggagcacca 240
cctgagtgag gtgcagaata tggcatctga ggagaagctg gagcaggtgc tgagttccat 300
gaaggagaac aaagtggcca tcattggaaa gattcatacc ccgatggagt ataaggggga 360
gctagcctcc tatgatatgc ggctgaggcg taagttggac t 401

<210> 376
<211> 284
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(284)
<223> n = A,T,C or G

<400> 376
ggaacaaggt cgtgaaaaaa aaggtcttgg tgaggtgccg ccatttcatc tgtcctcatt 60
ctctgcgcct ttcgcagagc ttccancagc tggtatgttg ggccagagca tccggaggtt 120
cacaacctct gtggtccgta ggagccacta tgaggagggc cctgggaaga atttgccatt 180
ttcagtggaa aacaagtggt cgttactagc taagatgtgt ttgtactttg gatctgcatt 240
tgctacaccc ttccttgtan taagacacca actgcttaaa acat 284

<210> 377
<211> 401
<212> DNA
<213> Homo sapien

<400> 377
atttatgtta ttgcactctc ggtgtgattt atcgtatgta tctgataggt tttatgaatt 60
gttttgagtt gtaaactcct ataccctta ttaaaatgga cctaattaag tgatttatgc 120
tttgtgcaat ttcttaaatc agatctctct aggattgaag ggatccatag gtatctttca 180
cttagtgtga agcctagtag tatactttta tattcctgaa gagagaccag cattaacata 240
aagagagaag tcttaggaaa aaatatacct aagaattatt tttaaaattc atactgtgaa 300
ggagaatctg cctgcctatt tcctctccaa atttcagaaa ataacacaga gtgctatttg 360
cctgaacttt aatgagcttg actttgttat gattcaggga g 401

<210> 378
<211> 401
<212> DNA
<213> Homo sapien

<400> 378

ccagaacaca ggtgtcgtga aaactacccc taaaagccaa aatgggaaag gaaaagactc 60
atatcaacat tgtcgtcatt ggacacgtag attcgggcaa gtccaccact actggccatc 120
tgatctataa atgcggtggc atcgacaaaa gaaccattga aaaatttgag aaggaggctg 180
ctgagatggg aaagggctcc ttcaagtatg cctgggtctt ggataaactg aaagctgagc 240
gtgaacgtgg tatcaccatt gatatctcct tgtggaaatt tgagaccagc aagtactatg 300
tgactatcat tgatgcccca ggacacagag actttatcaa aaacatgatt acagggacat 360
ctcaggctga ctgtgctgtc ctgattgttg ctgctggtgt t 401

<210> 379
<211> 401
<212> DNA
<213> Homo sapien

<400> 379
tcagatatca ggtggcttct tcaaatgatt tttaagtatc tcgatgatga tgaagaacaa 60
agacatcaat caggattcag gaagacagct tttgcggaaa atgcttaaag ggaagcatca 120
aggattggtg ttgatatttg aaagtttaag agtggtatac ttttattcag tcaacacatg 180
acaaatgtaa aaggcactca tttgttgttc ctggaagaag cctggcagca ttccattcag 240
acatctgccc tttcatcgtc ccacttttta cttattgcag tcctttcagt ctgaatattt 300
cctcctgacg catcttctgc cgtccgaaat gactccctgc tcccagatcc tgtagccctt 360
attattgaca cctttcattt agaaatttag cacatgtcac a 401

<210> 380
<211> 401
<212> DNA
<213> Homo sapien

<400> 380
cctgactctc tgaggctcat tttgcagttg ttgaaattgt ccccgcagtt ttcaatcatg 60
tctgaaccaa tcagagtcct tgtgactgga gcagctggtc aaattgcata ttcactgctg 120
tacagtattg gaaatggatc tgtctttggt aaagatcagc ctataattct tgtgctgttg 180
gatatcaccc ccatgatggg tgtcctggac ggtgtcctaa tggaactgca agactgtgcc 240
cttcccctcc tgaaagatgt catcgcaaca gataaagaag acgttgcctt caaagacctg 300
gatgtggcca ttcttgtggg ctccatgcca agaagggaag gcatggagag aaaagattta 360
ctgaaagcaa atgtgaaaat cttcaaatcc cagggtgcag c 401

<210> 381
<211> 401
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 381
ggggcttcgc tggcagtctg aacggcaagc ttgagcaacg cggtaaaaat attgcttcgg 60
tgggtgacgc ggtacagctg tccaagggcn ttngtaacgg gaatgccgaa gcgtgggaaa 120
aagggagcgg tggcggaaga cggggatgag ctcaggacag agccagaggc caagaagagt 180
aagacggccg caaagaaaaa tgacaaagag gcagcaggag agggcccagc cctgtatgag 240
gaccccccag atcagaaaac ctcacccagt ggcaaacctg ccacactcaa gatctgctct 300
tggaatgtgg atgggcttcg agcctggatt aagaagaaag gattagattg ggtaaaggaa 360
gaagccccag atatactgtg ccttcaagag accaaatgtt c 401

<210> 382
<211> 491
<212> DNA

<213> Homo sapien

<400> 382
gagcagcccc cggcggctga aagccggggc agaagtgctg gtctcggtcg ggattccggg 60
cttggtccca ccgaggcggc gactgcggta ggagggaaga ggttttggac gcgctggcct 120
cccgccgctg tgcattgcag cattatttca gttcaaaatg aactatatgc ctggcaccgc 180
cagcctcatc gaggacattg acaaaaagca cttggttctg cttcgagatg gaaggacact 240
tataggcttt ttaagaagca ttgatcaatt tgcaaactta gtgctacatc agactgtgga 300
gcgtattcat gtgggcaaaa aatacggtga tattcctcga gggatttttg tggtcagagg 360
agaaaatgtg gtcctactag gagaaataga cttggaaaag gagagtgaca cacccctcca 420
gcaagtatcc attgaagaaa ttctagaaga acaaagggtg gaacagcaga ccaagctgga 480
agcagagaag t 491

<210> 383
<211> 491
<212> DNA
<213> Homo sapien

<400> 383
gagtccatct cagcgcctgg aaaatgcagt gaaaaaacct gaagataaaa aggaagtttt 60
cagacccctc aagcctgctg gcgaagtgga tctgaccgca ctggccaaag agcttcgagc 120
agtggaagat gtacggccac ctcacaaagt aacggactac tcctcatcca gtgaggagtc 180
ggggacgacg gatgaggagg acgacgatgt ggagcaggaa ggggctgacg agtccacctc 240
aggaccagag gacaccagag cagcgtcatc tctgaatttg agcaatggtg aaacggaatc 300
tgtgaaaacc atgattgtcc atgatgatgt agaaagtgag ccggccatga ccccatccaa 360
ggagggcact ctaatcgtcc gccagagtac agttgaccaa aagcgtgcca gccatcatga 420
gagcaatggc tttgccggtc gcattcacct cttgccagat ctcttacagc aaagccattc 480
ctcctccact t 491

<210> 384
<211> 491
<212> DNA
<213> Homo sapien

<400> 384
gagcctaatc tcaggtggtc cacccgagac cccttgagca ccaaccctag tccccccgcgc 60
ggccccttat tcgctccgac aaggtacaaa aaggctctgg acggcggcgt ggtaggagga 120
cgggagcggg ggcgggaagt tccctgaagg agcgagacag ggagggacag ggcagaggag 180
gagaggaagg cgatgcgacg gacaggcgca cccgctcagg ctgactctcg gggggcgaggt 240
cgagccaggg gcggctgccc tgggggcgag gcgacgctgt ctcaacctcc acctcgcggc 300
ggaacccgag gacaggagcc tcagatgaaa gaaacaatca tgaaccagga aaaactcgcc 360
aaactgcagg cacaagtgcg cattggtggg aaaggaactg ctcgcagaaa gaagaaggtg 420
gttcatagaa cagccacagc agatgacaaa aaacttcagt tctccttaaa gaagttaggg 480
gtaaacaata t 491

<210> 385
<211> 483
<212> DNA
<213> Homo sapien

<400> 385
agccgctgcg aagggagccg ccgccatgtc tgcgcatctg caatggatgg tcgtgcggaa 60
ctgctccagt ttcctgatca agaggaataa gcagacctac agcactgagc ccaataactt 120
gaaggcccgc aattccttcc gctacaacgg actgattcac cgcaagactg tgggcgtgga 180
gccggcagcc gacggcaaag gtgtcgtggt ggtcattaag cggagatccg gccagcggaa 240
gcctgccacc tcctatgtgc ggaccaccat caacaagaat gctcgcgcca cgctcagcag 300
catcagacac atgatccgca agaacaagta ccgccccgac ctgcgcatgg cagccatccg 360
cagggccagc gccatcctgc gcagccagaa gcctgtgatg gtgaagagga agcggacccg 420

ccccaccaag agctcctgag ccccctgccc ccagagcaat aaagtcagct ggctttctca 480
cct 483

<210> 386
<211> 491
<212> DNA
<213> Homo sapien

<400> 386
aggtggaagg aaaaaacata aatgaagtta atgcacttct tttcctagcc caaaagtcac 60
tgtgattata ttttttaat gaagtttaga aaaaaagctg ttgtcttctc aattgtaaaa 120
ttagtttcaa aatgctgctt ctcttatcat tagtctagta attgttgaac ttttctgcaa 180
actgcatttt acaaaattga aacttggaag ctgtattaac ttttatagtt aaacattgta 240
ttaaataaac tatactataa taaacagttt ggttttgtat tttttaaatt gtattatcca 300
gccttttaaa aattaaaagc taaataatga aaataaacca attaaaacat acttttactc 360
tcagatatac aggtatttac attatgaaaa aactgaacaa agttttaaca atactgagct 420
ttaagaattt agccagcagg gaaaatttcc aggtttgaga atgttctaat gtaaatattt 480
aatcataata c 491

<210> 387
<211> 491
<212> DNA
<213> Homo sapien

<400> 387
ccacaccacc gtgtcccaag tccagccccc tccctccaag gcatcagcac ctgaaccccc 60
tgcagaagaa gaagtggcaa ctggtacaac ctcagcctct gatgacctgg aagccctggg 120
tacactgagc ctggggacca cagaggagaa ggcagcagct gaggcggctg tgcccaggac 180
cattggggcc gagctgatgg agctggtgcg gagaaacact ggcctgagcc acgaattatg 240
ccgggtggcc atcggcatca tagtgggtca catccaggcc tcggtgccgg ccagctcacc 300
agtcatggag caggtcctcc tctcactcgt agagggcaag gacctcagca tggccctgcc 360
ctcagggcag gtctgccacg accagcagag gctggaggtg atctttgcag acctggctcg 420
ccggaaggac gacgcccagc agcgcagttg ggcactatat gaggatgagg gtgtcatccg 480
ctgctaccta g 491

<210> 388
<211> 491
<212> DNA
<213> Homo sapien

<400> 388
gagactatca aactcctgag ccaacaactt aatatgacta gcttacacaa tagcttttat 60
agtaaagata cctctttacg gactccactt atgactccct aaagcccatg tcgaagcccc 120
catcgctggg tcaatagtac ttgccgcagt actcttgaaa ctaggcggct atggtataat 180
acgcctcaca ctcattctca accccctgac aaaacacata gcctacccct tccttgtact 240
atccctatga ggcataatta taacaagctc catctgccta cgacaaacag acctaaaatc 300
gctcattgca tactcttcaa tcagccacat agccctcgta gtaacagcca ttctcatcca 360
aaccccctga agcttcaccg gcgcagtcat tctcataatc gcccacggac ttacatcctc 420
attactattc tgcctagcaa actcaaacta cgaacgcact cacagtcgca tcataatcct 480
ctctcaagga c 491

<210> 389
<211> 511
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature

<222> (1)...(511)
<223> n = A,T,C or G

<400> 389
tactgatatc tctttaatac tttcatcatt caagtttgtt canaacatta caagaggcat 60
gaaagaaaaa ataattccat ttttaaaact ctgtctgtcc aaagtataac atatgaaacc 120
atgccattat ctnttaggaa acaaaagcat tcaaaattaa tttggtatta aagttcaaga 180
ttcanactaa cctcaaagta cggcatgtgc agtgtttaag tgcaanaagt attttcattc 240
caattatttt acananatgc tggagtgacg tgtgcaattt gaaatattca aatcctttaa 300
ggnttctgaa ctaagtgttt aaatgaaaac tgaaatgctg catagtttca gtggctttca 360
atttcctgtt tgatctcaga aatatatgga tgatctttgc cgtgagctac ttccatgatt 420
gcaatggcct tcttcagggc tttctcccct gcggctttgt gttccaggcc catgtagagt 480
ctccctagct tcaaccacat ggaggccacg t 511

<210> 390
<211> 1984
<212> DNA
<213> Homo sapien

<400> 390
cctggggtta gaggctgggg tgggtggggg gtaaggggc agtccttctc cccttcgacg 60
gcggctccga gtccagcccc ttccttcccg cgctcgctcg cccggccccc agccccctca 120
tgagggtgtc cgtgccgggt ccggcggccg ctgccgcccc cgcagccggc cgcgagccct 180
ccacgcccgg cgggggcagc ggaggcggag gcgccgtcgc tgcagcctca ggcgccgcgg 240
tgccgggctc cgtgcagttg gcgctgagcg tcctgcacgc cctgctctac gccgcgctgt 300
tcgcctttgc ctacctgcag ctgtggcggc tgctcctgta ccgcgagcgg cggctgagtt 360
accagagcct ctgcctcttc ctctgtctcc tgtgggcagc gctcaggacc accctcttct 420
ccgccgcctt ctcgctcagc ggctccctgc ccttgctccg gccgcccgct cacctgcact 480
tcttccccca ctggctgctc tactgcttcc cctcctgtct ccagttctcc acgctctgtc 540
tcctcaacct ctacctggcg gaggttatat gtaaagtcag atgtgccact gaacttgaca 600
gacacaaaat tctactgcat ttgggcttta taatggcaag cctgctcttt ttagtggtga 660
acttgacttg cgcaatgcta gttcatggag atgtcccaga aaatcagttg aagtggactg 720
tgtttgttcg agcattaatt aatgatagcc tgtttattct ttgtgccatc tctttagtgt 780
gttacatatg caaaattaca aaaatgtcat cagctaatgt ctacctcgaa tcaaagggta 840
tgtctctgtg ccagactgtc atcgtgggct ctgtagtcat tcttctgtac tcttccagag 900
cttgttataa tttggtggtg gtcaccatat ctcaggatac attagaaagt ccatttaatt 960
atggctggga taatctttca gataaggctc atgtagaaga cataagtgga gaagagtata 1020
tagtatttgg aatggtcctc tttctgtggg aacatgtgcc agcatggtcg gtggtactgt 1080
ttttccgggc acagagatta aaccagaatt tggcacctgc tggcatgata aatagtcaca 1140
gttatagttc cagagcttac tttttcgaca atccaagacg atatgatagt gatgatgacc 1200
tgccaagact gggaagttca agagaaggaa gtttaccaaa ttcgcaaagt ttgggctggt 1260
atggcaccat gactgggtgt ggcagcagca gttacacagt cactccccac ctgaatggac 1320
ctatgacaga tactgctcct ttgctcttta cttgtagtaa tttagatttg aacaatcatc 1380
atagcttata tgtgacacca caaaactgac agcatcacca agtcatgatt cttgagttgt 1440
ttttcataaa tgtgtatatt caatgtgttt aaattccatc tacataaaca ttccattatc 1500
tgttgcaact gaaaacaaaa tctggaagtg tggctgtgtt tggtaaataa cacagctatt 1560
atttttgacc tcttcatagt aaaatgaagt aaaatggaaa gtttggagta ggagaaaaga 1620
gagattagat cttaaggcac ttgatggcct ccaaaaatcc tgactttgga acatcaaatg 1680
catatgtgca cttttatctt tgttctgagt cactgcagtc cccaaagtca tatgccaatg 1740
ttcacactga aatactgtat tgtacaccaa actggaaggc aattttccta tgaaaatcaa 1800
agccggtata ttcattggta tgctctatac agatatctta ataaaaattt tatagtgtga 1860
acagtgcaca gagttaaggc ataaaaatgt atcattcttt ataaaaatct actgaaaatg 1920
tgtaatcatt gaagacagtt cttttaagca tgattttaaa atagcaactg aaattcaatc 1980
attt 1984

<210> 391
<211> 429
<212> PRT

<213> Homo sapien

<400> 391
```
Met Arg Val Ser Val Pro Gly Pro Ala Ala Ala Ala Ala Pro Ala Ala
                5                   10                  15
Gly Arg Glu Pro Ser Thr Pro Gly Gly Gly Ser Gly Gly Gly Gly Ala
            20                  25                  30
Val Ala Ala Ala Ser Gly Ala Ala Val Pro Gly Ser Val Gln Leu Ala
        35                  40                  45
Leu Ser Val Leu His Ala Leu Leu Tyr Ala Ala Leu Phe Ala Phe Ala
    50                  55                  60
Tyr Leu Gln Leu Trp Arg Leu Leu Leu Tyr Arg Glu Arg Arg Leu Ser
65                  70                  75                  80
Tyr Gln Ser Leu Cys Leu Phe Leu Cys Leu Leu Trp Ala Ala Leu Arg
                85                  90                  95
Thr Thr Leu Phe Ser Ala Ala Phe Ser Leu Ser Gly Ser Leu Pro Leu
            100                 105                 110
Leu Arg Pro Pro Ala His Leu His Phe Phe Pro His Trp Leu Leu Tyr
        115                 120                 125
Cys Phe Pro Ser Cys Leu Gln Phe Ser Thr Leu Cys Leu Leu Asn Leu
    130                 135                 140
Tyr Leu Ala Glu Val Ile Cys Lys Val Arg Cys Ala Thr Glu Leu Asp
145                 150                 155                 160
Arg His Lys Ile Leu Leu His Leu Gly Phe Ile Met Ala Ser Leu Leu
                165                 170                 175
Phe Leu Val Val Asn Leu Thr Cys Ala Met Leu Val His Gly Asp Val
            180                 185                 190
Pro Glu Asn Gln Leu Lys Trp Thr Val Phe Val Arg Ala Leu Ile Asn
        195                 200                 205
Asp Ser Leu Phe Ile Leu Cys Ala Ile Ser Leu Val Cys Tyr Ile Cys
    210                 215                 220
Lys Ile Thr Lys Met Ser Ser Ala Asn Val Tyr Leu Glu Ser Lys Gly
225                 230                 235                 240
Met Ser Leu Cys Gln Thr Val Ile Val Gly Ser Val Val Ile Leu Leu
                245                 250                 255
Tyr Ser Ser Arg Ala Cys Tyr Asn Leu Val Val Val Thr Ile Ser Gln
            260                 265                 270
Asp Thr Leu Glu Ser Pro Phe Asn Tyr Gly Trp Asp Asn Leu Ser Asp
        275                 280                 285
Lys Ala His Val Glu Asp Ile Ser Gly Glu Glu Tyr Ile Val Phe Gly
    290                 295                 300
Met Val Leu Phe Leu Trp Glu His Val Pro Ala Trp Ser Val Val Leu
305                 310                 315                 320
Phe Phe Arg Ala Gln Arg Leu Asn Gln Asn Leu Ala Pro Ala Gly Met
                325                 330                 335
Ile Asn Ser His Ser Tyr Ser Ser Arg Ala Tyr Phe Phe Asp Asn Pro
            340                 345                 350
Arg Arg Tyr Asp Ser Asp Asp Asp Leu Pro Arg Leu Gly Ser Ser Arg
        355                 360                 365
Glu Gly Ser Leu Pro Asn Ser Gln Ser Leu Gly Trp Tyr Gly Thr Met
    370                 375                 380
Thr Gly Cys Gly Ser Ser Ser Tyr Thr Val Thr Pro His Leu Asn Gly
385                 390                 395                 400
Pro Met Thr Asp Thr Ala Pro Leu Leu Phe Thr Cys Ser Asn Leu Asp
                405                 410                 415
Leu Asn Asn His His Ser Leu Tyr Val Thr Pro Gln Asn
            420                 425
```

<210> 392
<211> 1584
<212> DNA
<213> Homo sapiens

<400> 392
ggaagactgg agcctttgcg gcggcgctgc ccctcccctg gtccccgcga gctcggaggg 60
cccggctggt gctgcggggg ccccgggagg ttgaaaacta agcatgggga agagctgcaa 120
ggtggtcgtg tgtggccagg cgtctgtggg caaaacttca atcctggagc agcttctgta 180
tgggaaccat gtagtgggtt cggagatgat cgagacgcag gaggacatct acgtgggctc 240
cattgagaca gaccgggggg tgcgagagca ggtgcgtttc tatgacaccc gggggctccg 300
agatggggcc gaactgcccc gacactgctt ctcttgcact gatggctacg tcctggtcta 360
tagcacagat agcagagagt cttttcagcg tgtggagctg ctcaagaagg agattgacaa 420
atccaaggac aagaaggagg tcaccatcgt ggtccttggc aacaagtgtg acttacagga 480
gcagcggcgt gtagacccag atgtggctca gcactgggcc aagtcagaga aggtgaagct 540
gtgggaggtg tcagtggcgg accggcgctc cctcctggag ccctttgtct acttggccag 600
caagatgacg caaccccaga gcaagtctgc cttccccctc agccggaaga acaagggcag 660
cggctccttg gatggctgaa gagctgccgt tcctctttca cgatcccagc cccatttcag 720
tgtctggggc tctggtagat gtgttgaggg caaagtagag gacaagctgt ctttcccagt 780
cagccaggga gctccccgcc aggccacgcc ccagccactt tgctccctct cacctctggg 840
aagtgcaaat actcttggtt gacatcccct tcctcagccc tcccagccta ctccccatcc 900
cagcttttag aggatctgct ccactgtctc ctggggcagt tgtgggtcac tgtcccttcc 960
agctgcccca gacaggaagc agagtcacca cgcagcagtg tcccttcttg ggtctgagtt 1020
cctattatag gtagggggccc caccctctgg gcttcccatc agcgacacac acacacttat 1080
ggcaccagcc tggactccag aaaaagggtg tccaggtatt gtgtgtatgc atttagttgt 1140
gcacacacaa atatgctcct atactggcat taggcgtctc ctcatccctc accctgacct 1200
ttctcctgtc cttttcttgg ctggaagaag ttggcctcct gggagtgtag ttttctgttt 1260
taaatccccc accccctggct gggctcagtg gctcacccct gtaatcccag cactttggga 1320
ggccaaggcg ggtcgattac ttgaggtcag gagttcacga ccagcctggc caacattgtg 1380
aaaccccatc tctgccaaaa atacaaaagt tagccgggcg tagtggcaca tgcctgtaat 1440
cccagctacc cggggaggct gaggcaggag aattgcttga actcagaagg cggaggctgc 1500
agtgagccga gatcgtgcca ctgcactcca gcctggtcaa cagagcaaga ctccatctcg 1560
aaaaaaaaaa aaaaaaaact cgag 1584

<210> 393
<211> 191
<212> PRT
<213> Homo sapiens

<400> 393
Met Gly Lys Ser Cys Lys Val Val Val Cys Gly Gln Ala Ser Val Gly
5 10 15
Lys Thr Ser Ile Leu Glu Gln Leu Leu Tyr Gly Asn His Val Val Gly
20 25 30
Ser Glu Met Ile Glu Thr Gln Glu Asp Ile Tyr Val Gly Ser Ile Glu
35 40 45
Thr Asp Arg Gly Val Arg Glu Gln Val Arg Phe Tyr Asp Thr Arg Gly
50 55 60
Leu Arg Asp Gly Ala Glu Leu Pro Arg His Cys Phe Ser Cys Thr Asp
65 70 75 80
Gly Tyr Val Leu Val Tyr Ser Thr Asp Ser Arg Glu Ser Phe Gln Arg
85 90 95
Val Glu Leu Leu Lys Lys Glu Ile Asp Lys Ser Lys Asp Lys Lys Glu
100 105 110
Val Thr Ile Val Val Leu Gly Asn Lys Cys Asp Leu Gln Glu Gln Arg
115 120 125
Arg Val Asp Pro Asp Val Ala Gln His Trp Ala Lys Ser Glu Lys Val
130 135 140

```
Lys Leu Trp Glu Val Ser Val Ala Asp Arg Arg Ser Leu Leu Glu Pro
145                 150                 155                 160
Phe Val Tyr Leu Ala Ser Lys Met Thr Gln Pro Gln Ser Lys Ser Ala
                165                 170                 175
Phe Pro Leu Ser Arg Lys Asn Lys Gly Ser Gly Ser Leu Asp Gly
            180                 185                 190

<210> 394
<211> 1937
<212> DNA
<213> Homo sapiens

<400> 394
ccggttcccc cagctctggg tacccggctc tgcatcgcgt cgccatgatg ggccatcgtc 60
cagtgctcgt gctcagccag aacacaaagc gtgaatccgg aagaaaagtt caatctggaa 120
acatcaatgc tgccaagact attgcagata tcatccgaac atgtttggga cccaagtcca 180
tgatgaagat gcttttggac ccaatgggag gcattgtgat gaccaatgat ggcaatgcca 240
ttcttcgaga gattcaagtc cagcatccag cggccaagtc catgatcgaa attagccgga 300
cccaggatga agaggttgga gatgggacca catcagtaat tattcttgca ggggaaatgc 360
tgtctgtagc tgagcacttc ctggagcagc agatgcaccc aacagtggtg atcagtgctt 420
accgcaaggc attggatgat atgatcagca ccctaaagaa aataagtatc ccagtcgaca 480
tcagtgacag tgatatgatg ctgaacatca tcaacagctc tattactacc aaagccatca 540
gtcggtggtc atctttggct tgcaacattg ccctggatgc tgtcaagatg gtacagtttg 600
aggagaatgg tcggaaagag attgacataa aaaaatatgc aagagtggaa aagatacctg 660
gaggcatcat tgaagactcc tgtgtcttgc gtggagtcat gattaacaag gatgtgaccc 720
atccacgtat gcggcgctat atcaagaacc ctcgcattgt gctgctggat tcttctctgg 780
aatacaagaa aggagaaagc cagactgaca ttgagattac acgagaggag gacttcaccc 840
gaattctcca gatggaggaa gagtacatcc agcagctctg tgaggacatt atccaactga 900
agcccgatgt ggtcatcact gaaaagggca tctcagattt agctcagcac taccttatgc 960
gggccaatat cacagccatc cgcagagtcc ggaagacaga caataatcgc attgctagag 1020
cctgtggggc ccggatagtc agccgaccag aggaactgag agaagatgat gttggaacag 1080
gagcaggcct gttggaaatc aagaaaattg gagatgaata ctttactttc atcactgact 1140
gcaaagaccc caaggcctgc accattctcc tccggggggc tagcaaagag attctctcgg 1200
aagtagaacg caacctccag gatgccatgc aagtgtgtcg caatgttctc ctggaccctc 1260
agctggtgcc aggggggtggg gcctccgaga tggctgtggc ccatgccttg acagaaaaat 1320
ccaaggccat gactggtgtg gaacaatggc catacagggc tgttgcccag gccctagagg 1380
tcattcctcg taccctgatc cagaactgtg gggccagcac catccgtcta cttacctccc 1440
ttcgggccaa gcacacccag gagaactgtg agacctgggg tgtaaatggt gagacgggta 1500
ctttggtgga catgaaggaa ctgggcatat gggagccatt ggctgtgaag ctgcagactt 1560
ataagacagc agtggagacg gcagttctgc tactgcgaat tgatgacatc gtttcaggcc 1620
acaaaaagaa aggcgatgac cagagccggc aaggcggggc tcctgatgct ggccaggagt 1680
gagtgctagg caaggctact tcaatgcaca gaaccagcag agtctcccct tttcctgagc 1740
cagagtgcca ggaacactgt ggacgtcttt gttcagaagg gatcaggttg gggggcagcc 1800
cccagtccct ttctgtccca gctcagtttt ccaaaagaca ctgacatgta attcttctct 1860
attgtaaggt ttccatttag tttgcttccg atgattaaat ctaagtcatt tgaaaaaaaa 1920
aaaaaaaaaa actcgag                                                 1937

<210> 395
<211> 1675
<212> DNA
<213> Homo sapiens

<400> 395
gcgcgaatcg cggtcgcgag ccatggagga ggaggcatcg tccccggggc tgggctgcag 60
caagccgcac ctggagaagc tgaccctggg catcacgcgc atcctagaat cttccccagg 120
tgtgactgag gtgaccatca tagaaaagcc tcctgctgaa cgtcatatga tttcttcctg 180
ggaacaaaag aataactgtg tgatgcctga agatgtgaag aacttttacc tgatgaccaa 240
tggcttccac atgacatgga gtgtgaagct ggatgagcac atcattccac tgggaagcat 300
```

ggcaattaac agcatctcaa aactgactca gctcacccag tcttccatgt attcacttcc 360
taatgcaccc actctggcag acctggagga cgatacacat gaagccagtg atgatcagcc 420
agagaagcct cactttgact ctcgcagtgt gatatttgag ctggattcat gcaatggcag 480
tgggaaagtt tgccttgtct acaaaagtgg gaaaccagca ttagcagaag acactgagat 540
ctggttcctg gacagagcgt tatactggca ttttctcaca gacaccttta ctgcctatta 600
ccgcctgctc atcacccacc tgggcctgcc ccagtggcaa tatgccttca ccagctatgg 660
cattagccca caggccaagc aatggttcag catgtataaa cctatcacct acaacacaaa 720
cctgctcaca gaagagaccg actcctttgt gaataagcta gatcccagca aagtgtttaa 780
gagcaagaac aagatcgtaa tcccaaaaaa gaaagggcct gtgcagcctg caggtggcca 840
gaaagggccc tcaggaccct ccggtccctc cacttcctcc acttctaaat cctcctctgg 900
ctctggaaac ccccacccgga agtgagcacc cctccctcca actccctacc agctccagag 960
tggtggtttc catgcacaga tggccctagg ggtgacctcc agttttgcgt gtggaccgta 1020
ggcctctttc tagttgaatg accaaaattg taaggctttt agtcccaccg acattagcca 1080
ggctcgtagt gaggcctcca gagcaggttg tgctgtcccc tgcctctgga agcaatgggg 1140
aatttggaat cttgtgtaag tgcccaaata agtctgagtg ctttcctctt cttcaacact 1200
caaccctcaa tcccttagca ctgattgatt agagaggtcc cccaaagaaa ccactggttt 1260
tgacccatga agcattagaa ctgcattgtt cattcaggag ccactagtca catatgacta 1320
tttaaattta aagtaaattg tatgaaaaat tcatttcttc aattgcatta gccacatttt 1380
gagtattcat gtggctggta gattctgtat tagcacaaag atatggaaca tttccatcac 1440
cacagaaagt tctgttggac agcactgcat tagaatattt tcatactgct cttcctcaat 1500
taatttttgt tgttaatgtt gatgtcttca ttggatgggt cataatgttc catgaaacct 1560
ctcaagtaca caattgtatg ttctttgtat cccttaccac aaatatctcg ctctgctcat 1620
ttcttttgca gcttcctata aagtttgtct tcctcatcaa aaaaaaaaaa aaaaa 1675

<210> 396
<211> 559
<212> PRT
<213> Homo sapiens

<400> 396
Gly Ser Pro Ser Ser Gly Tyr Pro Ala Leu His Arg Val Ala Met Met
5 10 15
Gly His Arg Pro Val Leu Val Leu Ser Gln Asn Thr Lys Arg Glu Ser
20 25 30
Gly Arg Lys Val Gln Ser Gly Asn Ile Asn Ala Ala Lys Thr Ile Ala
35 40 45
Asp Ile Ile Arg Thr Cys Leu Gly Pro Lys Ser Met Met Lys Met Leu
50 55 60
Leu Asp Pro Met Gly Gly Ile Val Met Thr Asn Asp Gly Asn Ala Ile
65 70 75 80
Leu Arg Glu Ile Gln Val Gln His Pro Ala Ala Lys Ser Met Ile Glu
85 90 95
Ile Ser Arg Thr Gln Asp Glu Glu Val Gly Asp Gly Thr Thr Ser Val
100 105 110
Ile Ile Leu Ala Gly Glu Met Leu Ser Val Ala Glu His Phe Leu Glu
115 120 125
Gln Gln Met His Pro Thr Val Val Ile Ser Ala Tyr Arg Lys Ala Leu
130 135 140
Asp Asp Met Ile Ser Thr Leu Lys Lys Ile Ser Ile Pro Val Asp Ile
145 150 155 160
Ser Asp Ser Asp Met Met Leu Asn Ile Ile Asn Ser Ser Ile Thr Thr
165 170 175
Lys Ala Ile Ser Arg Trp Ser Ser Leu Ala Cys Asn Ile Ala Leu Asp
180 185 190
Ala Val Lys Met Val Gln Phe Glu Glu Asn Gly Arg Lys Glu Ile Asp
195 200 205
Ile Lys Lys Tyr Ala Arg Val Glu Lys Ile Pro Gly Gly Ile Ile Glu
210 215 220

Asp Ser Cys Val Leu Arg Gly Val Met Ile Asn Lys Asp Val Thr His
225 230 235 240
Pro Arg Met Arg Arg Tyr Ile Lys Asn Pro Arg Ile Val Leu Leu Asp
245 250 255
Ser Ser Leu Glu Tyr Lys Lys Gly Glu Ser Gln Thr Asp Ile Glu Ile
260 265 270
Thr Arg Glu Glu Asp Phe Thr Arg Ile Leu Gln Met Glu Glu Glu Tyr
275 280 285
Ile Gln Gln Leu Cys Glu Asp Ile Ile Gln Leu Lys Pro Asp Val Val
290 295 300
Ile Thr Glu Lys Gly Ile Ser Asp Leu Ala Gln His Tyr Leu Met Arg
305 310 315 320
Ala Asn Ile Thr Ala Ile Arg Arg Val Arg Lys Thr Asp Asn Asn Arg
325 330 335
Ile Ala Arg Ala Cys Gly Ala Arg Ile Val Ser Arg Pro Glu Glu Leu
340 345 350
Arg Glu Asp Asp Val Gly Thr Gly Ala Gly Leu Leu Glu Ile Lys Lys
355 360 365
Ile Gly Asp Glu Tyr Phe Thr Phe Ile Thr Asp Cys Lys Asp Pro Lys
370 375 380
Ala Cys Thr Ile Leu Leu Arg Gly Ala Ser Lys Glu Ile Leu Ser Glu
385 390 395 400
Val Glu Arg Asn Leu Gln Asp Ala Met Gln Val Cys Arg Asn Val Leu
405 410 415
Leu Asp Pro Gln Leu Val Pro Gly Gly Gly Ala Ser Glu Met Ala Val
420 425 430
Ala His Ala Leu Thr Glu Lys Ser Lys Ala Met Thr Gly Val Glu Gln
435 440 445
Trp Pro Tyr Arg Ala Val Ala Gln Ala Leu Glu Val Ile Pro Arg Thr
450 455 460
Leu Ile Gln Asn Cys Gly Ala Ser Thr Ile Arg Leu Leu Thr Ser Leu
465 470 475 480
Arg Ala Lys His Thr Gln Glu Asn Cys Glu Thr Trp Gly Val Asn Gly
485 490 495
Glu Thr Gly Thr Leu Val Asp Met Lys Glu Leu Gly Ile Trp Glu Pro
500 505 510
Leu Ala Val Lys Leu Gln Thr Tyr Lys Thr Ala Val Glu Thr Ala Val
515 520 525
Leu Leu Leu Arg Ile Asp Asp Ile Val Ser Gly His Lys Lys Lys Gly
530 535 540
Asp Asp Gln Ser Arg Gln Gly Gly Ala Pro Asp Ala Gly Gln Glu
545 550 555

<210> 397
<211> 307
<212> PRT
<213> Homo sapiens

<400> 397
Arg Glu Ser Arg Ser Arg Ala Met Glu Glu Glu Ala Ser Ser Pro Gly
5 10 15
Leu Gly Cys Ser Lys Pro His Leu Glu Lys Leu Thr Leu Gly Ile Thr
20 25 30
Arg Ile Leu Glu Ser Ser Pro Gly Val Thr Glu Val Thr Ile Ile Glu
35 40 45
Lys Pro Pro Ala Glu Arg His Met Ile Ser Ser Trp Glu Gln Lys Asn
50 55 60

```
Asn Cys Val Met Pro Glu Asp Val Lys Asn Phe Tyr Leu Met Thr Asn
 65                 70                  75                  80
Gly Phe His Met Thr Trp Ser Val Lys Leu Asp Glu His Ile Ile Pro
                85                  90                  95
Leu Gly Ser Met Ala Ile Asn Ser Ile Ser Lys Leu Thr Gln Leu Thr
            100                 105                 110
Gln Ser Ser Met Tyr Ser Leu Pro Asn Ala Pro Thr Leu Ala Asp Leu
        115                 120                 125
Glu Asp Asp Thr His Glu Ala Ser Asp Asp Gln Pro Glu Lys Pro His
    130                 135                 140
Phe Asp Ser Arg Ser Val Ile Phe Glu Leu Asp Ser Cys Asn Gly Ser
145                 150                 155                 160
Gly Lys Val Cys Leu Val Tyr Lys Ser Gly Lys Pro Ala Leu Ala Glu
                165                 170                 175
Asp Thr Glu Ile Trp Phe Leu Asp Arg Ala Leu Tyr Trp His Phe Leu
            180                 185                 190
Thr Asp Thr Phe Thr Ala Tyr Tyr Arg Leu Leu Ile Thr His Leu Gly
        195                 200                 205
Leu Pro Gln Trp Gln Tyr Ala Phe Thr Ser Tyr Gly Ile Ser Pro Gln
    210                 215                 220
Ala Lys Gln Trp Phe Ser Met Tyr Lys Pro Ile Thr Tyr Asn Thr Asn
225                 230                 235                 240
Leu Leu Thr Glu Glu Thr Asp Ser Phe Val Asn Lys Leu Asp Pro Ser
                245                 250                 255
Lys Val Phe Lys Ser Lys Asn Lys Ile Val Ile Pro Lys Lys Lys Gly
            260                 265                 270
Pro Val Gln Pro Ala Gly Gly Gln Lys Gly Pro Ser Gly Pro Ser Gly
        275                 280                 285
Pro Ser Thr Ser Ser Thr Ser Lys Ser Ser Ser Gly Ser Gly Asn Pro
    290                 295                 300
Thr Arg Lys
305


<210> 398
<211> 416
<212> DNA
<213> Homo sapiens

<400> 398
agaattcggc acgaggattg cctatctcca gtgcaacaac catcaagtgt gctgaaagtc 60
ttcagccggt tgctgcagca gtggaagaaa gggctacagg tccagtcttg ataagcaccg 120
ccgactttga ggggcctatg cccagtgcgc ccccagaagc tgaaagtcct cttgcctcaa 180
ccagcaagga ggagaaggat gaatgtgctc tcatttccac tagcatagca gaagaatgtg 240
aggcttctgt ttccggtgta gttgttgaaa gtgaaaatga gcgagctggc acagtcatgg 300
aagaaaaaga cgggagtggc atcatctcta cgagctcggt ggaagactgt gagggcccag 360
tgtccagtgc tgtccctcaa gaggaaggcg acccctcagt cacaccagcg gaagag     416

<210> 399
<211> 259
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(259)
<223> n = A,T,C or G
```

<400> 399
caaagaattc ggcacgaggg ggcgacctgc attcggacgt caccgaggcc atgctgtacg 60
aaaagttcag ccccgcgggg cctgtgctgt ncatccgggt ctgccgngat atgatcaccc 120
gccgctccct gggctatgcc tacgncaact tccancaacc ggccgacgct gatcgggctt 180
tggacaccat gaactttgat gtgattnagg gaaanccaat ccttatcntg tnnnaatcat 240
aggnatcctt ctttgacaa 259

<210> 400
<211> 410
<212> DNA
<213> Homo sapiens

<400> 400
ggcacgaggg gagagcggac cccagagagc cctgagcagc cccaccgccg ccgccggcct 60
agttaccatc acaccccggg aggagccgca gctgccgcag ccggccccag tcaccatcac 120
cgcaaccatg agcagcgagg ccgagaccca gcagccgccc gccgcccccc cccgccgccc 180
ccgccctcag cgccgccgac accaagcccg gcactacggg cagcggcgca gggagcggtg 240
gcccgggcgg cctcacatcg gcggcgcctg ccggcgggga caagaaggtc atcgcaacga 300
aggttttggg aacagtaaaa tggttcaatg taaggaacgg atatggtttc atcaacagga 360
atgacaccaa ggaagatgta tttgtacacc agactgccat aaagaagaat 410

<210> 401
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(433)
<223> n = A,T,C or G

<400> 401
ggnacgagga atcatggcgg ctgcgctgtt cgtgctgctg ggattcgcgc tgctgggcac 60
ccacggagcc tccggggctg ccggcacagt cttcactacc gtagaagacc ttggctccaa 120
gatactcctc acctgctcct tgaatgacag cgccacagag gtcacagggc accgctggct 180
gaaggggggc gtggtgctga aggaggacgc gctgcccggc cagaaaacgg agttcaaggt 240
ggactccgac gaccagtggg gagagtactc ctgcgtcttc ctccccgagc ccatgggcac 300
ggccaacatc cagctccacg ggcctcccag agtgaaggcc gtgaagtcgt cagaacacat 360
caacgagggg gagacggcca tgctggtctg caagtcagag tccgtgccac ctgtcactga 420
ctgggcctgg tac 433

<210> 402
<211> 434
<212> DNA
<213> Homo sapiens

<400> 402
ggcacgaggc tcggactgag caggactttc cttatcccag ttgattgtgc agaatacact 60
gcctgtcgct tgtcttctat tcaccatggc ttcttctgat atccaggtga aagaactgga 120
gaagcgtgcc tcaggccagg cttttgagct gattctcagc cctcggtcaa aaggatctgt 180
tccagaattc cccctttccc ctccaaagaa gaaggatctt tccctggagg aaattcagaa 240
gaaattagaa gctgcagaag aaagacgcaa gtcccatgaa gctgaggtct tgaagcagct 300
ggctgagaaa cgagagcacg agaaagaagt gcttcagaag gcaatagaag agaacaacaa 360
cttcagtaaa atggcagaag agaaactgac ccacaaaatg gaagctaata aagagaaccg 420
agaggcacaa atgg 434

<210> 403
<211> 435

<212> DNA
<213> Homo sapiens

<400> 403
ggcacgagga actgctgttg ccattcaaac cattgaggag catcctgcat cttttgactg 60
gagctctttt aagccaatgg gatttgaagt atcatttctg aagtttcttg aggagtctgc 120
agtgaagcag aagaaaaata ctgacaaaga ccatccgaat actggaaaca aaaaaggatc 180
ccattcaaat tcaagaaaaa atattgataa gactgctgtg actagtggaa atcatgtatg 240
tccttgtaaa gaaagcgaaa cgtttgtaca gtttgccaat ccatcacagc ttcagtgcag 300
tgataatgta aaaattgttt tagacaagaa tcttaaagat tgcactgagc ttgtcttaaa 360
gcaacttcag gaaatgaaac ctaccgtcag tctgaaaaaa cttgaagtac attcaaatga 420
tccagatatg tctgt 435

<210> 404
<211> 416
<212> DNA
<213> Homo sapiens

<400> 404
aaagaattcg gcacgaggcg ccgctccgcc acgaccaccg ccgcctcctg ccctgcagcc 60
accgccaccg cctgtgtcgc cgccgcctcg ggaccggctg tatgattagg ccacaatctt 120
caatgagtaa acatattcct caattctgtg gtgttcttgg tcacacattt atggagtttc 180
tgaagggcag tggagattac tgccaggcac agcacgacct ctatgcagac aagtgaactg 240
tagaaactga ttactgctcc accaagaagc ccccataaga gtggttatcc tggacacaga 300
agtgttgaat tgaaatccac agagcatttt acaagagttc tgacctggat ggggtaaacc 360
tcagtgcact tcttttctgt tggcctcagt attactggat tgaagaattg ctgctt 416

<210> 405
<211> 435
<212> DNA
<213> Homo sapiens

<400> 405
ggcacgaggg ctgccggagg gtcgttttaa agggcccgcg cgttgccgcc ccctcggccc 60
gccatgctgc tatccgtgcc gctgctgctc ggcctcctcg gcctggccgt cgccgagcct 120
gccgtctact tcaaggagca gtttctggac ggagacgggt ggacttcccg ctggatcgaa 180
tccaaacaca agtcagattt tggcaaattc gttctcagtt ccggcaagtt ctacggtgac 240
gaggagaaag ataaaggttt gcagacaagc caggatgcac gcttttatgc tctgtcggcc 300
agtttcgagc ctttcagcaa caaaggccag acgctggtgg tgcagttcac ggtgaaacat 360
gagcagaaca tcgactgtgg gggcggctat gtgaagctgt ttcctaatag tttggaccag 420
acagacatgc acgga 435

<210> 406
<211> 424
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(424)
<223> n = A,T,C or G

<400> 406
gcccaaaccc actccacctt actaccagac aaccttagcc aaaccattta cccaaataaa 60
gtataggcga tagaaattga aacctggcgc aatagatata gtaccgcaag ggaaagatga 120
aaaattataa ccaagcataa tatagcaagg actaacccct ataccttctg cataatgaat 180
taactagaaa taactttgca aggagagcca aagctaagac ccccgaaacc agacgagcta 240
cctaagaaca gctaaaagag cacacccgtc tatgtagcaa aatagtggga agatttatag 300

gtagaggcga caaacctacc gagcctggtg atagctggtt gtccaagata gaatcttagt 360
tcaactttaa atttgcccac agaaccctct aaatcccctt gnaaatttaa ctgntagtcc 420
aaag 424

<210> 407
<211> 423
<212> DNA
<213> Homo sapiens

<400> 407
gctcctaccg gcgcacgtgg tgccgccgct gctgcctccc gctcgccctg aacccagtgc 60
ctgcagccat ggctcccggc cagctcgcct tatttagtgt ctctgacaaa accggccttg 120
tggaatttgc aagaaacctg accgctcttg gtttgaatct ggtcgcttcc ggagggactg 180
caaaagctct cagggatgct ggtctggcag tcagagatgt ctctgagttg acgggatttc 240
ctgaaatgtt gggggacgt gtgaaaactt tgcatcctgc agtccatgct ggaatcctag 300
ctcgtaatat tccagaagat aatgctgaca tggccagact tgatttcaat cttataagag 360
ttgttgcctg caatctctat ccctttgtaa agacagtggc ttctccaggt gtaagtgttg 420
agg 423

<210> 408
<211> 424
<212> DNA
<213> Homo sapiens

<400> 408
gaaaaaaaat agcttactga attctataag atgtgtggga atctcaccta tcaaaaatag 60
gtaaaaagag cctccaaacc tgctttgatt ttattcacct attcttttag gccaggaact 120
aatttacctc tcactatcct gttccctctt gctatcttgt ggagtctcta aagacaaagg 180
tataaagagc ttttggtagg tgaattaata atcaactaga tggcatttcc aaatgggatt 240
gcacatactg tggggcaagt cccaagtgaa cttcaaagtg agacgtttat ttgagtaatc 300
cttccagatt aacaataatc ataatagcag ttaccacttc ctgagtactt tctatatgcc 360
atgtattgag cttgctcact tctttatgtg gattcttatt taatcttaat accaagatga 420
ggtg 424

<210> 409
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(398)
<223> n = A,T,C or G

<400> 409
gctcgactct tagcttgtcg gggacggtaa ccgggacccg gtgtctgctc ctgtcgcctt 60
cgcctcctaa tccctagcca ctatgcgtga gtgcatctcc atccacgttg gccaggctgg 120
tgtccagatt ggcaatgcct gctgggagct ctactgcctg gaacacggca tccagcccga 180
tggccagatg ccaagtgaca agaccattgg gggaggagat gactccttca acaccttctt 240
cagtgagacg ggcgctggca agcacgtgcc ccgggctgng tttgtagact tggaacccac 300
agtnattgat gaagntcgna ctggcaccta cccgcaggtc ttncaccctg ancanntcat 360
nacaggcaag gaagatgctg ncaaataact atgcccga 398

<210> 410
<211> 423
<212> DNA
<213> Homo sapiens

<400> 410
gccccacccc acctgcccgc tgcggctctc cgcgggagat ctcaccgttc tggagacagg 60
gctcgctcgc tctcacgctg cccggccagc ccgcttctct gcccggagcc atgaatctca 120
gtagcgccag tagcacggag gaaaaggcag tgacgaccgt gctctggggc tgcgagctca 180
gtcaggagag gcggacttgg accttcagac cccagctgga ggggaagcag agctgcaggc 240
tgttgcttca tacgatttgc ttgggggaga aagccaaaga ggagatgcat cgcgtggaga 300
tcctgccccc agcaaaccag gaggacaaga agatgcagcc ggtcaccatt gcctcactcc 360
aggcctcagt cctccccatg gtctccatgg taggagtgca gctttctccc ccagttactt 420
tcc 423

<210> 411
<211> 424
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(424)
<223> n = A,T,C or G

<400> 411
gcggaggcga ctagcggcgg cgggagcggc gccgagaggc cgtgcgggac gcgggcgcca 60
ggaccggccg aacgcagagg ttgattcttc accacactga aaccattagg aaaaatcctt 120
gtggttaaca gcagaggctt cagagtgtaa cctgtactcg ggcctagaaa ttatttaaaa 180
tggcgactga tacgtctcaa ggtgaactcg tccatcctaa ggcactccca cttatagtag 240
gagctcagct gatccacgcg gacaagttag gtgagaaggt agaagatagc accatgccga 300
ttcgtcgaac tgtgaattct acccgggaaa ctcctcccaa aagcaagctt gctgaagggg 360
aggaagaaan gccagaacca gacataagtt cagaggaatc tgtctccact gtagaagaac 420
aaga 424

<210> 412
<211> 430
<212> DNA
<213> Homo sapiens

<400> 412
ggcacgaggg gaagccggcg ccagttcgcg gggctccggg ccgccactca gagctatgag 60
ctacggccgc ccccctcccg atgtggaggg tatgacctcc ctcaaggtgg acaacctgac 120
ctaccgcacc tcgcccgaca cgctgaggcg cgtcttcgag aagtacgggc gcgtcggcga 180
cgtgtacatc ccgcgggatc gctacaccaa ggagtcccgc ggcttcgcct tcgttcgctt 240
tcacgacaag cgcgacgctg aggacgctat ggatgccatg gacggggccg tgctggacgg 300
ccgcgagctg cgggtgcaaa tggcgcgcta cggccgcccc ccggactcac accacagccg 360
ccggggaccg ccaccccgca ggtacggggg cggtggctac ggacgccgga gccgcagccc 420
taggcggcgt 430

<210> 413
<211> 429
<212> DNA
<213> Homo sapiens

<400> 413
ggcacgaggt cggcccggcc atcttgtggg aagagctgaa gcaggcgctc ttggctcggc 60
gcggcccgct gcaatccgtg gaggaacgcg ccgccgagcc accatcatgc ctgggcactt 120
acaggaaggc ttcggctgcg tggtcaccaa ccgattcgac cagttatttg acgacgaatc 180
ggaccccttc gaggtgctga aggcagcaga gaacaagaaa aaagaagccg gcgggggcgg 240
cgttgggggc cctgggggcca agagcgcagc tcaggccgcg gcccagacca actccaacgc 300
ggcaggcaaa cagctgcgca aggagtccca gaaagaccgc aagaacccgc tgccccccag 360
cgttggcgtg gttgacaaga aagaggagac gcagccgccc gtggcgctta agaaagaagg 420

aataagacg 429

<210> 414
<211> 429
<212> DNA
<213> Homo sapiens

<400> 414
ggcacgagga cgggcccggc tgccggcccc cgctctgccc tgcataataa aatggctaat 60
caggtgaatg gtaatgcggt acagttaaaa gaagaggaag aaccaatgga tacttccagt 120
gtaactcaca cagaacacta caagacactg atagaggcag gcctcccaca gaaggtggca 180
gaaagacttg atgaaatatt tcagacagga ttggtagctt atgtcgatct tgatgaaaga 240
gcaattgatg ctctcaggga atttaatgaa gaaggagctc tgtctgtact acagcagttc 300
aaggaaagtg acttatcaca tgttcagaac aaaagtgcat ttttatgtgg agttatgaag 360
acctacaggc agagagagaa acaggggagc aaggtgcaag agtccacaaa gggacctgat 420
gaagcgaag 429

<210> 415
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(398)
<223> n = A,T,C or G

<400> 415
gcggtcgtaa gggctgagga tttttggtcc gcacgctcct gctcctgact caccgctgtt 60
cgctctcgcc gaggaacaag tcggtcagga agcccgcgcg caacagccat ggcttttaag 120
gataccggaa aaacacccgt ggagccggag gtggcaattc accgaattcg aatcacccta 180
acaagccgca acgtaaaatc cttggaaaag gtgtgtgctg acttgataag aggcgcaaaa 240
gaaaagaatc tcaaagtact ttgagaatca ctacaagaaa aactccttgt ggtgaaggtt 300
ctaagacgtg ggatcgtttc cagatgagaa ttcacaagcg actcattgac ttgcacagtc 360
cttctgagat tgttaagcan attacttcca tcantatt 398

<210> 416
<211> 269
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(269)
<223> n = A,T,C or G

<400> 416
gccgaggcag gaagctgtga gtgcgcggtt gcggggtcgc attgtggcta cggctttgcg 60
tccccggcgg gcagccccag gctggtcccc gcctccgctc tccccaccgg cggggaaagc 120
agctggtgtg ggaggaaagg ctccatcccc cgccccctct ctcccgctgt tggctggcan 180
gatcttttgg cagtcctgtg gnctcnctcc ccgnccggat cctnctgacc ctganattcn 240
nggtntnacn nnccgtncac gccttgntt 269

<210> 417
<211> 408
<212> DNA
<213> Homo sapiens

<400> 417
ggccgggaga accgttcgcg gaggaaaggc gaactagtgt tgggatggcc accaactggg 60
ggagcctctt gcaggataaa cagcagctag aggagctggc acggcaggcc gtggaccggg 120
ccctggctga gggagtattg ctgaggacct cacaggagcc cacttcctcg gaggtggtga 180
gctatgcccc attcacgctc ttcccctcac tggtccccag tgccctgctg gagcaagcct 240
atgctgtgca gatggacttc aacctgctag tggatgctgt cagccagaac gctgccttcc 300
tggagcaaac tctttccagc accatcaaac aggatgactt taccgctcgt ctctttgaca 360
tccacaagca agtcctaaaa gagggcattg cccagactgt gttcctgg 408

<210> 418
<211> 402
<212> DNA
<213> Homo sapiens

<400> 418
gagccgggca gccgcttccc gcccccgagc aggagccggt gcgagcggag cagagccgag 60
gtcgggccgc gagcggagcc ggctgagcgg gcgccgagct cccgccatgg cccggaacac 120
gctgtcctcg cgcttccgcc gggtggacat cgacgaattt gacgagaaca aatttgtgga 180
cgagcaggag gaggcggcgg cggcggcggc ggagccaggc ccggacccga gcgaggtgga 240
cgggctcctg cggcaagggg acatgcttcg ggcattccat gcagccttgc ggaactctcc 300
cgtcaacacc aagaatcaag ctgtgaagga gcgagcccag ggcgtggtgc tgaaagtgct 360
cacaaacttc aagagcagtg agattgagca ggctgtgcag tc 402

<210> 419
<211> 406
<212> DNA
<213> Homo sapiens

<400> 419
gcccgggcta gcggcctggg ttgggctttg tagctgctcc gcaggcccag cccgggccgc 60
gctcgcagag tcctaggcgg tgcgcggcct cctgcctcct ccctcctcgg cggtcgcggc 120
ccgccggcct ccgcggtgcc tgccttcgct ctcaggttga ggagctcaag cttgggaaaa 180
tggtgtgcat tccttgtatc gtcattccag ttctgctctg gatctacaaa aaattcctgg 240
agccatatat ataccctctg gtttcccccct tcgttaagtc gtatatggcc taaaaaaaga 300
attcaaagaa atccaatgat ccaaacaaaa gggcaaaagt aaaaactttt aaaggggtgc 360
aagaacattg aaatgggaat tacccaacca aaaaagggaa cccaac 406

<210> 420
<211> 371
<212> DNA
<213> Homo sapiens

<400> 420
cagccatcgt ggtgtgttct tgactccgct gctcgccatg tcttctcaca agactttcag 60
gattaagcga ttcctggcca agaaacaaaa gcaaaatcgt cccattcccc agtggattcg 120
gatgaaaact ggaaataaaa tcaggtacaa ctccaaaagg agacattgga gaagaaccaa 180
gctgggtcta taaggaattg cacatgagat ggcacacata tttatgctgt ctgaaggtca 240
cgatcatgtt accatatcaa gctgaaaatg tcaccactat ctggagattt cgacgtgttt 300
tcctctctga atctgttatg aacacgttgg ttggctggat tcagtaataa atatgtaagg 360
cctttctttt t 371

<210> 421
<211> 51
<212> PRT
<213> Homo sapiens

<400> 421

Met Ser Ser His Lys Thr Phe Arg Ile Lys Arg Phe Leu Ala Lys Lys
5 10 15
Gln Lys Gln Asn Arg Pro Ile Pro Gln Trp Ile Arg Met Lys Thr Gly
20 25 30
Asn Lys Ile Arg Tyr Asn Ser Lys Arg Arg His Trp Arg Arg Thr Lys
35 40 45
Leu Gly Leu
50

<210> 422
<211> 12308
<212> DNA
<213> Homo sapiens

<400> 422
ttgttttcta gcagtgacaa gttcactttg aatcaggata tgtgtgtagt ttgtggcagt 60
tttggccaag gagcagaagg aagattactt gcctgttctc agtgtggtca gtgttaccat 120
ccatactgtg tcagtattaa gatcactaaa gtggttctta gcaaaggttg gaggtgtctt 180
gagtgcactg tgtgtgaggc ctgtgggaag gcaactgacc caggaagact cctgctgtgt 240
gatgactgtg acataagtta tcacacctac tgcctagacc ctccattgca gacagttccc 300
aaaggaggct ggaagtgcaa atggtgtgtt tggtgcagac actgtggagc aacatctgca 360
ggtctaagat gtgaatggca gaacaattac acacagtgcg ctccttgtgc aagcttatct 420
tcctgtccag tctgctatcg aaactataga gaagaagatc ttattctgca atgtagacaa 480
tgtgatagat ggatgcatgc agtttgtcag aacttaaata ctgaggaaga agtggaaaat 540
gtagcagaca ttggttttga ttgtagcatg tgcagaccct atatgcctgc gtctaatgtg 600
ccttcctcag actgctgtga atcttcactt gtagcacaaa ttgtcacaaa agtaaaagag 660
ctagacccac ccaagactta tacccaggat ggtgtgtgtt tgactgaatc agggatgact 720
cagttacaga gcctcacagt tacagttcca agaagaaaac ggtcaaaacc aaaattgaaa 780
ttgaagatta taaatcagaa tagcgtggcc gtccttcaga cccctccaga catccaatca 840
gagcattcaa gggatggtga aatggatgat agtcgagaag gagaacttat ggattgtgat 900
ggaaaatcag aatctagtcc tgagcgggaa gctgtggatg atgaaactaa gggagtggaa 960
ggaacagatg gtgtcaaaaa gagaaaaagg aaaccataca gaccaggtat tggtggattt 1020
atggtgcggc aaagaagtcg aactgggcaa gggaaaacca aaagatctgt gatcagaaaa 1080
gattcctcag gctctatttc cgagcagtta ccttgcagag atgatggctg gagtgagcag 1140
ttaccagata ctttagttga tgaatctgtt tctgttactg aaagcactga aaaaataaag 1200
aagagatacc gaaaaaggaa aaataagctt gaagaaactt tccctgccta tttacaagaa 1260
gctttctttg gaaaagatct tctagataca agtagacaaa gcaagataag tttagataat 1320
ctgtcagaag atggagctca gcttttatat aaaacaaaca tgaacacagg tttcttggat 1380
ccttccttag atccactact tagttcatcc tcggctccaa caaaatctgg aactcacggt 1440
cctgctgatg acccattagc tgatatttct gaagttttaa acacagatga tgacattctt 1500
ggaataattt cagatgatct agcaaaatca gttgatcatt cagatattgg tcctgtcact 1560
gatgatcctt cctctttgcc tcagccaaat gtcaatcaga gttcacgacc attaagtgaa 1620
gaacagctag atgggatcct cagtcctgaa ctagacaaaa tggtcacaga tggagcaatt 1680
cttggaaaat tatataaaat tccagagctt ggcggaaaag atgttgaaga cttatttaca 1740
gctgtactta gtcctgcgaa cactcagcca actccattgc cacagcctcc cccaccaaca 1800
cagctgttgc caatacacaa tcaggatgct tttcacgga tgcctctcat gaatggcctt 1860
attggatcca gtcctcatct cccacataat tctttgccac ctggaagcgg actgggaact 1920
ttctctgcaa ttgcacaatc ctcttatcct gatgccaggg ataaaaattc agcctttaat 1980
ccaatggcaa gtgatcctaa caactcttgg acatcatcag ctcccactgt ggaaggagaa 2040
aatgacacaa tgtcgaatgc ccagagaagc acgcttaagt gggagaaaga ggaggctctg 2100
ggtgaaatgg caactgttgc cccagttctc tacaccaata ttaatttccc caacttaaag 2160
gaagaattcc ctgattggac tactagagtg aagcaaattg ccaaattgtg gagaaaagca 2220
agctcacaag aaagagcacc atatgtgcaa aaagccagag ataacagagc tgctttacgc 2280
attaataaag tacagatgtc aaatgattcc atgaaaaggc agcaacagca agatagcatt 2340
gatcccagct ctcgtattga ttcggagctt tttaaagatc ctttaaagca aagagaatca 2400
gaacatgaac aggaatggaa atttagacag caaatgcgtc agaaaagtaa gcagcaagct 2460
aaaattgaag ccacacagaa acttgaacag gtgaaaaatg agcagcagca gcagcaacaa 2520
cagcaatttg gttctcagca tcttctggtg cagtctggtt cagatacacc aagtagtggg 2580

```
atacagagtc ccttgacacc tcagcctggc aatggaaata tgtctcctgc acagtcattc 2640
cataaagaac tgtttacaaa acagccaccc agtaccccta cgtctacatc ttcagatgat 2700
gtgtttgtaa agccacaagc tccacctcct cctccagccc catcccggat tcccatccag 2760
gatagtcttt ctcaggctca gacttctcag ccaccctcac cgcaagtgtt ttcacctggg 2820
tcctctaact cacgaccacc atctccaatg gatccatatg caaaaatggt tggtacccct 2880
cgaccacctc ctgtgggcca tagtttttcc agaagaaatt ctgctgcacc agtggaaaac 2940
tgtacacctt tatcatcggt atctaggccc cttcaaatga atgagacaac agcaaatagg 3000
ccatcccctg tcagagattt atgttcttct tccacgacaa ataatgaccc ctatgcaaaa 3060
cctccagaca cacctaggcc tgtgatgaca gatcaatttc ccaaatcctt gggcctatcc 3120
cggtctcctg tagtttcaga acaaactgca aaaggcccta tagcagctgg aaccagtgat 3180
cactttacta aaccatctcc tagggcagat gtgtttcaaa gacaaaggat acctgactca 3240
tatgcacgac ccttgttgac acctgcacct cttgatagtg gtcctggacc ttttaagact 3300
ccaatgcaac ctcctccatc ctctcaggat ccttatggat cagtgtcaca ggcatcaagg 3360
cgattgtctg ttgaccctta tgaaaggcct gctttgacac caagacctat agataatttt 3420
tctcataatc agtcaaatga tccatatagt cagcctcccc ttaccccaca tccagcagtg 3480
aatgaatctt ttgcccatcc ttcaagggct tttcccagc ctggaaccat atcaaggcca 3540
acatctcagg acccatactc ccaaccccca ggaactccac gacctgttgt agattcttat 3600
tcccaatctt caggaacagc taggtccaat acagaccctt actctcaacc tcctggaact 3660
ccccggccta ctactgttga cccatatagt cagcagcccc aaaccccaag accatctaca 3720
caaactgact tgtttgttac acctgtaaca aatcagaggc attctgatcc atatgctcat 3780
cctcctggaa caccaagacc tggaatttct gtcccttact ctcagccacc agcaacacca 3840
aggccaagga tttcagaggg ttttactagg tcctcaatga caagaccagt cctcatgcca 3900
aatcaggatc ctttcctgca agcagcacaa aaccgaggac cagctttacc tggcccgttg 3960
gtaaggccac ctgatacatg ttcccagaca cctaggcccc ctggacctgg tctttcagac 4020
acatttagcc gtgtttcccc atctgctgcc cgtgatccct atgatcagtc tccaatgact 4080
ccaagatctc agtctgactc ttttggaaca agtcaaactg cccatgatgt tgctgatcag 4140
ccaaggcctg gatcagaggg gagcttctgt gcatcttcaa actctccaat gcactcccaa 4200
ggccagcagt tctctggtgt ctcccaactt cctggacctg tgccaacttc aggagtaact 4260
gatacacaga atactgtaaa tatggcccaa gcagatacag agaaattgag acagcggcag 4320
aagttacgtg aaatcattct ccagcagcaa cagcagaaga agattgcagg tcgacaggag 4380
aaggggtcac aggactcacc cgcagtgcct catccagggc ctcttcaaca ctggcaacca 4440
gagaatgtta accaggcttt caccagaccc ccacctccct atcctgggaa cattaggtct 4500
cctgttgccc ctcctttagg acctagatat gctgttttcc caaaagatca gcgtggaccc 4560
tatcctcctg atgttgctag tatggggatg agacctcatg gatttagatt tggatttcca 4620
ggaggtagtc atggtaccat gccgagtcaa gagcgcttcc ttgtgcctcc tcagcaaata 4680
cagggatctg gagtttctcc acagctaaga agatcagtat ctgtagatat gcctaggcct 4740
ttaaataact cacaaatgaa taatccagtt ggacttcctc agcatttttc accacagagc 4800
ttgccagttc agcagcacaa catactgggc caagcatata ttgaactgag acatagggct 4860
cctgacggaa ggcaacggct gcctttcagt gctccacctg gcagcgttgt agaggcatct 4920
tctaatctga gacatggaaa cttcattccc cggccagact ttccgggccc tagacacaca 4980
gaccccatgc gacgacctcc ccagggtcta cctaatcagc tacctgtgca cccagatttg 5040
gaacaagtgc caccatctca acaagagcaa ggtcattctg tccattcatc ttctatggtc 5100
atgaggactc tgaaccatcc actaggtggt gaattttcag aagctccttt gtcaacatct 5160
gtaccgtctg aaacaacgtc tgataattta cagataacca cccagccttc tgatggtcta 5220
gaggaaaaac ttgattctga tgacccttct gtgaaggaac tggatgttaa agaccttgag 5280
ggggttgaag tcaaagactt agatgatgaa gatcttgaaa acttaaattt agatacagag 5340
gatggcaagg tagttgaatt ggatacttta gataatttgg aaactaatga tcccaacctg 5400
gatgacctct taaggtcagg agagtttgat atcattgcat atacagatcc agaacttgac 5460
atgggagata agaaaagcat gtttaatgag gaactagacc ttccaattga tgataagtta 5520
gataatcagt gtgtatctgt tgaaccaaaa aaaaaggaac aagaaaacaa aactctggtt 5580
ctctctgata aacattcacc acagaaaaaa tccactgtta ccaatgaggt aaaaacggaa 5640
gtactgtctc caaattctaa ggtggaatcc aaatgtgaaa ctgaaaaaaa tgatgagaat 5700
aaagataatg ttgacactcc ttgctcacag gcttctgctc actcagacct aaatgatgga 5760
gaaaagactt ctttgcatcc ttgtgatcca gatctatttg agaaaagaac caatcgagaa 5820
actgctggcc ccagtgcaaa tgtcattcag gcatccactc aactacctgc tcaagatgta 5880
ataaactctt gtggcataac tggatcaact ccagttctct caagtttact tgctaatgag 5940
aaatctgata attcagacat taggccatcg ggtctccac caccaccaac tctgccggcc 6000
tccccatcca atcatgtgtc aagtttgcct cctttcatag caccgcctgg ccgtgttttg 6060
```

gataatgcca tgaattctaa tgtgacagta gtctctaggg taaaccatgt tttttctcag 6120
ggtgtgcagg taaacccagg gctcattcca ggtcaatcaa cagttaacca cagtctgggg 6180
acaggaaaac ctgcaactca aactgggcct caaacaagtc agtctggtac cagtagcatg 6240
tctggacccc aacagctaat gattcctcaa acattagcac agcagaatag agagaggccc 6300
cttcttctag aagaacagcc tctacttcta caggatcttt tggatcaaga aaggcaagaa 6360
cagcagcagc aaagacagat gcaagccatg attcgtcagc gatcagaacc gttcttccct 6420
aatattgatt ttgatgcaat tacagatcct ataatgaaag ccaaaatggt ggcccttaaa 6480
ggtataaata aagtgatggc acaaaacaat ctgggcatgc caccaatggt gatgagcagg 6540
ttccctttta tgggccaggt ggtaactgga acacagaaca gtgaaggaca gaaccttgga 6600
ccacaggcca ttcctcagga tggcagtata acacatcaga tttctaggcc taatcctcca 6660
aattttggtc caggctttgt caatgattca cagcgtaagc agtatgaaga gtggctccag 6720
gagacccaac agctgcttca aatgcagcag aagtatcttg aagaacaaat tggtgctcac 6780
agaaaatcta agaaggccct ttcagctaaa caacgtactg ccaagaaagc tgggcgtgaa 6840
tttccagagg aagatgcaga acaactcaag catgttactg aacagcaaag catggttcag 6900
aaacagctag aacagattcg taaacaacag aaagaacatg ctgaattgat tgaagattat 6960
cggatcaaac agcagcagca atgtgcaatg gccccaccta ccatgatgcc cagtgtccag 7020
ccccagccac ccctaattcc aggtgccact ccacccacca tgagccaacc cacctttccc 7080
atggtgccac agcagcttca gcaccagcag cacacaacag ttatttctgg ccatactagc 7140
cctgttagaa tgcccagttt acctggatgg caacccaaca gtgctcctgc ccacctgccc 7200
ctcaatcctc ctagaattca gccccaattt gcccagttac caataaaaac ttgtacacca 7260
gccccaggga cagtctcaaa tgcaaatcca cagagtggac caccacctcg ggtagaattt 7320
gatgacaaca atccctttag tgaaagtttt caagaacggg aacgtaagga acgtttacga 7380
gaacagcaag agagacaacg gatccaactc atgcaggagg tagatagaca aagagctttg 7440
cagcagagga tggaaatgga gcagcatggt atggtgggct ctgagataag tagtagtagg 7500
acatctgtgt cccagattcc cttctacagt tccgacttac cttgtgattt tatgcaacct 7560
ctaggacccc ttcagcagtc tccacaacac caacagcaaa tggggcaggt tttacagcag 7620
cagaatatac aacaaggatc aattaattca ccctccaccc aaactttcat gcagactaat 7680
gagcgaaggc aggtaggccc tccttcattt gttcctgatt caccatcaat ccctgttgga 7740
agcccaaatt tttcttctgt gaagcaggga catggaaatc tttctgggac cagcttccag 7800
cagtccccag tgaggccttc ttttacacct gctttaccag cagcacctcc agtagctaat 7860
agcagtctcc catgtggcca agattctact ataacccatg gacacagtta tccgggatca 7920
acccaatcgc tcattcagtt gtattctgat ataatcccag aggaaaaagg gaaaaagaaa 7980
agaacaagaa agaagaaaag agatgatgat gcagaatcca ccaaggctcc atcaactccc 8040
cattcagata taactgcccc accgactcca ggcatctcag aaactacctc tactcctgca 8100
gtgagcacac ccagtgagct tcctcaacaa gccgaccaag agtcggtgga accagtcggc 8160
ccatccactc ccaatatggc agcaggccag ctatgtacag aattagagaa caaactgccc 8220
aatagtgatt tctcacaagc aactccaaat caacagacgt atgcaaattc agaagtagac 8280
aagctctcca tggaaacccc tgccaaaaca gaagagataa aactggaaaa ggctgagaca 8340
gagtcctgcc caggccaaga ggagcctaaa ttggaggaac agaatggtag taaggtagaa 8400
ggaaacgctg tagcctgtcc tgtctcctca gcacagagtc ctccccattc tgctggggcc 8460
cctgctgcca aaggagactc agggaatgaa cttctgaaac acttgttgaa aaataaaaag 8520
tcatcttctc ttttgaatca aaaacctgag ggcagtattt gttcagaaga tgactgtaca 8580
aaggataata aactagttga gaagcagaac ccagctgaag gactgcaaac tttgggggct 8640
caaatgcaag gtggttttgg atgtggcaac cagttgccaa aaacagatgg aggaagtgaa 8700
accaagaaac agcgaagcaa acggactcag aggacgggtg agaaagcagc acctcgctca 8760
aagaaaagga aaaaggacga agaggagaaa caagctatgt actctagcac tgacacgttt 8820
acccacttga aacaggtgag gcagctctct ctgctccctc taatggaacc aatcattgga 8880
gtgaactttg cgcactttct tccttatggc agtggccaat ttaatagtgg gaatcgactt 8940
ctaggaactt ttggcagtgc taccctggaa ggggtttcgg actactattc tcagttgatc 9000
tacaagcaga ataatttaag taatcctcca acaccccctg cctctcttcc tcctacacca 9060
cctcctatgg cttgtcagaa gatggccaat ggttttgcaa caactgaaga acttgctgga 9120
aaagccggag tgttagtgag ccatgaagtt accaaaactc taggacctaa accatttcag 9180
ctgcccttca gaccccagga cgacttgttg gcccgagctc ttgctcaggg ccccaagaca 9240
gttgatgtgc cagcctccct cccaacacca cctcataaca atcaggaaga attaaggata 9300
caggatcact gtggtgatcg agatactcct gacagttttg ttccctcatc ctctcctgag 9360
agtgtggttg gggtagaagt gagcaggtat ccagatctgt cattggtcaa ggaggagcct 9420
ccagaaccgg tgccgtcccc catcattcca attcttccta gcactgctgg gaaaagttca 9480
gaatcaagaa ggaatgacat caaaactgag ccaggcactt tatattttgc gtcacctttt 9540

ggtccttccc caaatggtcc cagatcaggt cttatatctg tagcaattac tctgcatcct 9600
acagctgctg agaacattag cagtgttgtg gctgcatttt ccgaccttct tcacgtccga 9660
atccctaaca gctatgaggt tagcagtgct ccagatgtcc catccatggg tttggtcagt 9720
agccacagaa tcaacccggg tttggagtat cgacagcatt tacttctccg tgggcctccg 9780
ccaggatctg caaaccctcc cagattagtg agctcttacc ggctgaagca gcctaatgta 9840
ccatttcctc caacaagcaa tggtctttct ggatataagg attctagtca tggtattgca 9900
gaaagcgcag cactcagacc acagtggtgt tgtcattgta aagtggttat tcttggaagt 9960
ggtgtgcgga aatctttcaa agatctgacc cttttgaaca aggattcccg agaaagcacc 10020
aagagggtag agaaggacat tgtcttctgt agtaataact gctttattct ttattcatca 10080
actgcacaag cgaaaaactc agaaaacaag gaatccattc cttcattgcc acaatcacct 10140
atgagagaaa cgccttccaa agcatttcat cagtacagca acaacatctc cactttggat 10200
gtgcactgtc tcccccagct cccagagaaa gcttctcccc ctgcctcacc acccatcgcc 10260
ttccctcctg cttttgaagc agcccaagtc gaggccaagc cagatgagct gaaggtgaca 10320
gtcaagctga agcctcggct aagagctgtc catggtgggt ttgaagattg caggccgctc 10380
aataaaaaat ggagaggaat gaaatggaag aagtggagca ttcatattgt aatccctaag 10440
gggacattta aaccaccttg tgaggatgaa atagatgaat ttctaaagaa attgggcact 10500
tcccttaaac ctgatcctgt gcccaaagac tatcggaaat gttgcttttg tcatgaagaa 10560
ggtgatggat tgacagatgg accagcaagg ctactcaacc ttgacttgga tctgtgggtc 10620
cacttgaact gcgctctgtg gtccacggag gtctatgaga ctcaggctgg tgccttaata 10680
aatgtggagc tagctctgag gagaggccta caaatgaaat gtgtcttctg tcacaagacg 10740
ggtgccacta gtggatgcca cagatttcga tgcaccaaca tttatcactt cacttgcgcc 10800
attaaagcac aatgcatgtt ttttaaggac aaaactatgc tttgccccat gcacaaacca 10860
aagggaattc atgagcaaga attaagttac tttgcagtct tcaggagggt ctatgttcag 10920
cgtgatgagg tgcgacagat tgctagcatc gtgcaacgag gagaacggga ccataccttt 10980
cgcgtgggta gcctcatctt ccacacaatt ggtcagctgc ttccacagca gatgcaagca 11040
ttccattctc ctaaagcact cttccctgtg ggctatgaag ccagccggct gtactggagc 11100
actcgctatg ccaataggcg ctgccgctac ctgtgctcca ttgaggagaa ggatgggcgc 11160
ccagtgtttg tcatcaggat tgtggaacaa ggccatgaag acctggttct aagtgacatc 11220
tcacctaaag gtgtctggga taagattttg gagcctgtgg catgtgtgag aaaaaagtct 11280
gaaatgctcc agcttttccc agcgtattta aaaggagagg atctgtttgg cctgaccgtc 11340
tctgcagtgg cacgcatagc ggaatcactt cctggggttg aggcatgtga aaattatacc 11400
ttccgatacg gccgaaatcc tctcatggaa cttcctcttg ccgttaaccc cacaggttgt 11460
gcccgttctg aacctaaaat gagtgcccat gtcaagaggc ctcacacctt aaacagcacc 11520
agcacctcaa agtcatttca gagcacagtc actggagaac tgaacgcacc ttatagtaaa 11580
cagtttgttc actccaagtc atcgcagtac cggaagatga aaactgaatg gaaatccaat 11640
gtgtatctgg cacggtctcg gattcagggg ctgggcctgt atgctgctcg agacattgag 11700
aaacacacca tggtcattga gtacatcggg actatcattc gaaacgaagt agccaacagg 11760
aaagagaagc tttatgagtc tcagaaccgt ggtgtgtaca tgttccgcat ggataacgac 11820
catgtgattg acgcgacgct cacaggaggg cccgcaaggt atatcaacca ttcgtgtgca 11880
cctaattgtg tggctgaagt ggtgactttt gagagaggac acaaaattat catcagctcc 11940
agtcggagaa tccagaaagg agaagagctc tgctatgact ataagtttga ctttgaagat 12000
gaccagcaca agattccgtg tcactgtgga gctgtgaact gccggaagtg gatgaactga 12060
aatgcattcc ttgctagctc agcgggcggc ttgtccctag gaagaggcga ttcaacacac 12120
cattggaatt ttgcagacag aaagagattt ttgttttctg ttttatgact ttttgaaaaa 12180
gcttctggga gttctgattt cctcagtcct ttaggttaaa gcagcgccag gaggaagctg 12240
acagaagcag cgttcctgaa gtggccgagg ttaaacggaa tcacagaatg gtccagcact 12300
tttgcttt 12308

<210> 423
<211> 596
<212> DNA
<213> Homo sapiens

<400> 423
ggccggtgaa ggaccgcgag gccttccaga ggctcaactt cctgtaccag gtgagtctgc 60
gacaagggcc ccacggggac ggtgctcggc gtcccagagt gactgctccc ctcccgcagg 120
ccgcccattg tgtccttgcc caggaccccg agaaccaggc gctggcgagg ttttactgct 180
acactgagag gaccattgcg aagcggctcg tcttgcggcg ggatccctcg gtgaagagga 240

ctctctgtcg aggctgctct tccctcctcg tcccgggcct cacctgcacc caccgccaga 300
gacgctgcag gggacagcgc tggaccgtac agacctgcct aacatgccag cgcagccaac 360
gcttcctcaa tgatcccggg catttactct ggggagacag gcctgaggcc cagctcggga 420
gccaagcaga ttccaaacca ctacaaccct tgccaaacac agcccactcc atttcagacc 480
gccttcctga ggagaaaatg cagactcagg gttccagtaa ccagtgatgg attcacccca 540
tctcccaaat aaagtttact tgttttacat tcaaaaaaaa aaaaaaaaaa ctcgag 596

<210> 424
<211> 1549
<212> DNA
<213> Homo sapiens

<400> 424
tgtgagaccg ccaagatggt ggtgggcgcg ttccctatgg cgaagctgct atacttgggc 60
atccggcagg tcagcaagcc gcttgccaac cgtattaagg aggccgcccg ccgaagcgag 120
ttcttcaaga cctatatctg cctcccgccg gctcaactgt atcactgggt ggagatgcgg 180
accaagatgc gcatcatggg cttccggggc acggtcatca agccgctgaa cgaggaggcg 240
gcagccgagc tgggcgcaga gctgctgggc gaagccacca tcttcatcgt gggcggcggc 300
tgcctagtgc tggagtactg gcgccaccag gcgcagcagc gccacaagga ggaggagcag 360
cgtgctgcct ggaacgcgct gcgggacgag gtgggccacc tggcgctggc gctggaagcg 420
ctgcaggcgc aggtgcaggc ggcgccgcca cagggcgccc tggaggaact gcgcacagag 480
ctgcaagagg tgcgcgccca gctctgcaat cccggccggt ccgcttccca cgcagtgcct 540
gcgtccaaga aataggagct tgctggatgg aacctgaatt tggacatggc ctatgtacct 600
aacgtggcct tcttcccgca ccacccttgc ctgcgctggc ccagtggaaa ccaccaggat 660
cttgatgcaa cttggcattt ggttacccct gctgataaga gcagccatta cctgccactg 720
ggaccagcag gtgaagcgtt gcaacatagc cccctccatc atccttcacc tcctatcccc 780
cactccaaac caggacgacc tgcaaggtcc cagccagcag gacaccgtgg gcactctggc 840
aaatgaaaaa atggaacctg gtcttgagct gaatcaatgt gttattgtta cccccacccc 900
cggtttacct gatcagtgtt aacctttact gggacactca tctgttacac tggaacacct 960
tcttcttttt gtcaatcggc acagaccact gtaaggaaat gcagtgtgtt gcagtggcct 1020
tttctccccc tcaccttcta aggtcagctc tagctgagca tcagtgctct cttaaggagg 1080
aaaaaaacgg tgcggctggg agcggtggct cacgcctgta atcctagcac cttgggaggc 1140
cgaggcgggc ggatcacttg aggtcaggag ttccagacca gcctggccaa catggtgaaa 1200
ctccgtctct actaaaaata caaaaattag ccgggtgtgg tggggtgcgc ttgtaatccc 1260
agctactcgg gaggctgagg caggagaatt gcttgaaccc atgaggtgga ggttgcggtg 1320
agccaagatg gcaccattgc accctagcct gggcaacaga gcaagacacc gtcttaaaac 1380
caaaagttaa ccgggcgtgg tggtgggtgc ctgtaatcct agctacttgg gaggctgagg 1440
caggagaatt gcttgaactt gggaggtgga ggccaagatt gtaccactgt attccagccc 1500
gggtgacaga gcaagactgt gtctcaaaaa aaaaaaaaaa aaactcgag 1549

<210> 425
<211> 4019
<212> PRT
<213> Homo sapiens

<400> 425
Leu Phe Ser Ser Ser Asp Lys Phe Thr Leu Asn Gln Asp Met Cys Val
5 10 15
Val Cys Gly Ser Phe Gly Gln Gly Ala Glu Gly Arg Leu Leu Ala Cys
20 25 30
Ser Gln Cys Gly Gln Cys Tyr His Pro Tyr Cys Val Ser Ile Lys Ile
35 40 45
Thr Lys Val Val Leu Ser Lys Gly Trp Arg Cys Leu Glu Cys Thr Val
50 55 60
Cys Glu Ala Cys Gly Lys Ala Thr Asp Pro Gly Arg Leu Leu Leu Cys
65 70 75 80
Asp Asp Cys Asp Ile Ser Tyr His Thr Tyr Cys Leu Asp Pro Pro Leu
85 90 95

```
Gln Thr Val Pro Lys Gly Gly Trp Lys Cys Lys Trp Cys Val Trp Cys
            100                 105                 110
Arg His Cys Gly Ala Thr Ser Ala Gly Leu Arg Cys Glu Trp Gln Asn
        115                 120                 125
Asn Tyr Thr Gln Cys Ala Pro Cys Ala Ser Leu Ser Ser Cys Pro Val
    130                 135                 140
Cys Tyr Arg Asn Tyr Arg Glu Glu Asp Leu Ile Leu Gln Cys Arg Gln
145                 150                 155                 160
Cys Asp Arg Trp Met His Ala Val Cys Gln Asn Leu Asn Thr Glu Glu
                165                 170                 175
Glu Val Glu Asn Val Ala Asp Ile Gly Phe Asp Cys Ser Met Cys Arg
            180                 185                 190
Pro Tyr Met Pro Ala Ser Asn Val Pro Ser Ser Asp Cys Cys Glu Ser
        195                 200                 205
Ser Leu Val Ala Gln Ile Val Thr Lys Val Lys Glu Leu Asp Pro Pro
    210                 215                 220
Lys Thr Tyr Thr Gln Asp Gly Val Cys Leu Thr Glu Ser Gly Met Thr
225                 230                 235                 240
Gln Leu Gln Ser Leu Thr Val Thr Val Pro Arg Arg Lys Arg Ser Lys
                245                 250                 255
Pro Lys Leu Lys Leu Lys Ile Ile Asn Gln Asn Ser Val Ala Val Leu
            260                 265                 270
Gln Thr Pro Pro Asp Ile Gln Ser Glu His Ser Arg Asp Gly Glu Met
        275                 280                 285
Asp Asp Ser Arg Glu Gly Glu Leu Met Asp Cys Asp Gly Lys Ser Glu
    290                 295                 300
Ser Ser Pro Glu Arg Glu Ala Val Asp Asp Glu Thr Lys Gly Val Glu
305                 310                 315                 320
Gly Thr Asp Gly Val Lys Lys Arg Lys Arg Lys Pro Tyr Arg Pro Gly
                325                 330                 335
Ile Gly Gly Phe Met Val Arg Gln Arg Ser Arg Thr Gly Gln Gly Lys
            340                 345                 350
Thr Lys Arg Ser Val Ile Arg Lys Asp Ser Ser Gly Ser Ile Ser Glu
        355                 360                 365
Gln Leu Pro Cys Arg Asp Asp Gly Trp Ser Glu Gln Leu Pro Asp Thr
    370                 375                 380
Leu Val Asp Glu Ser Val Ser Val Thr Glu Ser Thr Glu Lys Ile Lys
385                 390                 395                 400
Lys Arg Tyr Arg Lys Arg Lys Asn Lys Leu Glu Glu Thr Phe Pro Ala
                405                 410                 415
Tyr Leu Gln Glu Ala Phe Phe Gly Lys Asp Leu Leu Asp Thr Ser Arg
            420                 425                 430
Gln Ser Lys Ile Ser Leu Asp Asn Leu Ser Glu Asp Gly Ala Gln Leu
        435                 440                 445
Leu Tyr Lys Thr Asn Met Asn Thr Gly Phe Leu Asp Pro Ser Leu Asp
    450                 455                 460
Pro Leu Leu Ser Ser Ser Ser Ala Pro Thr Lys Ser Gly Thr His Gly
465                 470                 475                 480
Pro Ala Asp Asp Pro Leu Ala Asp Ile Ser Glu Val Leu Asn Thr Asp
                485                 490                 495
Asp Asp Ile Leu Gly Ile Ile Ser Asp Asp Leu Ala Lys Ser Val Asp
            500                 505                 510
His Ser Asp Ile Gly Pro Val Thr Asp Asp Pro Ser Ser Leu Pro Gln
        515                 520                 525
Pro Asn Val Asn Gln Ser Ser Arg Pro Leu Ser Glu Glu Gln Leu Asp
    530                 535                 540
Gly Ile Leu Ser Pro Glu Leu Asp Lys Met Val Thr Asp Gly Ala Ile
545                 550                 555                 560
```

```
Leu Gly Lys Leu Tyr Lys Ile Pro Glu Leu Gly Gly Lys Asp Val Glu
                565                 570                 575
Asp Leu Phe Thr Ala Val Leu Ser Pro Ala Asn Thr Gln Pro Thr Pro
            580                 585                 590
Leu Pro Gln Pro Pro Pro Pro Thr Gln Leu Leu Pro Ile His Asn Gln
        595                 600                 605
Asp Ala Phe Ser Arg Met Pro Leu Met Asn Gly Leu Ile Gly Ser Ser
    610                 615                 620
Pro His Leu Pro His Asn Ser Leu Pro Pro Gly Ser Gly Leu Gly Thr
625                 630                 635                 640
Phe Ser Ala Ile Ala Gln Ser Ser Tyr Pro Asp Ala Arg Asp Lys Asn
                645                 650                 655
Ser Ala Phe Asn Pro Met Ala Ser Asp Pro Asn Asn Ser Trp Thr Ser
            660                 665                 670
Ser Ala Pro Thr Val Glu Gly Glu Asn Asp Thr Met Ser Asn Ala Gln
        675                 680                 685
Arg Ser Thr Leu Lys Trp Glu Lys Glu Glu Ala Leu Gly Glu Met Ala
    690                 695                 700
Thr Val Ala Pro Val Leu Tyr Thr Asn Ile Asn Phe Pro Asn Leu Lys
705                 710                 715                 720
Glu Glu Phe Pro Asp Trp Thr Thr Arg Val Lys Gln Ile Ala Lys Leu
                725                 730                 735
Trp Arg Lys Ala Ser Ser Gln Glu Arg Ala Pro Tyr Val Gln Lys Ala
            740                 745                 750
Arg Asp Asn Arg Ala Ala Leu Arg Ile Asn Lys Val Gln Met Ser Asn
        755                 760                 765
Asp Ser Met Lys Arg Gln Gln Gln Gln Asp Ser Ile Asp Pro Ser Ser
    770                 775                 780
Arg Ile Asp Ser Glu Leu Phe Lys Asp Pro Leu Lys Gln Arg Glu Ser
785                 790                 795                 800
Glu His Glu Gln Glu Trp Lys Phe Arg Gln Gln Met Arg Gln Lys Ser
                805                 810                 815
Lys Gln Gln Ala Lys Ile Glu Ala Thr Gln Lys Leu Glu Gln Val Lys
            820                 825                 830
Asn Glu Gln Gln Gln Gln Gln Gln Gln Gln Phe Gly Ser Gln His Leu
        835                 840                 845
Leu Val Gln Ser Gly Ser Asp Thr Pro Ser Ser Gly Ile Gln Ser Pro
    850                 855                 860
Leu Thr Pro Gln Pro Gly Asn Gly Asn Met Ser Pro Ala Gln Ser Phe
865                 870                 875                 880
His Lys Glu Leu Phe Thr Lys Gln Pro Pro Ser Thr Pro Thr Ser Thr
                885                 890                 895
Ser Ser Asp Asp Val Phe Val Lys Pro Gln Ala Pro Pro Pro Pro Pro
            900                 905                 910
Ala Pro Ser Arg Ile Pro Ile Gln Asp Ser Leu Ser Gln Ala Gln Thr
        915                 920                 925
Ser Gln Pro Pro Ser Pro Gln Val Phe Ser Pro Gly Ser Ser Asn Ser
    930                 935                 940
Arg Pro Pro Ser Pro Met Asp Pro Tyr Ala Lys Met Val Gly Thr Pro
945                 950                 955                 960
Arg Pro Pro Pro Val Gly His Ser Phe Ser Arg Arg Asn Ser Ala Ala
                965                 970                 975
Pro Val Glu Asn Cys Thr Pro Leu Ser Ser Val Ser Arg Pro Leu Gln
            980                 985                 990
Met Asn Glu Thr Thr Ala Asn Arg Pro Ser Pro Val Arg Asp Leu Cys
        995                 1000                1005
Ser Ser Ser Thr Thr Asn Asn Asp Pro Tyr Ala Lys Pro Pro Asp Thr
    1010                1015                1020
```

```
Pro Arg Pro Val Met Thr Asp Gln Phe Pro Lys Ser Leu Gly Leu Ser
1025                1030                1035                1040
Arg Ser Pro Val Val Ser Glu Gln Thr Ala Lys Gly Pro Ile Ala Ala
                1045                1050                1055
Gly Thr Ser Asp His Phe Thr Lys Pro Ser Pro Arg Ala Asp Val Phe
            1060                1065                1070
Gln Arg Gln Arg Ile Pro Asp Ser Tyr Ala Arg Pro Leu Leu Thr Pro
        1075                1080                1085
Ala Pro Leu Asp Ser Gly Pro Gly Pro Phe Lys Thr Pro Met Gln Pro
    1090                1095                1100
Pro Pro Ser Ser Gln Asp Pro Tyr Gly Ser Val Ser Gln Ala Ser Arg
1105                1110                1115                1120
Arg Leu Ser Val Asp Pro Tyr Glu Arg Pro Ala Leu Thr Pro Arg Pro
                1125                1130                1135
Ile Asp Asn Phe Ser His Asn Gln Ser Asn Asp Pro Tyr Ser Gln Pro
            1140                1145                1150
Pro Leu Thr Pro His Pro Ala Val Asn Glu Ser Phe Ala His Pro Ser
        1155                1160                1165
Arg Ala Phe Ser Gln Pro Gly Thr Ile Ser Arg Pro Thr Ser Gln Asp
    1170                1175                1180
Pro Tyr Ser Gln Pro Pro Gly Thr Pro Arg Pro Val Val Asp Ser Tyr
1185                1190                1195                1200
Ser Gln Ser Ser Gly Thr Ala Arg Ser Asn Thr Asp Pro Tyr Ser Gln
                1205                1210                1215
Pro Pro Gly Thr Pro Arg Pro Thr Thr Val Asp Pro Tyr Ser Gln Gln
            1220                1225                1230
Pro Gln Thr Pro Arg Pro Ser Thr Gln Thr Asp Leu Phe Val Thr Pro
        1235                1240                1245
Val Thr Asn Gln Arg His Ser Asp Pro Tyr Ala His Pro Pro Gly Thr
    1250                1255                1260
Pro Arg Pro Gly Ile Ser Val Pro Tyr Ser Gln Pro Pro Ala Thr Pro
1265                1270                1275                1280
Arg Pro Arg Ile Ser Glu Gly Phe Thr Arg Ser Ser Met Thr Arg Pro
                1285                1290                1295
Val Leu Met Pro Asn Gln Asp Pro Phe Leu Gln Ala Ala Gln Asn Arg
            1300                1305                1310
Gly Pro Ala Leu Pro Gly Pro Leu Val Arg Pro Pro Asp Thr Cys Ser
        1315                1320                1325
Gln Thr Pro Arg Pro Pro Gly Pro Gly Leu Ser Asp Thr Phe Ser Arg
    1330                1335                1340
Val Ser Pro Ser Ala Ala Arg Asp Pro Tyr Asp Gln Ser Pro Met Thr
1345                1350                1355                1360
Pro Arg Ser Gln Ser Asp Ser Phe Gly Thr Ser Gln Thr Ala His Asp
                1365                1370                1375
Val Ala Asp Gln Pro Arg Pro Gly Ser Glu Gly Ser Phe Cys Ala Ser
            1380                1385                1390
Ser Asn Ser Pro Met His Ser Gln Gly Gln Gln Phe Ser Gly Val Ser
        1395                1400                1405
Gln Leu Pro Gly Pro Val Pro Thr Ser Gly Val Thr Asp Thr Gln Asn
    1410                1415                1420
Thr Val Asn Met Ala Gln Ala Asp Thr Glu Lys Leu Arg Gln Arg Gln
1425                1430                1435                1440
Lys Leu Arg Glu Ile Ile Leu Gln Gln Gln Gln Gln Lys Lys Ile Ala
                1445                1450                1455
Gly Arg Gln Glu Lys Gly Ser Gln Asp Ser Pro Ala Val Pro His Pro
            1460                1465                1470
Gly Pro Leu Gln His Trp Gln Pro Glu Asn Val Asn Gln Ala Phe Thr
        1475                1480                1485
```

Arg Pro Pro Pro Pro Tyr Pro Gly Asn Ile Arg Ser Pro Val Ala Pro
1490 1495 1500
Pro Leu Gly Pro Arg Tyr Ala Val Phe Pro Lys Asp Gln Arg Gly Pro
1505 1510 1515 1520
Tyr Pro Pro Asp Val Ala Ser Met Gly Met Arg Pro His Gly Phe Arg
1525 1530 1535
Phe Gly Phe Pro Gly Gly Ser His Gly Thr Met Pro Ser Gln Glu Arg
1540 1545 1550
Phe Leu Val Pro Pro Gln Gln Ile Gln Gly Ser Gly Val Ser Pro Gln
1555 1560 1565
Leu Arg Arg Ser Val Ser Val Asp Met Pro Arg Pro Leu Asn Asn Ser
1570 1575 1580
Gln Met Asn Asn Pro Val Gly Leu Pro Gln His Phe Ser Pro Gln Ser
1585 1590 1595 1600
Leu Pro Val Gln Gln His Asn Ile Leu Gly Gln Ala Tyr Ile Glu Leu
1605 1610 1615
Arg His Arg Ala Pro Asp Gly Arg Gln Arg Leu Pro Phe Ser Ala Pro
1620 1625 1630
Pro Gly Ser Val Val Glu Ala Ser Ser Asn Leu Arg His Gly Asn Phe
1635 1640 1645
Ile Pro Arg Pro Asp Phe Pro Gly Pro Arg His Thr Asp Pro Met Arg
1650 1655 1660
Arg Pro Pro Gln Gly Leu Pro Asn Gln Leu Pro Val His Pro Asp Leu
1665 1670 1675 1680
Glu Gln Val Pro Pro Ser Gln Gln Glu Gln Gly His Ser Val His Ser
1685 1690 1695
Ser Ser Met Val Met Arg Thr Leu Asn His Pro Leu Gly Gly Glu Phe
1700 1705 1710
Ser Glu Ala Pro Leu Ser Thr Ser Val Pro Ser Glu Thr Thr Ser Asp
1715 1720 1725
Asn Leu Gln Ile Thr Thr Gln Pro Ser Asp Gly Leu Glu Glu Lys Leu
1730 1735 1740
Asp Ser Asp Asp Pro Ser Val Lys Glu Leu Asp Val Lys Asp Leu Glu
1745 1750 1755 1760
Gly Val Glu Val Lys Asp Leu Asp Asp Glu Asp Leu Glu Asn Leu Asn
1765 1770 1775
Leu Asp Thr Glu Asp Gly Lys Val Val Glu Leu Asp Thr Leu Asp Asn
1780 1785 1790
Leu Glu Thr Asn Asp Pro Asn Leu Asp Asp Leu Leu Arg Ser Gly Glu
1795 1800 1805
Phe Asp Ile Ile Ala Tyr Thr Asp Pro Glu Leu Asp Met Gly Asp Lys
1810 1815 1820
Lys Ser Met Phe Asn Glu Glu Leu Asp Leu Pro Ile Asp Asp Lys Leu
1825 1830 1835 1840
Asp Asn Gln Cys Val Ser Val Glu Pro Lys Lys Lys Glu Gln Glu Asn
1845 1850 1855
Lys Thr Leu Val Leu Ser Asp Lys His Ser Pro Gln Lys Lys Ser Thr
1860 1865 1870
Val Thr Asn Glu Val Lys Thr Glu Val Leu Ser Pro Asn Ser Lys Val
1875 1880 1885
Glu Ser Lys Cys Glu Thr Glu Lys Asn Asp Glu Asn Lys Asp Asn Val
1890 1895 1900
Asp Thr Pro Cys Ser Gln Ala Ser Ala His Ser Asp Leu Asn Asp Gly
1905 1910 1915 1920
Glu Lys Thr Ser Leu His Pro Cys Asp Pro Asp Leu Phe Glu Lys Arg
1925 1930 1935
Thr Asn Arg Glu Thr Ala Gly Pro Ser Ala Asn Val Ile Gln Ala Ser
1940 1945 1950

```
Thr Gln Leu Pro Ala Gln Asp Val Ile Asn Ser Cys Gly Ile Thr Gly
        1955                1960                1965
Ser Thr Pro Val Leu Ser Ser Leu Leu Ala Asn Glu Lys Ser Asp Asn
    1970                1975                1980
Ser Asp Ile Arg Pro Ser Gly Ser Pro Pro Pro Pro Thr Leu Pro Ala
1985                1990                1995                2000
Ser Pro Ser Asn His Val Ser Ser Leu Pro Pro Phe Ile Ala Pro Pro
                2005                2010                2015
Gly Arg Val Leu Asp Asn Ala Met Asn Ser Asn Val Thr Val Val Ser
            2020                2025                2030
Arg Val Asn His Val Phe Ser Gln Gly Val Gln Val Asn Pro Gly Leu
        2035                2040                2045
Ile Pro Gly Gln Ser Thr Val Asn His Ser Leu Gly Thr Gly Lys Pro
    2050                2055                2060
Ala Thr Gln Thr Gly Pro Gln Thr Ser Gln Ser Gly Thr Ser Ser Met
2065                2070                2075                2080
Ser Gly Pro Gln Gln Leu Met Ile Pro Gln Thr Leu Ala Gln Gln Asn
                2085                2090                2095
Arg Glu Arg Pro Leu Leu Leu Glu Glu Gln Pro Leu Leu Leu Gln Asp
            2100                2105                2110
Leu Leu Asp Gln Glu Arg Gln Glu Gln Gln Gln Gln Arg Gln Met Gln
        2115                2120                2125
Ala Met Ile Arg Gln Arg Ser Glu Pro Phe Phe Pro Asn Ile Asp Phe
    2130                2135                2140
Asp Ala Ile Thr Asp Pro Ile Met Lys Ala Lys Met Val Ala Leu Lys
2145                2150                2155                2160
Gly Ile Asn Lys Val Met Ala Gln Asn Asn Leu Gly Met Pro Pro Met
                2165                2170                2175
Val Met Ser Arg Phe Pro Phe Met Gly Gln Val Val Thr Gly Thr Gln
            2180                2185                2190
Asn Ser Glu Gly Gln Asn Leu Gly Pro Gln Ala Ile Pro Gln Asp Gly
        2195                2200                2205
Ser Ile Thr His Gln Ile Ser Arg Pro Asn Pro Pro Asn Phe Gly Pro
    2210                2215                2220
Gly Phe Val Asn Asp Ser Gln Arg Lys Gln Tyr Glu Glu Trp Leu Gln
2225                2230                2235                2240
Glu Thr Gln Gln Leu Leu Gln Met Gln Gln Lys Tyr Leu Glu Glu Gln
                2245                2250                2255
Ile Gly Ala His Arg Lys Ser Lys Lys Ala Leu Ser Ala Lys Gln Arg
            2260                2265                2270
Thr Ala Lys Lys Ala Gly Arg Glu Phe Pro Glu Glu Asp Ala Glu Gln
        2275                2280                2285
Leu Lys His Val Thr Glu Gln Gln Ser Met Val Gln Lys Gln Leu Glu
    2290                2295                2300
Gln Ile Arg Lys Gln Gln Lys Glu His Ala Glu Leu Ile Glu Asp Tyr
2305                2310                2315                2320
Arg Ile Lys Gln Gln Gln Gln Cys Ala Met Ala Pro Pro Thr Met Met
                2325                2330                2335
Pro Ser Val Gln Pro Gln Pro Pro Leu Ile Pro Gly Ala Thr Pro Pro
            2340                2345                2350
Thr Met Ser Gln Pro Thr Phe Pro Met Val Pro Gln Gln Leu Gln His
        2355                2360                2365
Gln Gln His Thr Thr Val Ile Ser Gly His Thr Ser Pro Val Arg Met
    2370                2375                2380
Pro Ser Leu Pro Gly Trp Gln Pro Asn Ser Ala Pro Ala His Leu Pro
2385                2390                2395                2400
Leu Asn Pro Pro Arg Ile Gln Pro Pro Ile Ala Gln Leu Pro Ile Lys
                2405                2410                2415
```

Thr Cys Thr Pro Ala Pro Gly Thr Val Ser Asn Ala Asn Pro Gln Ser
2420 2425 2430
Gly Pro Pro Pro Arg Val Glu Phe Asp Asp Asn Asn Pro Phe Ser Glu
2435 2440 2445
Ser Phe Gln Glu Arg Glu Arg Lys Glu Arg Leu Arg Glu Gln Gln Glu
2450 2455 2460
Arg Gln Arg Ile Gln Leu Met Gln Glu Val Asp Arg Gln Arg Ala Leu
2465 2470 2475 2480
Gln Gln Arg Met Glu Met Glu Gln His Gly Met Val Gly Ser Glu Ile
2485 2490 2495
Ser Ser Ser Arg Thr Ser Val Ser Gln Ile Pro Phe Tyr Ser Ser Asp
2500 2505 2510
Leu Pro Cys Asp Phe Met Gln Pro Leu Gly Pro Leu Gln Gln Ser Pro
2515 2520 2525
Gln His Gln Gln Gln Met Gly Gln Val Leu Gln Gln Gln Asn Ile Gln
2530 2535 2540
Gln Gly Ser Ile Asn Ser Pro Ser Thr Gln Thr Phe Met Gln Thr Asn
2545 2550 2555 2560
Glu Arg Arg Gln Val Gly Pro Pro Ser Phe Val Pro Asp Ser Pro Ser
2565 2570 2575
Ile Pro Val Gly Ser Pro Asn Phe Ser Ser Val Lys Gln Gly His Gly
2580 2585 2590
Asn Leu Ser Gly Thr Ser Phe Gln Gln Ser Pro Val Arg Pro Ser Phe
2595 2600 2605
Thr Pro Ala Leu Pro Ala Ala Pro Pro Val Ala Asn Ser Ser Leu Pro
2610 2615 2620
Cys Gly Gln Asp Ser Thr Ile Thr His Gly His Ser Tyr Pro Gly Ser
2625 2630 2635 2640
Thr Gln Ser Leu Ile Gln Leu Tyr Ser Asp Ile Ile Pro Glu Glu Lys
2645 2650 2655
Gly Lys Lys Lys Arg Thr Arg Lys Lys Lys Arg Asp Asp Asp Ala Glu
2660 2665 2670
Ser Thr Lys Ala Pro Ser Thr Pro His Ser Asp Ile Thr Ala Pro Pro
2675 2680 2685
Thr Pro Gly Ile Ser Glu Thr Thr Ser Thr Pro Ala Val Ser Thr Pro
2690 2695 2700
Ser Glu Leu Pro Gln Gln Ala Asp Gln Glu Ser Val Glu Pro Val Gly
2705 2710 2715 2720
Pro Ser Thr Pro Asn Met Ala Ala Gly Gln Leu Cys Thr Glu Leu Glu
2725 2730 2735
Asn Lys Leu Pro Asn Ser Asp Phe Ser Gln Ala Thr Pro Asn Gln Gln
2740 2745 2750
Thr Tyr Ala Asn Ser Glu Val Asp Lys Leu Ser Met Glu Thr Pro Ala
2755 2760 2765
Lys Thr Glu Glu Ile Lys Leu Glu Lys Ala Glu Thr Glu Ser Cys Pro
2770 2775 2780
Gly Gln Glu Glu Pro Lys Leu Glu Glu Gln Asn Gly Ser Lys Val Glu
2785 2790 2795 2800
Gly Asn Ala Val Ala Cys Pro Val Ser Ser Ala Gln Ser Pro Pro His
2805 2810 2815
Ser Ala Gly Ala Pro Ala Ala Lys Gly Asp Ser Gly Asn Glu Leu Leu
2820 2825 2830
Lys His Leu Leu Lys Asn Lys Lys Ser Ser Ser Leu Leu Asn Gln Lys
2835 2840 2845
Pro Glu Gly Ser Ile Cys Ser Glu Asp Asp Cys Thr Lys Asp Asn Lys
2850 2855 2860
Leu Val Glu Lys Gln Asn Pro Ala Glu Gly Leu Gln Thr Leu Gly Ala
2865 2870 2875 2880

Gln Met Gln Gly Gly Phe Gly Cys Gly Asn Gln Leu Pro Lys Thr Asp
2885 2890 2895
Gly Gly Ser Glu Thr Lys Lys Gln Arg Ser Lys Arg Thr Gln Arg Thr
2900 2905 2910
Gly Glu Lys Ala Ala Pro Arg Ser Lys Lys Arg Lys Lys Asp Glu Glu
2915 2920 2925
Glu Lys Gln Ala Met Tyr Ser Ser Thr Asp Thr Phe Thr His Leu Lys
2930 2935 2940
Gln Val Arg Gln Leu Ser Leu Leu Pro Leu Met Glu Pro Ile Ile Gly
2945 2950 2955 2960
Val Asn Phe Ala His Phe Leu Pro Tyr Gly Ser Gly Gln Phe Asn Ser
2965 2970 2975
Gly Asn Arg Leu Leu Gly Thr Phe Gly Ser Ala Thr Leu Glu Gly Val
2980 2985 2990
Ser Asp Tyr Tyr Ser Gln Leu Ile Tyr Lys Gln Asn Asn Leu Ser Asn
2995 3000 3005
Pro Pro Thr Pro Pro Ala Ser Leu Pro Pro Thr Pro Pro Pro Met Ala
3010 3015 3020
Cys Gln Lys Met Ala Asn Gly Phe Ala Thr Thr Glu Glu Leu Ala Gly
3025 3030 3035 3040
Lys Ala Gly Val Leu Val Ser His Glu Val Thr Lys Thr Leu Gly Pro
3045 3050 3055
Lys Pro Phe Gln Leu Pro Phe Arg Pro Gln Asp Asp Leu Leu Ala Arg
3060 3065 3070
Ala Leu Ala Gln Gly Pro Lys Thr Val Asp Val Pro Ala Ser Leu Pro
3075 3080 3085
Thr Pro Pro His Asn Asn Gln Glu Glu Leu Arg Ile Gln Asp His Cys
3090 3095 3100
Gly Asp Arg Asp Thr Pro Asp Ser Phe Val Pro Ser Ser Ser Pro Glu
3105 3110 3115 3120
Ser Val Val Gly Val Glu Val Ser Arg Tyr Pro Asp Leu Ser Leu Val
3125 3130 3135
Lys Glu Glu Pro Pro Glu Pro Val Pro Ser Pro Ile Ile Pro Ile Leu
3140 3145 3150
Pro Ser Thr Ala Gly Lys Ser Ser Glu Ser Arg Arg Asn Asp Ile Lys
3155 3160 3165
Thr Glu Pro Gly Thr Leu Tyr Phe Ala Ser Pro Phe Gly Pro Ser Pro
3170 3175 3180
Asn Gly Pro Arg Ser Gly Leu Ile Ser Val Ala Ile Thr Leu His Pro
3185 3190 3195 3200
Thr Ala Ala Glu Asn Ile Ser Ser Val Val Ala Ala Phe Ser Asp Leu
3205 3210 3215
Leu His Val Arg Ile Pro Asn Ser Tyr Glu Val Ser Ser Ala Pro Asp
3220 3225 3230
Val Pro Ser Met Gly Leu Val Ser Ser His Arg Ile Asn Pro Gly Leu
3235 3240 3245
Glu Tyr Arg Gln His Leu Leu Leu Arg Gly Pro Pro Pro Gly Ser Ala
3250 3255 3260
Asn Pro Pro Arg Leu Val Ser Ser Tyr Arg Leu Lys Gln Pro Asn Val
3265 3270 3275 3280
Pro Phe Pro Pro Thr Ser Asn Gly Leu Ser Gly Tyr Lys Asp Ser Ser
3285 3290 3295
His Gly Ile Ala Glu Ser Ala Ala Leu Arg Pro Gln Trp Cys Cys His
3300 3305 3310
Cys Lys Val Val Ile Leu Gly Ser Gly Val Arg Lys Ser Phe Lys Asp
3315 3320 3325
Leu Thr Leu Leu Asn Lys Asp Ser Arg Glu Ser Thr Lys Arg Val Glu
3330 3335 3340

Lys Asp Ile Val Phe Cys Ser Asn Asn Cys Phe Ile Leu Tyr Ser Ser
3345 3350 3355 3360
Thr Ala Gln Ala Lys Asn Ser Glu Asn Lys Glu Ser Ile Pro Ser Leu
3365 3370 3375
Pro Gln Ser Pro Met Arg Glu Thr Pro Ser Lys Ala Phe His Gln Tyr
3380 3385 3390
Ser Asn Asn Ile Ser Thr Leu Asp Val His Cys Leu Pro Gln Leu Pro
3395 3400 3405
Glu Lys Ala Ser Pro Pro Ala Ser Pro Pro Ile Ala Phe Pro Pro Ala
3410 3415 3420
Phe Glu Ala Ala Gln Val Glu Ala Lys Pro Asp Glu Leu Lys Val Thr
3425 3430 3435 3440
Val Lys Leu Lys Pro Arg Leu Arg Ala Val His Gly Gly Phe Glu Asp
3445 3450 3455
Cys Arg Pro Leu Asn Lys Lys Trp Arg Gly Met Lys Trp Lys Lys Trp
3460 3465 3470
Ser Ile His Ile Val Ile Pro Lys Gly Thr Phe Lys Pro Pro Cys Glu
3475 3480 3485
Asp Glu Ile Asp Glu Phe Leu Lys Lys Leu Gly Thr Ser Leu Lys Pro
3490 3495 3500
Asp Pro Val Pro Lys Asp Tyr Arg Lys Cys Cys Phe Cys His Glu Glu
3505 3510 3515 3520
Gly Asp Gly Leu Thr Asp Gly Pro Ala Arg Leu Leu Asn Leu Asp Leu
3525 3530 3535
Asp Leu Trp Val His Leu Asn Cys Ala Leu Trp Ser Thr Glu Val Tyr
3540 3545 3550
Glu Thr Gln Ala Gly Ala Leu Ile Asn Val Glu Leu Ala Leu Arg Arg
3555 3560 3565
Gly Leu Gln Met Lys Cys Val Phe Cys His Lys Thr Gly Ala Thr Ser
3570 3575 3580
Gly Cys His Arg Phe Arg Cys Thr Asn Ile Tyr His Phe Thr Cys Ala
3585 3590 3595 3600
Ile Lys Ala Gln Cys Met Phe Phe Lys Asp Lys Thr Met Leu Cys Pro
3605 3610 3615
Met His Lys Pro Lys Gly Ile His Glu Gln Glu Leu Ser Tyr Phe Ala
3620 3625 3630
Val Phe Arg Arg Val Tyr Val Gln Arg Asp Glu Val Arg Gln Ile Ala
3635 3640 3645
Ser Ile Val Gln Arg Gly Glu Arg Asp His Thr Phe Arg Val Gly Ser
3650 3655 3660
Leu Ile Phe His Thr Ile Gly Gln Leu Leu Pro Gln Gln Met Gln Ala
3665 3670 3675 3680
Phe His Ser Pro Lys Ala Leu Phe Pro Val Gly Tyr Glu Ala Ser Arg
3685 3690 3695
Leu Tyr Trp Ser Thr Arg Tyr Ala Asn Arg Arg Cys Arg Tyr Leu Cys
3700 3705 3710
Ser Ile Glu Glu Lys Asp Gly Arg Pro Val Phe Val Ile Arg Ile Val
3715 3720 3725
Glu Gln Gly His Glu Asp Leu Val Leu Ser Asp Ile Ser Pro Lys Gly
3730 3735 3740
Val Trp Asp Lys Ile Leu Glu Pro Val Ala Cys Val Arg Lys Lys Ser
3745 3750 3755 3760
Glu Met Leu Gln Leu Phe Pro Ala Tyr Leu Lys Gly Glu Asp Leu Phe
3765 3770 3775
Gly Leu Thr Val Ser Ala Val Ala Arg Ile Ala Glu Ser Leu Pro Gly
3780 3785 3790
Val Glu Ala Cys Glu Asn Tyr Thr Phe Arg Tyr Gly Arg Asn Pro Leu
3795 3800 3805

Met Glu Leu Pro Leu Ala Val Asn Pro Thr Gly Cys Ala Arg Ser Glu
3810 3815 3820
Pro Lys Met Ser Ala His Val Lys Arg Pro His Thr Leu Asn Ser Thr
3825 3830 3835 3840
Ser Thr Ser Lys Ser Phe Gln Ser Thr Val Thr Gly Glu Leu Asn Ala
3845 3850 3855
Pro Tyr Ser Lys Gln Phe Val His Ser Lys Ser Ser Gln Tyr Arg Lys
3860 3865 3870
Met Lys Thr Glu Trp Lys Ser Asn Val Tyr Leu Ala Arg Ser Arg Ile
3875 3880 3885
Gln Gly Leu Gly Leu Tyr Ala Ala Arg Asp Ile Glu Lys His Thr Met
3890 3895 3900
Val Ile Glu Tyr Ile Gly Thr Ile Ile Arg Asn Glu Val Ala Asn Arg
3905 3910 3915 3920
Lys Glu Lys Leu Tyr Glu Ser Gln Asn Arg Gly Val Tyr Met Phe Arg
3925 3930 3935
Met Asp Asn Asp His Val Ile Asp Ala Thr Leu Thr Gly Gly Pro Ala
3940 3945 3950
Arg Tyr Ile Asn His Ser Cys Ala Pro Asn Cys Val Ala Glu Val Val
3955 3960 3965
Thr Phe Glu Arg Gly His Lys Ile Ile Ile Ser Ser Ser Arg Arg Ile
3970 3975 3980
Gln Lys Gly Glu Glu Leu Cys Tyr Asp Tyr Lys Phe Asp Phe Glu Asp
3985 3990 3995 4000
Asp Gln His Lys Ile Pro Cys His Cys Gly Ala Val Asn Cys Arg Lys
4005 4010 4015
Trp Met Asn

<210> 426
<211> 174
<212> PRT
<213> Homo sapiens

<400> 426
Pro Val Lys Asp Arg Glu Ala Phe Gln Arg Leu Asn Phe Leu Tyr Gln
5 10 15
Val Ser Leu Arg Gln Gly Pro His Gly Asp Gly Ala Arg Arg Pro Arg
20 25 30
Val Thr Ala Pro Leu Pro Gln Ala Ala His Cys Val Leu Ala Gln Asp
35 40 45
Pro Glu Asn Gln Ala Leu Ala Arg Phe Tyr Cys Tyr Thr Glu Arg Thr
50 55 60
Ile Ala Lys Arg Leu Val Leu Arg Arg Asp Pro Ser Val Lys Arg Thr
65 70 75 80
Leu Cys Arg Gly Cys Ser Ser Leu Leu Val Pro Gly Leu Thr Cys Thr
85 90 95
His Arg Gln Arg Arg Cys Arg Gly Gln Arg Trp Thr Val Gln Thr Cys
100 105 110
Leu Thr Cys Gln Arg Ser Gln Arg Phe Leu Asn Asp Pro Gly His Leu
115 120 125
Leu Trp Gly Asp Arg Pro Glu Ala Gln Leu Gly Ser Gln Ala Asp Ser
130 135 140
Lys Pro Leu Gln Pro Leu Pro Asn Thr Ala His Ser Ile Ser Asp Arg
145 150 155 160
Leu Pro Glu Glu Lys Met Gln Thr Gln Gly Ser Ser Asn Gln
165 170

<210> 427
<211> 184
<212> PRT
<213> Homo sapiens

<400> 427
Cys Glu Thr Ala Lys Met Val Val Gly Ala Phe Pro Met Ala Lys Leu
5 10 15
Leu Tyr Leu Gly Ile Arg Gln Val Ser Lys Pro Leu Ala Asn Arg Ile
20 25 30
Lys Glu Ala Ala Arg Arg Ser Glu Phe Phe Lys Thr Tyr Ile Cys Leu
35 40 45
Pro Pro Ala Gln Leu Tyr His Trp Val Glu Met Arg Thr Lys Met Arg
50 55 60
Ile Met Gly Phe Arg Gly Thr Val Ile Lys Pro Leu Asn Glu Glu Ala
65 70 75 80
Ala Ala Glu Leu Gly Ala Glu Leu Leu Gly Glu Ala Thr Ile Phe Ile
85 90 95
Val Gly Gly Gly Cys Leu Val Leu Glu Tyr Trp Arg His Gln Ala Gln
100 105 110
Gln Arg His Lys Glu Glu Glu Gln Arg Ala Ala Trp Asn Ala Leu Arg
115 120 125
Asp Glu Val Gly His Leu Ala Leu Ala Leu Glu Ala Leu Gln Ala Gln
130 135 140
Val Gln Ala Ala Pro Pro Gln Gly Ala Leu Glu Glu Leu Arg Thr Glu
145 150 155 160
Leu Gln Glu Val Arg Ala Gln Leu Cys Asn Pro Gly Arg Ser Ala Ser
165 170 175
His Ala Val Pro Ala Ser Lys Lys
180

<210> 428
<211> 6476
<212> DNA
<213> Homo sapiens

<400> 428
cactgactgg actgaaaaca gggccaagaa aactgctgct gcagggggtc ctgaaaacag 60
ctggaacccg gcagtgatgt gggacctaac ttgaagttaa cctgtggtgg tgaggttgga 120
accagttgga ttatgattta ttttctacac tcttgtacgg aatgcagagc tgttgtatcc 180
tgatgaatct actgctaaat atagtcattt ggaataattt taagtattga tcttaaaact 240
tgtaccacaa caagagtgtc taaaaagcac ggcaagctca ttacgttctt acgaacattc 300
atgaagtctc gtccaacaaa acagaagctg aagcagcggg gaatcttgaa agagagggtg 360
tttggttgtg acctggggga gcaccttcta aattctggtt ttgaagtgcc gcagttcttc 420
aaagctgcac agcattcatt gagagatatg gcatcgtgga tggaatctat cgcctttctg 480
gtgttgcctc caatatccag agactacgcc atgaatttga ctctgagcac gtccccgacc 540
tgacgaaaga accgtatgtt caggacatcc attctgtggg ttccctatgt aagctgtact 600
tccgggaact cccaaaccct ctgcttacct accagctgta tgagaaattt tctgatgcag 660
tttcagcagc aacagatgaa gaaaggctga taaaaatcca cgatgtcatc cagcagctcc 720
ccccaccaca ctacagaaca ctggagttcc tgatgagaca cttgtctctt ctagctgact 780
attgttccat cacaaatatg catgcaaaaa atctagcaat tgtttgggct ccaaacctgt 840
taagatcaaa acagatagaa tctgcctgct tcagtggaac agcagctttc atggaagtga 900
ggattcagtc tgtggttgtt gagttcatcc tgaatcacgt tgatgtgctg ttcagcggca 960
gaatcagcat ggccatgcaa gagggggcag cttctctatc aaggcccaag tccctcctgg 1020
tatcctctcc atccaccaaa ctgctgacat tggaagaggc ccaggcacga acacaagctc 1080
aggtcaattc tccaattgtg acggaaaata aatatatcga agtaggagaa ggacctgctg 1140

```
cacttcaggg gaaatttcat accataattg agttcccact tgaaagaaag aggcctcaaa 1200
ataagatgaa aaagtctcct gtgggtagct ggcgttcctt tttcaacttg gggaaatcat 1260
catctgtttc taaacgaaag ctgcagcgga atgagagtga gccttcagag atgaaagcca 1320
tggctctgaa aggtggcagg gcagaaggaa ccctccgttc agctaaaagt gaggagtctc 1380
ttacatctct ccatgcagtt gatggtgatt ctaagctctt ccgacccaga agacccagat 1440
cttccagtga tgcactgtct gcctctttta atggagaaat gctggggaac cgctgtaact 1500
cctatgataa tctgcctcat gacaatgaga gtgaggagga aggagggctg cttcatatcc 1560
cagcccttat gtctcctcat tcagctgagg atgttgactt gagcccacca gacattggag 1620
tagccagcct ggattttgat ccaatgtcat ttcaatgtag tcctcctaag gccgaatcag 1680
aatgtctgga gagtggtgct tcctttttag attcaccagg atactccaag gataaaccaa 1740
gtgccaataa aaaggatgca gaaacaggta gtagccaatg tcagactcca ggaagcacag 1800
caagctctga acctgtctct cctcttcagg agaaactgag tccattcttt accctggact 1860
tgagcccaac tgaagataaa tcatctaagc catcctcctt tactgaaaag gtcgtctatg 1920
ctttctctcc gaagatagga cggaaattaa gcaaatcacc ttctatgagc atatctgagc 1980
caatttcagt gaccctacca ccacgggtgt cagaagtcat tggtacagtc tcaaatacca 2040
cagctcagaa tgcatcatct tcaacctggg acaaatgcgt tgaagaaagg gatgccacaa 2100
atagatcccc cacccagata gtaaagatga aaacaaatga gacagttgcc caagaagcat 2160
atgaatctga agtccagccc ctggaccagg tggctgctga agaagtagaa ttgccaggga 2220
aagaggatca gtctgtctca agcagtcaga gtaaggctgt agcttctgga cagactcaga 2280
caggagcagt tacccatgac ccccctcagg attccgttcc tgtcagttca gtctctctta 2340
tcccaccacc accgcctccg aaaaatgttg cccgaatgtt ggcgctagca ttagctgagt 2400
ccgcacagca agcctcaact cagtcattga agagaccagg gacctctcag gctgggtata 2460
caaattatgg agacatagcg gtggctacaa ctgaagataa tctgtccagt tcttactctg 2520
cagttgctct agataaggcc tatttccaaa ccgatcgacc agcagagcag ttccacctcc 2580
agaataatgc accaggaaac tgtgaccatc ctctaccaga gacaacagct actggggatc 2640
ctacccattc caacacaact gaatctgggg agcaacatca ccaagtagac ttaacaggga 2700
atcagccaca tcaagcatat ttatctgggg acccagaaaa ggccagaatt acttcagttc 2760
ccttagactc agagaagtct gatgatcatg taagtttccc tgaagaccag tctgggaaga 2820
acagtatgcc aactgtctcc ttcttggatc aggaccagtc tccaccccgt ttctacagtg 2880
gagatcagcc tccttcttat cttggtgcaa gtgtggataa actccatcac cctttagaat 2940
ttgcagacaa atctcccaca cctcctaatt tacctagcga taaaatctac cctccttctg 3000
ggtcccccga agagaatacc agcacagcca ccatgactta catgacaact actccagcaa 3060
cagcccaaat gagcaccaag gaagccagct gggatgtggc tgaacaaccc accactgctg 3120
attttgctgc tgccacactt cagcgcacgc acagaactaa tcgtcccctt ccccctccgc 3180
cttcccagag atctgcagag cagccaccag ttgtggggca ggtacaagca gcaaccaata 3240
taggattaaa taattcccac aaggttcaag gagtagttcc agttccagag aggccacctg 3300
aacctcgagc catggatgac cctgcgtctg ccttcatcag tgacagtggt gctgctgctg 3360
ctcagtgtcc catggctaca gctgtccagc caggcctgcc tgagaaagtg cgggacggtg 3420
cccgggtccc gctgctgcac ctgcgcgccg agtctgtccc tgcgcatccc tgtggctttc 3480
ctgcaccact gccccccacc aggatgatgg agagtaagat gattgctgcc atacactcca 3540
gcagtgcaga tgccaccagc agttcaaatt atcattcctt tgtcactgct tcatccacct 3600
ctgtggacga tgcattgcct ttaccacttc ctgtcccaca acctaagcat gcttctcaga 3660
aaacagttta ctcctccttt gctaggcccg atgtcaccac tgaacccttt ggtccagata 3720
actgtttgca tttcaatatg actccaaact gccagtaccg tccccagagt gtacctcccc 3780
atcacaataa attggagcag caccaagtgt atggtgccag gtcagagcca ccagcctcca 3840
tgggtcttcg ttataacaca tatgtggccc caggaagaaa cgcatctgga caccactcca 3900
agccatgcag ccgggtcgag tatgtgtctt ctttgagctc ctctgtcagg aatacctgtt 3960
accccgaaga cattccaccg taccctacca tccggagagt gcagtctctc catgctccgc 4020
cgtcttccat gattcgctct gttcccattt cacggacaga agttccccca gatgatgagc 4080
cagcctactg cccaagacct ctgtaccaat ataagccata tcagtcctcc caggcccgct 4140
cagattatca tgtcactcag cttcagcctt actttgagaa tggccgggtc cactacaggt 4200
atagcccata ttccagttct tctagttcct attacagtcc agatggggcc ctgtgtgatg 4260
tggatgccta tggcacagtc cagttgagac cccttcaccg ccttcccaat cgagactttg 4320
ctttctacaa tcctaggctg caaggaaaga gcttgtacag ttatgctggt ttggctccac 4380
gtccccgggc caacgtgact ggctatttct ctcccaacga ccataatgta gtcagcatgc 4440
ctccggctgc tgatgtgaag cacacctaca cctcatggga tcttgaggac atggaaaaat 4500
accgcatgca gtccatccgg agagagagcc gtgctcggca gaaggtgaaa gggcctgtca 4560
tgtcccaata tgataacatg accccggcgg tgcaggacga cttgggtggg atctatgtca 4620
```

tccatctgcg tagtaaatca gatcctggga aaactggact tctctcagtg gcagaaggaa 4680
aggagagccg ccatgcagcc aaggccatca gtcccgaggg agaggaccgc ttctatagga 4740
ggcatcccga ggcagagatg gacagagccc accatcacgg aggccatggt agcacgcagc 4800
cggagaagcc atccctgcct cagaagcaga gcagcctgag gagcaggaag cttcctgaca 4860
tgggctgcag tcttcctgag cacagggcac accaagaagc aagccatagg cagttctgtg 4920
agtcaaagaa tgggcccccct tatccccagg gagctggcca gttagattat gggtccaaag 4980
ggattccaga cacttctgag ccagtcagct accacaactc tggagtaaaa tatgctgcat 5040
ccgggcaaga atctttaaga ctgaaccaca aagaggtaag gctctccaaa gagatggagc 5100
gaccctgggt taggcagcct tctgccccag agaaacactc cagagactgc tacaaggagg 5160
aagaacacct cactcagtca atcgtcccac cccctaaacc agagaggagt catagcctca 5220
aactccatca tacccagaac gtggagaggg accccagtgt gctgtaccag taccaaccac 5280
acggcaagcg ccagagcagt gtgactgttg tgtcccagta tgataacctg gaagattacc 5340
actccctgcc tcagcaccag cgaggagtct ttggaggggg cggcatgggg acgtatgtgc 5400
cccctggctt tccccatcca cagagcagga cctatgctac agcgttgggt caaggggcct 5460
tcctgcccgc agagttgtcc ttgcagcatc ctgaaacaca gatccatgca gaatgagccc 5520
tgcgagcaat agagttgaag cagcctctgc tggacagtgg actgttctat ttttttcaat 5580
aaccaaaaag attaaacaaa aaatactata aaaccccctga ccacatttaa aaaatgataa 5640
taaaagtaaa caaatcagca tctttttccc cttccctgct tcattacccc ctcttccatc 5700
tatagacttt gtcatttttg tctttagaaa agatctgaag gatggtaaag ccccgtgctg 5760
aaacccagta gagaaacctg tctcaggaca cacttgccat ctagggctag cttgaaagag 5820
cctgaggact gcctttaact gaatttgaat tcagcattgt cctttcttct tagtatttgc 5880
tgcataattg agagcagttc acatcgattt cctggtaggc gtctgcattc cctgttgtgt 5940
tcctgcttct ccttcagtag ctgcacaact tgcgcagatc gacacactgt tgtcacttca 6000
ttctccccgt ctgagaagga tcttgtgttc agttagagtc gtggaaaaat ccctgatcct 6060
tcaaggtcag tcagacagtt ggcaacatta taattaaaaa taagaaatta agactttaaa 6120
ttaaacattt ggtagagtca tcataaaaca ccagaccact tagactcagg ctgaaccata 6180
ctctttctat tcttattttt catccttgtt cctcacggtt cagtgaacag gctcatatca 6240
tgacagaatg gacttttaaa agttagtact taaggaaact tctttaggtg gaagaaagta 6300
aagttcttat tgtcagtgaa ctttattagc accagaaatc tctattgatg cttttaatgc 6360
attgcctgcc ttcaggtttt cttcttaccc cacccctcaa taagatttgg tgaattgtaa 6420
ttctagtaaa acatgtcata ccattggttt tcctaaatta tcaactttct ttcatt 6476

<210> 429
<211> 732
<212> DNA
<213> Homo sapiens

<400> 429
tgggatttgg tctctttgac taatcaccaa aaagcaacca actcctccga ctcttccttg 60
gcttcaacct tagctggggc tgcagcagca gagcgagcag ctgtggtggc agcagcaacg 120
gggcagcagc acaaaggcag atggatcagc caagaaggcc ttgacctttt cagcaagtgg 180
gaaggtgtaa tccgtctcca cagacaaggc caggaccggc gtcaaaggtg aagcaggaca 240
tgcctccgcc gggggctat gggcccatcg actacaaacg gaacttgccg cgtcgaggac 300
tgtcgggcta cagcatgctg gccataggga ttggaaccct gatctacggg cactggagca 360
taatgaagtg gaaccgtgag cgcaggcgcc tacaaatcga ggacttcgag gctcgcatcg 420
cgctgttgcc actgttacag gcagaaaccg accggaggac cttgcagatg cttcgggaga 480
acctggagga ggaggccatc atcatgaagg acgtgcccga ctggaaggtg ggggagtctg 540
tgttccacac aacccgctgg gtgcccccct tgatcgggga gctgtacggg ctgcgcacca 600
cagaggaggc tctccatgcc agccacggct tcatgtggta cacgtaggcc ctgtgccctc 660
cggccacctg gatccctgcc cctccccact gggacggaat aaatgctctg cagacctgaa 720
aaaaaaaaaa aa 732

<210> 430
<211> 2843
<212> DNA
<213> Homo sapiens

<400> 430

gcgggcccag gaggcggcgg cggcggcggc ggacgggccc cccgcggcag acggcgagga 60
cggacaggac ccgcacagca agcacctgta cacggccgac atgttcacgc acgggatcca 120
gagcgccgcg cacttcgtca tgttcttcgc gccctggtgt ggacactgcc agcggctgca 180
gccgacttgg aatgacctgg gagacaaata caacagcatg gaagatgcca aagtctatgt 240
ggctaaagtg gactgcacgg cccactccga cgtgtgctcc gcccaggggg tgcgaggata 300
ccccaccctta aagcttttca agccaggcca agaagctgtg aagtaccagg gtcctcggga 360
cttccagaca ctggaaaact ggatgctgca gacactgaac gaggagccag tgacaccaga 420
gccggaagtg gaaccgccca gtgcccccga gctcaagcaa gggctgtatg agctctcagc 480
aagcaacttt gagctgcacg ttgcacaagg cgaccacttt atcaagttct tcgctccgtg 540
gtgtggtcac tgcaaagccc tggctccaac ctgggagcag ctggctctgg gccttgaaca 600
ttccgaaact gtcaagattg gcaaggttga ttgtacacag cactatgaac tctgctccgg 660
aaaccaggtt cgtggctatc ccactcttct ctggttccga gatgggaaaa aggtggatca 720
gtacaaggga aagcgggatt tggagtcact gagggagtac gtggagtcgc agctgcagcg 780
cacagagact ggagcgacgg agaccgtcac gccctcagag gccccggtgc tggcagctga 840
gcccgaggct gacaagggca ctgtgttggc actcactgaa aatactttcg atgacaccat 900
tgcagaagga ataaccttca tcaagtttta tgctccatgg tgtggtcatt gtaagactct 960
ggctcctact tgggaggaac tctctaaaaa ggaattccct ggtctggcgg gggtcaagat 1020
cgccgaagta gactgcactg ctgaacggaa tatctgcagc aagtattcgg tacgaggcta 1080
ccccacgtta ttgcttttcc gaggagggaa gaaagtcagt gagcacagtg gaggcagaga 1140
ccttgactcg ttacaccgct ttgtcctgag ccaagcgaaa gacgaacttt aggaacacag 1200
ttggaggtca cctctcctgc ccagctcccg caccctgcgt ttaggagttc agtcccacag 1260
aggccactgg gttcccagtg gtggctgttc agaaagcaga acatactaag cgtgaggtat 1320
cttctttgtg tgtgtgtttt ccaagccaac acactctaca gattctttat taagttaagt 1380
ttctctaagt aaatgtgtaa ctcatggtca ctgtgtaaac attttcagtg gcgatatatc 1440
ccctttgacc ttctcttgat gaaatttaca tggtttcctt tgagactaaa atagcgttga 1500
gggaaatgaa attgctggac tatttgtggc tcctgagttg agtgattttg gtgaaagaaa 1560
gcacatccaa agcatagttt acctgcccac gagttctgga aaggtggcct tgtggcagta 1620
ttgacgttcc tctgatctta aggtcacagt tgactcaata ctgtgttggt ccgtagcatg 1680
gagcagattg aaatgcaaaa acccacacct ctggaagata ccttcacggc cgctgctgga 1740
gcttctgttg ctgtgaatac ttctctcagt gtgagaggtt agccgtgatg aaagcagcgt 1800
tacttctgac cgtgcctgag taagagaatg ctgatgccat aactttatgt gtcgatactt 1860
gtcaaatcag ttactgttca ggggatcctt ctgtttctca cggggtgaaa catgtcttta 1920
gttcctcatg ttaacacgaa gccagagccc acatgaactg ttggatgtct tccttagaaa 1980
gggtaggcat ggaaaattcc acgaggctca ttctcagtat ctcattaact cattgaaaga 2040
ttccagttgt atttgtcacc tggggtgaca agaccagaca ggctttccca ggcctgggta 2100
tccagggagg ctctgcagcc ctgctgaagg gccctaacta gagttctaga gtttctgatt 2160
ctgtttctca gtagtccttt tagaggcttg ctatacttgg tctgcttcaa ggaggtcgac 2220
cttctaatgt atgaagaatg ggatgcattt gatctcaaga ccaaagacag atgtcagtgg 2280
gctgctctgg ccctggtgtg cacggctgtg gcagctgttg atgccagtgt cctctaactc 2340
atgctgtcct tgtgattaaa cacctctatc tcccttggga ataagcacat acaggcttaa 2400
gctctaagat agataggtgt ttgtcctttt accatcgagc tacttcccat aataaccact 2460
ttgcatccaa cactcttcac ccacctccca tacgcaaggg gatgtggata cttggcccaa 2520
agtaactggt ggtaggaatc ttagaaacaa gaccacttat actgtctgtc tgaggcagaa 2580
gataacagca gcatctcgac cagcctctgc cttaaaggaa atctttatta atcacgtatg 2640
gttcacagat aattcttttt ttaaaaaaac ccaacctcct agagaagcac aactgtcaag 2700
agtcttgtac acacaacttc agctttgcat cacgagtctt gtattccaag aaaatcaaag 2760
tggtacaatt tgtttgttta cactatgata ctttctaaat aaactctttt ttttaaaaaa 2820
aaaaaaaaaa aaaaaaactc gag 2843

<210> 431
<211> 640
<212> DNA
<213> Homo sapiens

<400> 431
ggtaacgtta tagtatttgt cagaagttgg ggtctccgtg ggcattgtga tccgtcccag 60
gcagtggatt aggaggccag aaggagatcc cttccacggt gctaggctga gatggatcct 120
ctcagggccc aacagctggc tgcggagctg gaggtggaga tgatggccga tatgtacaac 180

agaatgacca gtgcctgcca ccggaagtgt gtgcctcctc actacaagga agcagagctc 240
tccaagggcg agtctgtgtg cctggaccga tgtgtctcta agtacctgga catccatgag 300
cggatgggca aaaagttgac agagttgtct atgcaggatg aagagctgat gaagagggtg 360
cagcagagct ctgggcctgc atgaggtccc tgtcagtata caccctgggg tgtaccccac 420
cccttcccac tttaataaac gtgctccctg ttgggtgtca tctgtgaaga ctgccaggcc 480
taggctctct gtagagagtc ttcaagatcc cggagtggta gcgctgtctc ctggtgaagg 540
agtatttgtc acactggaat gtgactgtgt gtgtatgtat gtgtatatat atatatatat 600
atatatataa acaagtttgt tgacacctac aaaaaaaaaa 640

<210> 432
<211> 2068
<212> DNA
<213> Homo sapiens

<400> 432
cctcagaagt ccgtgccagt gaccggaggc ggcggcggcg agcggttcct tgtgggctag 60
aagaatcctg caaaaatgtc tctctatcca tctctcgaag acttgaaggt agacaaagta 120
attcaggctc aaactgcttt ttctgcaaac cctgccaatc cagcaatttt gtcagaagct 180
tctgctccta tccctcacga tggaaatctc tatcccagac tgtatccaga gctctctcaa 240
tacatggggc tgagtttaaa tgaagaagaa atacgtgcaa atgtggccgt ggtttctggt 300
gcaccacttc aggggcagtt ggtagcaaga ccttccagta taaactatat ggtggctcct 360
gtaactggta atgatgttgg aattcgtaga gcagaaatta agcaagggat tcgtgaagtc 420
attttgtgta aggatcaaga tggaaaaatt ggactcaggc ttaaatcaat agataatggt 480
atatttgttc agctagtcca ggctaattct ccagcctcat tggttggtct gagatttggg 540
gaccaagtac ttcagatcaa tggtgaaaac tgtgcaggat ggagctctga taaagcgcac 600
aaggtgctca aacaggcttt tggagagaag attaccatga ccattcgtga caggcccttt 660
gaacggacga ttaccatgca taaggatagc actggacatg ttggttttat ctttaaaaat 720
ggaaaaataa catccatagt gaaagatagc tctgcagcca gaaatggtct tctcacggaa 780
cataacatct gtgaaatcaa tggacagaat gtcattggat tgaaggactc tcaaattgca 840
gacatactgt caacatctgg gactgtagtt actattacaa tcatgcctgc ttttatcttt 900
gaacatatta ttaagcggat ggcaccaagc attatgaaaa gcctaatgga ccacaccatt 960
cctgaggttt aaaattcacg gcaccatgga aatgtagctg aacgtctcca gtttccttct 1020
ttggcaactt ctgtattatg cacgtgaagc cttcccggag ccagcgagca tatgctgcat 1080
gaggaccttt ctatcttaca ttatggctgg gaatcttact ctttcatctg ataccttgtt 1140
cagatttcaa aatagttgta gccttatcct ggttttacag atgtgaaact ttcaagagat 1200
ttactgactt tcctagaata gtttctctac tggaaacctg atgcttttat aagccattgt 1260
gattaggatg actgttacag gcttagcttt gtgtgaaaac cagtcacctt tctcctaggt 1320
aatgagtagt gctgttcata ttactttagt tctatagcat actgcatctt taacatgcta 1380
tcatagtaca tttagaatga ttgcctttga tttttttttt aaattctgtg tgtgtgtgtg 1440
taaaatgcca attaagaaca ctggtttcat tccatgtaag cattaaacag tgtatgtagg 1500
tttcaagaga ttgtgatgat tcttaaattt taactacctt cacttaatat gcttgaactg 1560
tcgccttaac tatgttaagc atctagacta aaagccaaaa tataattatt gctgcctttc 1620
taaaaaccca aaatgtagtt ctctattaac ctgaaatgta cactagccca gaacagttta 1680
atggtactta ctgagctata gcatagctgc ttagttgttt ttgagagttt ttagtcaaca 1740
cataatggaa acttctttct tctaaaagtt gccagtgcca cttttaagaa gtgaatcact 1800
atatgtgatg taaaagttat tacactaaac aggataaact tttgactccc cttttgttca 1860
tttgtggatt aagtggtata atacttaatt ttggcatttg actcttaaga ttatgtaacc 1920
tagctacttt gggatggtct tagaatattt ttctgataac ttgttccttt tcctgactcc 1980
tccttgcaaa caaaatgata gttgacactt tatcctgatt tttttcttct ttttggttta 2040
tgtctattct aattaaatat gtataaat 2068

<210> 433
<211> 1723
<212> DNA
<213> Homo sapiens

<400> 433
tttctttgtt aagtcgttcc ctctacaaag gacttcctag tgggtgtgaa aggcagcggt 60

ggccacagag gcggcggaga gatggccttc agcggttccc aggctcccta cctgagtcca 120
gctgtcccct tttctgggac tattcaagga ggtctccagg acggacttca gatcactgtc 180
aatgggaccg ttctcagctc cagtggaacc aggtttgctg tgaactttca gactggcttc 240
agtggaaatg acattgcctt ccacttcaac cctcggtttg aagatggagg gtacgtggtg 300
tgcaacacga ggcagaacgg aagctggggg cccgaggaga ggaagacaca catgcctttc 360
cagaagggga tgccctttga cctctgcttc ctggtgcaga gctcagattt caaggtgatg 420
gtgaacggga tcctcttcgt gcagtacttc caccgcgtgc ccttccaccg tgtggacacc 480
atctccgtca atggctctgt gcagctgtcc tacatcagct tccagaaccc ccgcacagtc 540
cctgttcagc ctgcctttcc acggtgccgt tctcccagcc tgtctgtttc ccacccaggc 600
ccaggggggcg cagacaaaaa cctcccggcg tgtggcctgc caacccggct cccattaccc 660
agacagtcat ccacacagtg cagagcgccc ctggacagat gttctctact cccgccatcc 720
cacctatgat gtaccccac cccgcctatc cgatgccttt catcaccacc attctgggag 780
ggctgtaccc atccaagtcc atcctcctgt caggcactgt cctgcccagt gctcagaggt 840
tccacatcaa cctgtgctct gggaaccaca tcgccttcca cctgaacccc cgttttgatg 900
agaatgctgt ggtccgcaac acccagatcg acaactcctg gggtctgag gagcgaagtc 960
tgccccgaaa aatgcccttc gtccgtggcc agagcttctc agtgtggatc ttgtgtgaag 1020
ctcactgcct caaggtggcc gtggatggtc agcacctgtt tgaatactac catcgcctga 1080
ggaacctgcc caccatcaac agactggaag tgggggggcga catccagctg acccatgtgc 1140
agacataggc ggcttcctgg ccctggggcc gggggctggg gtgtggggca gtctgggtcc 1200
tctcatcatc cccacttccc aggcccagcc tttccaaccc tgcctgggat ctgggcttta 1260
atgcagaggc catgtccttg tctggtcctg cttctggcta cagccaccct ggaacggaga 1320
aggcagctga cggggattgc cttcctcagc cgcagcagca cctggggctc cagctgctgg 1380
aatcctacca tcccaggagg caggcacagc cagggagagg ggaggagtgg gcagtgaaga 1440
tgaagcccca tgctcagtcc cctcccatcc cccacgcagc tccaccccag tcccaagcca 1500
ccagctgtct gctcctggtg ggaggtggcc tcctcagccc ctcctctctg acctttaacc 1560
tcactctcac cttgcaccgt gcaccaaccc ttcacccctc ctggaaagca ggcctgatgg 1620
cttcccactg gcctccacca cctgaccaga gtgttctctt cagaggactg gctcctttcc 1680
cagtgtcctt aaaataaaga aatgaaaatg cttgttggca cat 1723

<210> 434
<211> 1702
<212> PRT
<213> Homo sapiens

<400> 434
Ala Ala Val Leu Gln Ser Cys Thr Ala Phe Ile Glu Arg Tyr Gly Ile
5 10 15
Val Asp Gly Ile Tyr Arg Leu Ser Gly Val Ala Ser Asn Ile Gln Arg
20 25 30
Leu Arg His Glu Phe Asp Ser Glu His Val Pro Asp Leu Thr Lys Glu
35 40 45
Pro Tyr Val Gln Asp Ile His Ser Val Gly Ser Leu Cys Lys Leu Tyr
50 55 60
Phe Arg Glu Leu Pro Asn Pro Leu Leu Thr Tyr Gln Leu Tyr Glu Lys
65 70 75 80
Phe Ser Asp Ala Val Ser Ala Ala Thr Asp Glu Glu Arg Leu Ile Lys
85 90 95
Ile His Asp Val Ile Gln Gln Leu Pro Pro Pro His Tyr Arg Thr Leu
100 105 110
Glu Phe Leu Met Arg His Leu Ser Leu Leu Ala Asp Tyr Cys Ser Ile
115 120 125
Thr Asn Met His Ala Lys Asn Leu Ala Ile Val Trp Ala Pro Asn Leu
130 135 140
Leu Arg Ser Lys Gln Ile Glu Ser Ala Cys Phe Ser Gly Thr Ala Ala
145 150 155 160
Phe Met Glu Val Arg Ile Gln Ser Val Val Val Glu Phe Ile Leu Asn
165 170 175
His Val Asp Val Leu Phe Ser Gly Arg Ile Ser Met Ala Met Gln Glu

```
                180                 185                 190
Gly Ala Ala Ser Leu Ser Arg Pro Lys Ser Leu Leu Val Ser Ser Pro
        195                 200                 205
Ser Thr Lys Leu Leu Thr Leu Glu Glu Ala Gln Ala Arg Thr Gln Ala
    210                 215                 220
Gln Val Asn Ser Pro Ile Val Thr Glu Asn Lys Tyr Ile Glu Val Gly
225                 230                 235                 240
Glu Gly Pro Ala Ala Leu Gln Gly Lys Phe His Thr Ile Ile Glu Phe
                245                 250                 255
Pro Leu Glu Arg Lys Arg Pro Gln Asn Lys Met Lys Lys Ser Pro Val
            260                 265                 270
Gly Ser Trp Arg Ser Phe Phe Asn Leu Gly Lys Ser Ser Ser Val Ser
        275                 280                 285
Lys Arg Lys Leu Gln Arg Asn Glu Ser Glu Pro Ser Glu Met Lys Ala
    290                 295                 300
Met Ala Leu Lys Gly Gly Arg Ala Glu Gly Thr Leu Arg Ser Ala Lys
305                 310                 315                 320
Ser Glu Glu Ser Leu Thr Ser Leu His Ala Val Asp Gly Asp Ser Lys
                325                 330                 335
Leu Phe Arg Pro Arg Arg Pro Arg Ser Ser Ser Asp Ala Leu Ser Ala
            340                 345                 350
Ser Phe Asn Gly Glu Met Leu Gly Asn Arg Cys Asn Ser Tyr Asp Asn
        355                 360                 365
Leu Pro His Asp Asn Glu Ser Glu Glu Glu Gly Gly Leu Leu His Ile
    370                 375                 380
Pro Ala Leu Met Ser Pro His Ser Ala Glu Asp Val Asp Leu Ser Pro
385                 390                 395                 400
Pro Asp Ile Gly Val Ala Ser Leu Asp Phe Asp Pro Met Ser Phe Gln
                405                 410                 415
Cys Ser Pro Pro Lys Ala Glu Ser Glu Cys Leu Glu Ser Gly Ala Ser
            420                 425                 430
Phe Leu Asp Ser Pro Gly Tyr Ser Lys Asp Lys Pro Ser Ala Asn Lys
        435                 440                 445
Lys Asp Ala Glu Thr Gly Ser Ser Gln Cys Gln Thr Pro Gly Ser Thr
    450                 455                 460
Ala Ser Ser Glu Pro Val Ser Pro Leu Gln Glu Lys Leu Ser Pro Phe
465                 470                 475                 480
Phe Thr Leu Asp Leu Ser Pro Thr Glu Asp Lys Ser Ser Lys Pro Ser
                485                 490                 495
Ser Phe Thr Glu Lys Val Val Tyr Ala Phe Ser Pro Lys Ile Gly Arg
            500                 505                 510
Lys Leu Ser Lys Ser Pro Ser Met Ser Ile Ser Glu Pro Ile Ser Val
        515                 520                 525
Thr Leu Pro Pro Arg Val Ser Glu Val Ile Gly Thr Val Ser Asn Thr
    530                 535                 540
Thr Ala Gln Asn Ala Ser Ser Ser Thr Trp Asp Lys Cys Val Glu Glu
545                 550                 555                 560
Arg Asp Ala Thr Asn Arg Ser Pro Thr Gln Ile Val Lys Met Lys Thr
                565                 570                 575
Asn Glu Thr Val Ala Gln Glu Ala Tyr Glu Ser Glu Val Gln Pro Leu
            580                 585                 590
Asp Gln Val Ala Ala Glu Glu Val Glu Leu Pro Gly Lys Glu Asp Gln
        595                 600                 605
Ser Val Ser Ser Ser Gln Ser Lys Ala Val Ala Ser Gly Gln Thr Gln
    610                 615                 620
Thr Gly Ala Val Thr His Asp Pro Pro Gln Asp Ser Val Pro Val Ser
625                 630                 635                 640
Ser Val Ser Leu Ile Pro Pro Pro Pro Pro Pro Lys Asn Val Ala Arg
```

```
                    645                     650                     655
Met Leu Ala Leu Ala Leu Ala Glu Ser Ala Gln Gln Ala Ser Thr Gln
                660                     665                     670
Ser Leu Lys Arg Pro Gly Thr Ser Gln Ala Gly Tyr Thr Asn Tyr Gly
            675                     680                     685
Asp Ile Ala Val Ala Thr Thr Glu Asp Asn Leu Ser Ser Ser Tyr Ser
    690                     695                     700
Ala Val Ala Leu Asp Lys Ala Tyr Phe Gln Thr Asp Arg Pro Ala Glu
705                     710                     715                     720
Gln Phe His Leu Gln Asn Asn Ala Pro Gly Asn Cys Asp His Pro Leu
                    725                     730                     735
Pro Glu Thr Thr Ala Thr Gly Asp Pro Thr His Ser Asn Thr Thr Glu
                740                     745                     750
Ser Gly Glu Gln His His Gln Val Asp Leu Thr Gly Asn Gln Pro His
            755                     760                     765
Gln Ala Tyr Leu Ser Gly Asp Pro Glu Lys Ala Arg Ile Thr Ser Val
    770                     775                     780
Pro Leu Asp Ser Glu Lys Ser Asp Asp His Val Ser Phe Pro Glu Asp
785                     790                     795                     800
Gln Ser Gly Lys Asn Ser Met Pro Thr Val Ser Phe Leu Asp Gln Asp
                    805                     810                     815
Gln Ser Pro Pro Arg Phe Tyr Ser Gly Asp Gln Pro Pro Ser Tyr Leu
                820                     825                     830
Gly Ala Ser Val Asp Lys Leu His His Pro Leu Glu Phe Ala Asp Lys
            835                     840                     845
Ser Pro Thr Pro Pro Asn Leu Pro Ser Asp Lys Ile Tyr Pro Pro Ser
    850                     855                     860
Gly Ser Pro Glu Glu Asn Thr Ser Thr Ala Thr Met Thr Tyr Met Thr
865                     870                     875                     880
Thr Thr Pro Ala Thr Ala Gln Met Ser Thr Lys Glu Ala Ser Trp Asp
                    885                     890                     895
Val Ala Glu Gln Pro Thr Thr Ala Asp Phe Ala Ala Ala Thr Leu Gln
                900                     905                     910
Arg Thr His Arg Thr Asn Arg Pro Leu Pro Pro Pro Pro Ser Gln Arg
            915                     920                     925
Ser Ala Glu Gln Pro Pro Val Val Gly Gln Val Gln Ala Ala Thr Asn
    930                     935                     940
Ile Gly Leu Asn Asn Ser His Lys Val Gln Gly Val Val Pro Val Pro
945                     950                     955                     960
Glu Arg Pro Pro Glu Pro Arg Ala Met Asp Asp Pro Ala Ser Ala Phe
                    965                     970                     975
Ile Ser Asp Ser Gly Ala Ala Ala Ala Gln Cys Pro Met Ala Thr Ala
                980                     985                     990
Val Gln Pro Gly Leu Pro Glu Lys Val Arg Asp Gly Ala Arg Val Pro
            995                     1000                    1005
Leu Leu His Leu Arg Ala Glu Ser Val Pro Ala His Pro Cys Gly Phe
    1010                    1015                    1020
Pro Ala Pro Leu Pro Pro Thr Arg Met Met Glu Ser Lys Met Ile Ala
1025                    1030                    1035                    1040
Ala Ile His Ser Ser Ser Ala Asp Ala Thr Ser Ser Ser Asn Tyr His
                    1045                    1050                    1055
Ser Phe Val Thr Ala Ser Ser Thr Ser Val Asp Asp Ala Leu Pro Leu
                1060                    1065                    1070
Pro Leu Pro Val Pro Gln Pro Lys His Ala Ser Gln Lys Thr Val Tyr
            1075                    1080                    1085
Ser Ser Phe Ala Arg Pro Asp Val Thr Thr Glu Pro Phe Gly Pro Asp
    1090                    1095                    1100
Asn Cys Leu His Phe Asn Met Thr Pro Asn Cys Gln Tyr Arg Pro Gln
```

1105 1110 1115 1120
Ser Val Pro Pro His His Asn Lys Leu Glu Gln His Gln Val Tyr Gly
1125 1130 1135
Ala Arg Ser Glu Pro Pro Ala Ser Met Gly Leu Arg Tyr Asn Thr Tyr
1140 1145 1150
Val Ala Pro Gly Arg Asn Ala Ser Gly His His Ser Lys Pro Cys Ser
1155 1160 1165
Arg Val Glu Tyr Val Ser Ser Leu Ser Ser Ser Val Arg Asn Thr Cys
1170 1175 1180
Tyr Pro Glu Asp Ile Pro Pro Tyr Pro Thr Ile Arg Arg Val Gln Ser
1185 1190 1195 1200
Leu His Ala Pro Pro Ser Ser Met Ile Arg Ser Val Pro Ile Ser Arg
1205 1210 1215
Thr Glu Val Pro Pro Asp Asp Glu Pro Ala Tyr Cys Pro Arg Pro Leu
1220 1225 1230
Tyr Gln Tyr Lys Pro Tyr Gln Ser Ser Gln Ala Arg Ser Asp Tyr His
1235 1240 1245
Val Thr Gln Leu Gln Pro Tyr Phe Glu Asn Gly Arg Val His Tyr Arg
1250 1255 1260
Tyr Ser Pro Tyr Ser Ser Ser Ser Ser Ser Tyr Tyr Ser Pro Asp Gly
1265 1270 1275 1280
Ala Leu Cys Asp Val Asp Ala Tyr Gly Thr Val Gln Leu Arg Pro Leu
1285 1290 1295
His Arg Leu Pro Asn Arg Asp Phe Ala Phe Tyr Asn Pro Arg Leu Gln
1300 1305 1310
Gly Lys Ser Leu Tyr Ser Tyr Ala Gly Leu Ala Pro Arg Pro Arg Ala
1315 1320 1325
Asn Val Thr Gly Tyr Phe Ser Pro Asn Asp His Asn Val Val Ser Met
1330 1335 1340
Pro Pro Ala Ala Asp Val Lys His Thr Tyr Thr Ser Trp Asp Leu Glu
1345 1350 1355 1360
Asp Met Glu Lys Tyr Arg Met Gln Ser Ile Arg Arg Glu Ser Arg Ala
1365 1370 1375
Arg Gln Lys Val Lys Gly Pro Val Met Ser Gln Tyr Asp Asn Met Thr
1380 1385 1390
Pro Ala Val Gln Asp Asp Leu Gly Gly Ile Tyr Val Ile His Leu Arg
1395 1400 1405
Ser Lys Ser Asp Pro Gly Lys Thr Gly Leu Leu Ser Val Ala Glu Gly
1410 1415 1420
Lys Glu Ser Arg His Ala Ala Lys Ala Ile Ser Pro Glu Gly Glu Asp
1425 1430 1435 1440
Arg Phe Tyr Arg Arg His Pro Glu Ala Glu Met Asp Arg Ala His His
1445 1450 1455
His Gly Gly His Gly Ser Thr Gln Pro Glu Lys Pro Ser Leu Pro Gln
1460 1465 1470
Lys Gln Ser Ser Leu Arg Ser Arg Lys Leu Pro Asp Met Gly Cys Ser
1475 1480 1485
Leu Pro Glu His Arg Ala His Gln Glu Ala Ser His Arg Gln Phe Cys
1490 1495 1500
Glu Ser Lys Asn Gly Pro Pro Tyr Pro Gln Gly Ala Gly Gln Leu Asp
1505 1510 1515 1520
Tyr Gly Ser Lys Gly Ile Pro Asp Thr Ser Glu Pro Val Ser Tyr His
1525 1530 1535
Asn Ser Gly Val Lys Tyr Ala Ala Ser Gly Gln Glu Ser Leu Arg Leu
1540 1545 1550
Asn His Lys Glu Val Arg Leu Ser Lys Glu Met Glu Arg Pro Trp Val
1555 1560 1565
Arg Gln Pro Ser Ala Pro Glu Lys His Ser Arg Asp Cys Tyr Lys Glu

```
    1570                1575                1580
Glu Glu His Leu Thr Gln Ser Ile Val Pro Pro Pro Lys Pro Glu Arg
1585                1590                1595                1600
Ser His Ser Leu Lys Leu His His Thr Gln Asn Val Glu Arg Asp Pro
                1605                1610                1615
Ser Val Leu Tyr Gln Tyr Gln Pro His Gly Lys Arg Gln Ser Ser Val
            1620                1625                1630
Thr Val Val Ser Gln Tyr Asp Asn Leu Glu Asp Tyr His Ser Leu Pro
        1635                1640                1645
Gln His Gln Arg Gly Val Phe Gly Gly Gly Gly Met Gly Thr Tyr Val
    1650                1655                1660
Pro Pro Gly Phe Pro His Pro Gln Ser Arg Thr Tyr Ala Thr Ala Leu
1665                1670                1675                1680
Gly Gln Gly Ala Phe Leu Pro Ala Glu Leu Ser Leu Gln His Pro Glu
                1685                1690                1695
Thr Gln Ile His Ala Glu
            1700


<210> 435
<211> 160
<212> PRT
<213> Homo sapiens

<400> 435
Pro Phe Gln Gln Val Gly Arg Cys Asn Pro Ser Pro Gln Thr Arg Pro
                5                   10                  15
Gly Pro Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro Gly Gly Tyr
            20                  25                  30
Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly Leu Ser Gly
        35                  40                  45
Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr Gly His Trp
    50                  55                  60
Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln Ile Glu Asp
65                  70                  75                  80
Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala Glu Thr Asp
                85                  90                  95
Arg Arg Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu Glu Ala Ile
            100                 105                 110
Ile Met Lys Asp Val Pro Asp Trp Lys Val Gly Glu Ser Val Phe His
        115                 120                 125
Thr Thr Arg Trp Val Pro Pro Leu Ile Gly Glu Leu Tyr Gly Leu Arg
    130                 135                 140
Thr Thr Glu Glu Ala Leu His Ala Ser His Gly Phe Met Trp Tyr Thr
145                 150                 155                 160


<210> 436
<211> 396
<212> PRT
<213> Homo sapiens

<400> 436
Arg Ala Gln Glu Ala Ala Ala Ala Ala Ala Asp Gly Pro Pro Ala Ala
                5                   10                  15
Asp Gly Glu Asp Gly Gln Asp Pro His Ser Lys His Leu Tyr Thr Ala
            20                  25                  30
Asp Met Phe Thr His Gly Ile Gln Ser Ala Ala His Phe Val Met Phe
```

35 40 45
Phe Ala Pro Trp Cys Gly His Cys Gln Arg Leu Gln Pro Thr Trp Asn
50 55 60
Asp Leu Gly Asp Lys Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val
65 70 75 80
Ala Lys Val Asp Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly
85 90 95
Val Arg Gly Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala
100 105 110
Val Lys Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met
115 120 125
Leu Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu
130 135 140
Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser Ala
145 150 155 160
Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His Phe Ile Lys Phe
165 170 175
Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro Thr Trp Glu
180 185 190
Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val Lys Ile Gly Lys
195 200 205
Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser Gly Asn Gln Val Arg
210 215 220
Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp Gly Lys Lys Val Asp Gln
225 230 235 240
Tyr Lys Gly Lys Arg Asp Leu Glu Ser Leu Arg Glu Tyr Val Glu Ser
245 250 255
Gln Leu Gln Arg Thr Glu Thr Gly Ala Thr Glu Thr Val Thr Pro Ser
260 265 270
Glu Ala Pro Val Leu Ala Ala Glu Pro Glu Ala Asp Lys Gly Thr Val
275 280 285
Leu Ala Leu Thr Glu Asn Thr Phe Asp Asp Thr Ile Ala Glu Gly Ile
290 295 300
Thr Phe Ile Lys Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu
305 310 315 320
Ala Pro Thr Trp Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala
325 330 335
Gly Val Lys Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys
340 345 350
Ser Lys Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly
355 360 365
Gly Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu
370 375 380
His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu
385 390 395

<210> 437
<211> 92
<212> PRT
<213> Homo sapiens

<400> 437
Ala Glu Met Asp Pro Leu Arg Ala Gln Gln Leu Ala Ala Glu Leu Glu
5 10 15
Val Glu Met Met Ala Asp Met Tyr Asn Arg Met Thr Ser Ala Cys His
20 25 30
Arg Lys Cys Val Pro Pro His Tyr Lys Glu Ala Glu Leu Ser Lys Gly

```
         35                      40                      45
Glu Ser Val Cys Leu Asp Arg Cys Val Ser Lys Tyr Leu Asp Ile His
     50                  55                      60
Glu Arg Met Gly Lys Lys Leu Thr Glu Leu Ser Met Gln Asp Glu Glu
 65                  70                      75                  80
Leu Met Lys Arg Val Gln Gln Ser Ser Gly Pro Ala
                 85                      90


<210> 438
<211> 303
<212> PRT
<213> Homo sapiens

<400> 438
Lys Asn Pro Ala Lys Met Ser Leu Tyr Pro Ser Leu Glu Asp Leu Lys
                 5                      10                      15
Val Asp Lys Val Ile Gln Ala Gln Thr Ala Phe Ser Ala Asn Pro Ala
             20                  25                      30
Asn Pro Ala Ile Leu Ser Glu Ala Ser Ala Pro Ile Pro His Asp Gly
         35                      40                      45
Asn Leu Tyr Pro Arg Leu Tyr Pro Glu Leu Ser Gln Tyr Met Gly Leu
     50                  55                      60
Ser Leu Asn Glu Glu Glu Ile Arg Ala Asn Val Ala Val Val Ser Gly
 65                  70                      75                  80
Ala Pro Leu Gln Gly Gln Leu Val Ala Arg Pro Ser Ser Ile Asn Tyr
                 85                      90                      95
Met Val Ala Pro Val Thr Gly Asn Asp Val Gly Ile Arg Arg Ala Glu
             100                 105                     110
Ile Lys Gln Gly Ile Arg Glu Val Ile Leu Cys Lys Asp Gln Asp Gly
         115                     120                     125
Lys Ile Gly Leu Arg Leu Lys Ser Ile Asp Asn Gly Ile Phe Val Gln
     130                     135                     140
Leu Val Gln Ala Asn Ser Pro Ala Ser Leu Val Gly Leu Arg Phe Gly
145                 150                     155                     160
Asp Gln Val Leu Gln Ile Asn Gly Glu Asn Cys Ala Gly Trp Ser Ser
                 165                     170                     175
Asp Lys Ala His Lys Val Leu Lys Gln Ala Phe Gly Glu Lys Ile Thr
             180                 185                     190
Met Thr Ile Arg Asp Arg Pro Phe Glu Arg Thr Ile Thr Met His Lys
         195                     200                     205
Asp Ser Thr Gly His Val Gly Phe Ile Phe Lys Asn Gly Lys Ile Thr
     210                     215                     220
Ser Ile Val Lys Asp Ser Ser Ala Ala Arg Asn Gly Leu Leu Thr Glu
225                 230                     235                     240
His Asn Ile Cys Glu Ile Asn Gly Gln Asn Val Ile Gly Leu Lys Asp
                 245                     250                     255
Ser Gln Ile Ala Asp Ile Leu Ser Thr Ser Gly Thr Val Val Thr Ile
             260                 265                     270
Thr Ile Met Pro Ala Phe Ile Phe Glu His Ile Ile Lys Arg Met Ala
         275                     280                     285
Pro Ser Ile Met Lys Ser Leu Met Asp His Thr Ile Pro Glu Val
     290                     295                     300


<210> 439
<211> 378
<212> PRT
```

<213> Homo sapiens

<400> 439
Val Val Pro Ser Thr Lys Asp Phe Leu Val Gly Val Lys Gly Ser Gly
5 10 15
Gly His Arg Gly Gly Gly Glu Met Ala Phe Ser Gly Ser Gln Ala Pro
20 25 30
Tyr Leu Ser Pro Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu
35 40 45
Gln Asp Gly Leu Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser
50 55 60
Gly Thr Arg Phe Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp
65 70 75 80
Ile Ala Phe His Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val
85 90 95
Cys Asn Thr Arg Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr
100 105 110
His Met Pro Phe Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val
115 120 125
Gln Ser Ser Asp Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln
130 135 140
Tyr Phe His Arg Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn
145 150 155 160
Gly Ser Val Gln Leu Ser Tyr Ile Ser Phe Gln Asn Pro Arg Thr Val
165 170 175
Pro Val Gln Pro Ala Phe Ser Thr Val Pro Phe Ser Gln Pro Val Cys
180 185 190
Phe Pro Pro Arg Pro Arg Gly Arg Arg Gln Lys Pro Pro Gly Val Trp
195 200 205
Pro Ala Asn Pro Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln
210 215 220
Ser Ala Pro Gly Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met
225 230 235 240
Tyr Pro His Pro Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly
245 250 255
Gly Leu Tyr Pro Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro
260 265 270
Ser Ala Gln Arg Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala
275 280 285
Phe His Leu Asn Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr
290 295 300
Gln Ile Asp Asn Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys
305 310 315 320
Met Pro Phe Val Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu
325 330 335
Ala His Cys Leu Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr
340 345 350
Tyr His Arg Leu Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly
355 360 365
Gly Asp Ile Gln Leu Thr His Val Gln Thr
370 375

<210> 440
<211> 2239
<212> DNA
<213> Homo sapiens

<400> 440
ggaggttgaa gtgagcagag atcatgccag cctgggtgac agtgagactc tgtctcaaac 60
agaattaagg aaaaaagaaa gaaagaaaaa gagagagagg aaattccagg ccaattgtgg 120
catagatttt atcatattct ggatttttg gattcttttg ttttctcatc actggattca 180
ggaaagcctg ttgtgtccac catctccaaa ggaggttacc tgcagggaaa tgttaacggg 240
aggctgcctt ccctgggcaa caaggagcca cctgggcagg acgccttttc aggaagagac 300
gccttttcag gaagagacgc cttttcagga agagagaaag tgcagctgaa gaggaaagtc 360
actttactga ggggagtctc cattatcatt ggcaccatca ttggagcagg aatcttcatc 420
tctcctaagg gcgtgctcca gaacacgggc agcgtgggca tgtctctgac catctggacg 480
gtgtgtgggg tcctgtcact atttggagct ttgtcttatg ctgaattggg aacaactata 540
aagaaatctg gaggtcatta cacatatatt ttggaagtct ttggtccatt accagctttt 600
gtacgagtct gggtggaact cctcataata cgccctgcag ctactgctgt gatatccctg 660
gcatttggac gctacattct ggaaccattt tttattcaat gtgaaatccc tgaacttgcg 720
atcaagctca ttacagctgt gggcataact gtagtgatgg tcctaaatag catgagtgtc 780
agctggagcg cccggatcca gattttctta accttttgca agctcacagc aattctgata 840
attatagtcc ctggagttat gcagctaatt aaaggtcaaa cgcagaactt taaagacgcc 900
ttttcaggaa gagattcaag tattacgcgg ttgccactgg ctttttatta tggaatgtat 960
gcatatgctg gctggtttta cctcaacttt gttactgaag aagtagaaaa ccctgaaaaa 1020
accattcccc ttgcaatatg tatatccatg gccattgtca ccattggcta tgtgctgaca 1080
aatgtggcct actttacgac cattaatgct gaggagctgc tgctttcaaa tgcagtggca 1140
gtgacctttt ctgagcggct actgggaaat ttctcattag cagttccgat ctttgttgcc 1200
ctctcctgct ttggctccat gaacggtggt gtgtttgctg tctccaggtt attctatgtt 1260
gcgtctcgag agggtcacct tccagaaatc ctctccatga ttcatgtccg caagcacact 1320
cctctaccag ctgttattgt tttgcaccct ttgacaatga taatgctctt ctctggagac 1380
ctcgacagtc ttttgaattt cctcagtttt gccaggtggc tttttattgg gctggcagtt 1440
gctgggctga tttatcttcg atacaaatgc ccagatatgc atcgtccttt caaggtgcca 1500
ctgttcatcc cagctttgtt ttccttcaca tgcctcttca tggttgccct ttccctctat 1560
tcggacccat ttagtacagg gattggcttc gtcatcactc tgactggagt ccctgcgtat 1620
tatctcttta ttatatggga caagaaaccc aggtggttta gaataatgtc agagaaaata 1680
accagaacat tacaaataat actggaagtt gtaccagaag aagataagtt atgaactaat 1740
ggacttgaga tcttggcaat ctgcccaagg ggagacacaa aatagggatt tttacttcat 1800
tttctgaaag tctagagaat tacaactttg gtgataaaca aaaggagtca gttattttta 1860
ttcatatatt ttagcatatt cgaactaatt tctaagaaat ttagttataa ctctatgtag 1920
ttatagaaag tgaatatgca gttattctat gagtcgcaca attcttgagt ctctgatacc 1980
tacctattgg ggttaggaga aaagactaga caattactat gtggtcattc tctacaacat 2040
atgttagcac ggcaaagaac cttcaaattg aagactgaga tttttctgta tatatgggtt 2100
ttgtaaagat ggttttacac actacagatg tctatactgt gaaaagtgtt ttcaattctg 2160
aaaaaaagca tacatcatga ttatggcaaa gaggagagaa ggtagagctg ttcttaaatt 2220
tattaaaaaa aaaaaaaaa 2239

<210> 441
<211> 5981
<212> DNA
<213> Homo sapiens

<400> 441
aggttgaagt gagcagagat catgccagcc tgggtgacag tgagactctg tctcaaacag 60
aattaaggaa aaaagaaaga aagaaaaaga gagagaggaa attccaggcc aattgtggca 120
tagattttat catattctgg atttttgga ttcttttgtt ttctcatcac tggattcagg 180
aaagcctgtt gtgtccacca tctccaaagg aggttacctg cagggaaatg ttaacgggag 240
gctgccttcc ctgggcaaca aggagccacc tgggcaggag aaagtgcagc tgaagaggaa 300
agtcacttta ctgaggggag tctccattat cattggcacc atcattggag caggaatctt 360
catctctcct aagggcgtgc tccagaacac gggcagcgtg ggcatgtctc tgaccatctg 420
gacggtgtgt ggggtcctgt cactatttgg agctttgtct tatgctgaat tgggaacaac 480
tataaagaaa tctggaggtc attacacata tattttggaa gtctttggtc cattaccagc 540
ttttgtacga gtctgggtgg aactcctcat aatacgccct gcagctactg ctgtgatatc 600

cctggcattt ggacgctaca ttctggaacc atttttatt caatgtgaaa tccctgaact 660
tgcgatcaag ctcattacag ctgtgggcat aactgtagtg atggtcctaa atagcatgag 720
tgtcagctgg agcgcccgga tccagatttt cttaaccttt tgcaagctca cagcaattct 780
gataattata gtccctggag ttatgcagct aattaaaggt caaacgcaga actttaaaga 840
cgccttttca ggaagagatt caagtattac gcggttgcca ctggcttttt attatggaat 900
gtatgcatat gctggctggt tttacctcaa ctttgttact gaagaagtag aaaaccctga 960
aaaaaccatt ccccttgcaa tatgtatatc catggccatt gtcaccattg gctatgtgct 1020
gacaaatgtg gcctacttta cgaccattaa tgctgaggag ctgctgcttt caaatgcagt 1080
ggcagtgacc ttttctgagc ggctactggg aaatttctca ttagcagttc cgatctttgt 1140
tgccctctcc tgctttggct ccatgaacgg tggtgtgttt gctgtctcca ggttattcta 1200
tgttgcgtct cgagagggtc accttccaga aatcctctcc atgattcatg tccgcaagca 1260
cactcctcta ccagctgtta ttgttttgca ccctttgaca atgataatgc tcttctctgg 1320
agacctcgac agtcttttga atttcctcag ttttgccagg tggcttttta ttgggctggc 1380
agttgctggg ctgatttatc ttcgatacaa atgcccagat atgcatcgtc ctttcaaggt 1440
gccactgttc atcccagctt tgttttcctt cacatgcctc ttcatggttg ccctttccct 1500
ctattcggac ccatttagta cagggattgg cttcgtcatc actctgactg gagtccctgc 1560
gtattatctc tttattatat gggacaagaa acccaggtgg tttagaataa tgtcagagaa 1620
aataaccaga acattacaaa taatactgga agttgtacca gaagaagata agttatgaac 1680
taatggactt gagatcttgg caatctgccc aaggggagac acaaaatagg gatttttact 1740
tcattttctg aaagtctaga gaattacaac tttggtgata aacaaaagga gtcagttatt 1800
tttattcata tattttagca tattcgaact aatttctaag aaatttagtt ataactctat 1860
gtagttatag aaagtgaata tgcagttatt ctatgagtcg cacaattctt gagtctctga 1920
tacctaccta ttggggttag gagaaaagac tagacaatta ctatgtggtc attctctaca 1980
acatatgtta gcacggcaaa gaaccttcaa attgaagact gagattttc tgtatatatg 2040
ggttttgtaa agatggtttt acacactaca gatgtctata ctgtgaaaag tgttttcaat 2100
tctgaaaaaa agcatacatc atgattatgg caaagaggag agaaagaaat ttattttaca 2160
ttgacattgc attgcttccc cttagatacc aatttagata acaaacactc atgctttaat 2220
ggattatacc cagagcactt tgaacaaagg tcagtgggga ttgttgaata cattaaagaa 2280
gagtttctag ggctactgt ttatgagaca catccaggag ttatgtttaa gtaaaaatcc 2340
ttgagaattt attatgtcag atgtttttc attcattatc aggaagtttt agttatctgt 2400
catttttttt tttcacatca gtttgatcag gaaagtgtat aacacatctt agagcaagag 2460
ttagtttggt attaaatcct cattagaaca accacctgtt tcactaataa cttacccctg 2520
atgagtctat ctaaacatat gcattttaag ccttcaaatt acattatcaa catgagagaa 2580
atcaccaaca aagaagatgt tcaaaataat agtcccatat ctgtaatcat atctacatgc 2640
aatgttagta attctgaagt tttttaaatt tatggctatt tttacacgat gatgaatttt 2700
gacagtttgt gcattttctt tatacatttt atattcttct gttaaaatat ctcttcagat 2760
gaaactgtcc agattaatta ggaaaaggca tatattaaca taaaaattgc aaaagaaatg 2820
tcgctgtaaa taagatttac aactgatgtt tctagaaaat ttccacttct atatctaggc 2880
tttgtcagta atttccacac acacacacac ttttatata tatatatata tatatatata 2940
tagtggaact tacaaatgag agtaatataa tgatgaaatt ttgaactgtt atttataaac 3000
atctaaggta aaatggttag tcatggccag agtatgtttc atcctttaat ttttgtccat 3060
ttgaaaataa ggatttttga aagaattata ccaattaaaa ttattaaagg caaacataga 3120
attcataaaa aattgtccaa agtagaaatg atgacctata atttggagca tttccaattc 3180
agtaatttca attttgctct tgaaaacatt taatatatat ccaagactga catttcttta 3240
gctgaaccta acgtttgggt ctctgagtga atttataata actccttcct tccttagcat 3300
agggttttca aaatttgatt tataattcct atttccagta aatattgttc atttgtccac 3360
atctctccct atgatatgtt gctggaggta agaatttctt tcatattcct attttttttt 3420
tccccataga ctaggctcat agaatttaaa caagcaaatt ttcctgagct ttttcttgcc 3480
aaatgaaaga agactggtaa attctcatag agaggtttgt gtagttcttg gctcttcctg 3540
gggttaatgt gcttatattc acagtggcaa attggtctca gactttaatt tatttatttt 3600
tgatttgaat ttctctttaa aagtatcaat ttaaaaggta actagaatta ttctttctca 3660
ttttcaaaag tgatttttgc attattaaat ttccctgcca ttgtaatgcc atttcacgca 3720
gaaaaaaagt cagccagtaa ttaagaaaaa aagtgatgga gattaagtag tattttggct 3780
tatttttagg actcatcatg agaagacaca gttcctttaa tcaggaaatt aatatccata 3840
attttcactc aaaattgcag tatgtaaagc agattctcaa aaactctcct gaacacttat 3900
ttatatatat gtttttatat aagtaaaatt tttctcatat ttttatacga tatgcacaca 3960
cacacataca tgcacatact acttactaca tgttctgtac ttgtactttg taccatgcat 4020
attcaaatgt ttatatacat aagtttatta taacataaac agtaaaagta atgaatactg 4080

tttaaaataa ctaatatagt attttttaat ttttgtgggg atggattctc aaatacttgt 4140
gattttaaaa gattctaaag ctaaaacaca acttgatttt aaaaagaatg attctcctta 4200
cacaattata aatatttgca gtaaatattt tccttataat actgttttga ccccatttaa 4260
aaagtattag attatattcc tttgatccaa tgaaaactga accttataaa tggttagctg 4320
aaagtagacc ttattcttgt ccttctttag aagagtaaag atttgtccta gggaagatgg 4380
ctgacttcgg ttcccaacat gcgtatgcat ttagactgta gctcctcagc cctgtggaca 4440
caaaatttgg acagcttatt aggttacgtt agcaatgcat gacggtttct ccaacactaa 4500
gatattcacg ttgaaacaga tttcctgttc gtcttatgtg tctggtaaaa ttgtttcccc 4560
aattacaatt tgacatatca atagagggtt aacaagagta taattacata acagaattcc 4620
tcatgaactg taatcagtct acaggaaaat cattatttta tcttgatttg cagatgaata 4680
tactgctaag aaagggagca actctgacct ttgttaaagt tgatcttttg taattgaggt 4740
ataaggtatg aaaagataaa aaaccgaagg ccagagaatc aggaaatgaa agatagtatg 4800
gactgaaggt aacaatattt taatgttatg caatatagcc agagaaatat taaaaattag 4860
ttgtttgctg tgcataggtg gatctcgcag gaagctaatg aaacctaagc ttcagtgcct 4920
ctcacttaga catgttccat tcgaggtcct gaacctaact ttgtattagg aattctgtac 4980
taattttgtt gaagaagacc agcaaagttg tgtacacttc taccccccaca aaatctgcat 5040
tgtccatgtg agtaaagtaa aataattcct gttatttttt tctgttagaa ataagtatgg 5100
aggatatgtt tttaaaaatt tatgagttaa ttgaaatatc catatataac aagtgacttt 5160
ctcacaatat atatgatgtg atatataggg agatagtttc actttcatca tattttatac 5220
gttgattctg aactatagaa aaataataaa tgggatttta attatagctc ttagttggga 5280
aagaaatata gagagatgtg ggatttgaat gcccatgaaa gacattttat tttacttgaa 5340
tatattcttg cttcacttta ccctccataa tatgttgtac attagtgctg atcaagttta 5400
cagagttaca ttttgctttc ctaaccattc agtcaggaat taaaatatgg cattgtataa 5460
caactgggaa gaagctcata gtggatataa attagagtag ataatgggtc accttgatag 5520
cctctgttta cattacttgt atatgggcaa aataattatt acctatacgt gtatttaagc 5580
ttaattttca tataaacagt atttttaatc tatgttaaaa tagataatat ctaaaagtgt 5640
gatctctagg tagtccttag tttattagta ctgtacttca aaaagatttt taaataggtc 5700
cggcacggtg gctcatgcct gtaatcccag cactttggga ggctgaggcg ggcgaatcac 5760
ctgaggtcag gagttcgaga tcagcctggc caacatggtg aaaccctgtc tcaactaaaa 5820
atataaaaat tagccgggcg tggtggcagg cgcctgtaat cccagctact cgggaggctg 5880
aggcaggaga atcacttgaa cccaaggggc agaagctgca gttagccaag atcgcatcat 5940
tgcactccag cctaggggac aagagcgcga gacttcatct c 5981

<210> 442
<211> 337
<212> DNA
<213> Homo sapiens

<400> 442
gatggaggtt gaagtgagca gagatcatgc cagcctgggt gacagtgaga ctctgtctca 60
aacagaatta aggaaaaaag aaagaaagaa aaagagagag aggaaattcc aggccaattg 120
tggcatagat tttatcatat tctggatttt ttggattctt ttgttttctc atcactggat 180
tcaggaaagc ctgttgtgtc caccatctcc aaaggaggtt acctgcaggg aaatgttaac 240
gggaggctgc cttccctggg caacaaggag ccacctgggc aggagaaagt gcagctgaag 300
aggaaagtca ctttactgag gggagtctcc attatca 337

<210> 443
<211> 739
<212> DNA
<213> Homo sapiens

<400> 443
gaattcgaac cccttcggat tctaatcaag aaaatgattt gctatgggaa gagaagtttc 60
ctgaaagaac aactgttact gaattacctc agacttcaca tgtatcattc tccgagcctg 120
atattccgtc ctcaaaaagt actgagttac ctgtggactg gagtattaaa acgcgactcc 180
ttttcacctc ttctcaaccc tttacctggg cagatcattt gaaagcacag gaagaagctc 240
aaggtcttgt ccagcattgt agggcaacag aagttacttt gcctaaaagt atacaggatc 300

ccaaactctc ctctgagctc cgttgtacct tccagcagag ccttatctat tggctccacc 360
ctgctttgtc ttggctacca ctgttccctc gtattggagc tgatagaaaa atggctggaa 420
agacaagtcc ttggtcaaat gatgcaaccc tgcagcatgt tttaatgagt gactggtctg 480
tgagctttac ttctctatat aatttgctga agacaaaact ttgcccctat ttctacgttt 540
gtacctatca gtttactgtc ctgttccgag cagcaggatt agctggaagt gacttaatca 600
cagctctcat atctccaaca actcgaggtt taagagaagc tatgagaaat gaaggtattg 660
aattttctct gcctttaata aaagaaagtg gccataagaa ggagacagca tctggaacaa 720
gcttgggata tggggagga 739

<210> 444
<211> 738
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(738)
<223> n = A,T,C or G

<400> 444
ttttttttt ttcgttnaaa agaaatttta tttctanant ggaatgattt ggatgtgacc 60
tgataaatac agtttgttat tgnggtctca ttaaattaat cagcttttc acactggggt 120
aaagaaacag atgatgatac tagggaatgg aaacaaaatt ggaaacctgg gttatttggg 180
gatttatatt gtactctgca cagttgccct tttttttagg cgtgttccct ggaaaagagg 240
gacggatgaa cctggaagta agtaaaagac attctaggtg tgtagcatca aggcagttaa 300
tatccaagca tcagctttct ctttatacat ctacactgca tggcctgcac caaataagga 360
actgaaccag gggtatgttt ttacctccac agctgcctcc ttccatcana gcaccttgat 420
gaacttaatg tctagtcaca cgtcattggc atgttttctc cccagcattt aattacaaag 480
ctttctttct ttggatagga tcagttctta agagcagccc cggtaactgg aggaatggga 540
gccgttttga tganaaaaat gggtttggtg ttcaggatct ccaattataa atgtagtctc 600
tcagcaccac attccgtaaa gatgatttcc caagtaacgg tatttgacta agttgctcca 660
gagtgttagg ggcaaaccac agttagtaag ctccttatga acaaccccca tatcaagtac 720
tttgtccatt tgcaggca 738

<210> 445
<211> 716
<212> DNA
<213> Homo sapiens

<400> 445
gcggccgcta gtgctccagc tcgcgctccg ccctcaggca cagcatcccc acgggcctcc 60
acgccaacct gtccgagggc cgccccgtgg gtccggcccg ccgtggcgcc tcatcgctgc 120
tcggcccgga aggcttcttc cttggcaaga tgggattccg ggaggcggtg gcggccggag 180
acgtggattt gcctcaggtg cggagccgca gctacaggag gatgctcgcg aggaccccca 240
gagctccgcc cggagggtac tgtgaggccg ttaggagctg gcggtggatg acttccgcat 300
tcaaacactg gagccatcac acggaagcac gaggagggta tcctcggcag ctactcccgg 360
tcgctcaagg tgtctctcgc tcgccctcta ggtgcgggag gagctcgagg cccaactaag 420
ctgcttccgg gagctgctgg gcagggcccc cacgcacgcg gacgggcacc agcacgtgca 480
cgtgctccca ggtggacaga cgccttcgtg ggcctgagca cttgcggccg gcacatgtcc 540
gctcaccgcg tgtccggggc cctggcgcgg gtcctggaag gtaccctagc gggccacacc 600
ctgacagccg agctgatggc gcaccccggc taccccagtg tgcctcccac cggcggctgc 660
ggtgaaggcc ccgacgcttt ctctttgctc ttgggaagcg gcttgcattg agcttg 716

<210> 446
<211> 641
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(641)
<223> n = A,T,C or G

<400> 446
gctncagctc gcgctccgcc ctcaggcaca gcatccccac gggcctccac gccaacctgt 60
ccgaggnccg ccccgtgggt ccggcccgcc gtggcgcctc atcgctgctc ggcccggaag 120
gcttnttcct tggcaagatg ggattccggg aggcggnggc ggccggagac gtggatttgc 180
ctcaggtgcg gagccgcagc tacaggagga tgctcgcgag gacccccaga gctccgcccg 240
gagggtactg tgaggccgtt aggagctggc ggnggatgac ttccgcattc aaacactgga 300
gccatcacac ggaagcacga ggagggtatc ctcggcagct actcccggtc gctcaaggtg 360
tctntcgctc gccctctagg ngcgggagga gctcgaggcc caactaanct gcttccggga 420
gctgctgggc agggccccca cgcacgcgga cgggcaccag cacgtgcacg tgctcccagg 480
nggacagacg ccttcgtggg cctgancact tgcggccggn acatgttccc tcacccgcgg 540
gtccgggccc ttggcgcggg tcctggaagg taccctacgg gccacaccct gacagccgaa 600
ctgatggccc accccggcta ccccangtgt gcctccaccc g 641

<210> 447
<211> 652
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(652)
<223> n = A,T,C or G

<400> 447
gaattcgaac cccttcgctt ttagaaaatt gtatatgcag ctggatgaag gcagcctcac 60
ctttaatgcc aacccagatg agggagtgaa ctactttatg tccaagggta tcctggatga 120
ttcgccaaag gaaatagcaa agtttatctt ctgtacaaga acactaaatt ggaaaaaact 180
gagaatctat cttgatgaaa ggagagatgt cttggatgac cttgtaacat tgcataattt 240
tagaaatcag ttcttgccaa atgcactgag agaatttttt cgtcatatcc atgcccctga 300
agagcgtgga gagtatcttg aaactcttat aacaaagttc tcacatagat tctgtgcttg 360
caaccctgat ttaatgcgag aacttggcct tagtcctgat gctgtctatg tactgtgcta 420
ctctttgatt ctactttcca ttgacctcac tagccctcat gtgaagaata aaatgtcaaa 480
aagggaattt attcgaaata ccccgcgcgc tgctcaaaat attagtgaag aattttgtan 540
ggcatcttta tgacaatatc taccctattt gggccatggn ggctggcata aaaaagcacc 600
aattggctaa ggactttcaa gtttttttact ttcagaactt aaaagcttac cc 652

<210> 448
<211> 677
<212> DNA
<213> Homo sapiens

<400> 448
gaattcgaac cccttcggcg cctggcagag gtgaaggact ccctggacat cgaggtcaag 60
cagaacttca ttgacccccct ccagaacctg tgcgagaaag acctgaagga gatccagcac 120
cacctgaaga aactggaggg ccgccgcctg gactttgact acaagaagaa gcggcagggc 180
aagatccccg atgaggagct acgccaggcg ctggagaagt tcgaggagtc caaggaggtg 240
gcagaaacca gcatgcacaa cctcctggag actgacatcg agcaggtgag tcagctctcg 300
gccctggtgg atgcacagct ggactaccac cggcaggccg tgcagatcct ggacgagctg 360
gcggagaagc tcaagcgcag gatgcgggaa gcttcctcac gccctaagcg ggagtataag 420
ccgaagcccc gggagccctt tgaccttgga gagcctgagc agtccaacgg gggcttcccc 480
tgcaccacag cccccaagat cgcagcttca tcgtctttcc gatcttccga caagcccatc 540
cggacccccta gccggagcat gccgcccctg gaccagccga gctgcaaggc gctgtacgac 600
ttcgagcccg agaacgacgg ggagctgggc ttcatgaggg cgacgtcatc acgctgacca 660

accagatcga tgagaac 677

<210> 449
<211> 603
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(603)
<223> n = A,T,C or G

<400> 449
ttttttgtan aaagagacat ttaatacttc tgtttacaaa attcaggcgt acatttcagt 60
ttgccctgga ccgtgcccaa agctgtgtgc tcatctctgc gcccctcatg tacttctgac 120
gagggggtg cagggcaggg cagagcagag cctggggtcc ggaggcttca ctggaccaca 180
gggggagggg aatgtgaatg tggcctggcc canagaactc cccatttcat cgattttgca 240
ttgggcgata gaggaagcag atgtcggggc tgcctgcctt ggtctanagg agatggctgg 300
ggccacttcc cacagggtga agtggcagcg gctcagcaag gggagcctgg ccaccagggg 360
ctgggacatg cgctcactgg aacctttgtg cttggccctc ggcagcgcgg ctgtggtccc 420
gtgtgaggtg tgctggggtg gggtgtgggt ggctggtggt ggcagcttgt gccagagtga 480
cacaggcctc cctgggttgg gatgggggca agttaaaaag ctgaaaaggt acttggcttt 540
ctgagggcgg gcttgggagc aggccctgca gganaccatg ttctctgtcc tcagcagatc 600
cac 603

<210> 450
<211> 678
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(678)
<223> n = A,T,C or G

<400> 450
gaattcgaac cccttcgcat caatataana tgccacccat ctgcagttaa tttcttttcc 60
tcatcatgtg attaaaagtg gtgattcagt gggaactggg aatgttttta gctggtggta 120
gaaggctgcc tacactgggc actgttttag attctcatat catttaaaca gcaaggaggt 180
tcagggaaga ataaccgtag ccttgggtaa tccactaggg cttttgtgag taggagagct 240
gatacctcac attcttagca ggtgaaaact tgccatgatg gaaacagata gtgaagagtt 300
actgacgtat cccaaattat atgctgtgac ataaattccc agcatgccca gccctgattt 360
ctgagttcat aagtaattct agtgaacctt agtaggaatt ctgggtaaga aaatgaggtt 420
gccattggtc ttgtttgcat caccaagacc agacatccag aagagcccct caccttgaaa 480
agcagacaga ttttaaatta accccctcct tcccactcac cttcatctcc ctaagagttt 540
tggccattta attccacatt ttgaaaggaa tacattggtg aaatttggga agagaatctg 600
tgctatgcaa tgtttcatta aaatcttcag tttttcaagt ctctctaaaa ataatttgta 660
gatctatctt ggatggat 678

<210> 451
<211> 651
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(651)
<223> n = A,T,C or G

<400> 451
tttttcatca acaaaaatca agcattttcn ttttttgaa acaagaaaag cgcatcgtan 60
aaaccaagat tctgtacaat attctaacat tatatgtaca taaaattata ttactcataa 120
ctatattgaa aagtcttatt tgtagaatat ggctggcaac aaagaaagac ccataccatt 180
tagcgtttga agcagggcag gtagcaagag aacattagca aagacacctt tgtgcctgga 240
tacacaatcc tgctactaag ttatgtgact aaccagcaca ctctaagttc tgtggtttgt 300
tcgttgtttc acattctagt agggaattct gcagcaggcg atgcgaaaaa naanacatgg 360
tcaaatgaaa tgtgaaatgc tgtttaaaat ctgcatattg gctatgataa tgggtttgng 420
aatccaagtt gcattggaag ttcactcatt ctccattcat tatgcatgcc tccagtgatt 480
taatgaattt cagcaggngg aaaagacagc tttgaacaga tcagatgggc tgtgagtcan 540
attcttgatt ctttttcctc atttggctcc tgaatgttgc anaaaactgg ttttgtacac 600
tggggaagga gagagtgaag accctccagt tggttcctca gtcagctccg t 651

<210> 452
<211> 679
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(679)
<223> n = A,T,C or G

<400> 452
gaattcgaac cccttcgcat tgctcagccn nctaccactg ctaagagcca tctccaccag 60
aagcctggcc agacctggaa gaacaaagag catcatctct ctgacagaga gtttgtgttc 120
aaagaacctc agcaggtagt acgtagagct cctgagccac gagtgattga cagagagggt 180
gtgtatgaaa tcagcctgtc acccacaggt gtatctaggg tctgtttgta tcctggcttt 240
gttgacgtga aagaagctga ctggatattg gaacagcttt gtcaagatgt tccctggaaa 300
cagaggaccg gcatcagaga ggatataact tatcagcaac caagacttac agcatggtat 360
ggagaacttc cttacactta ttcaagaatc actatggaac caaatcctca ctggcaccct 420
gtgctgcgca cactaaagaa ccgcattgaa gagaacactg gccacacctt caactcctta 480
ctctgcaatc tttatcgcaa tgagaaggac agcgtggact ggcacagtga tgatgaaccc 540
tcactaggga ggtgccccat tattgcttca ctaagttttg gtgccacacg cacatttgag 600
atgagaaaga agccaccacc agaagagaat ggagactaca catatgtgga aagagtgaag 660
ataccettgg atcatggta 679

<210> 453
<211> 630
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(630)
<223> n = A,T,C or G

<400> 453
gaattcgaac cccttcggaa ggccaagggn ntagaaggng gctccggccc cagctgtcgt 60
gaagaagcag gaggctaaga aagtggtgaa tcccctgttt gagaaaaggc ctaagaattt 120
tggcattgga caggacatcc agcccaaaag agacctcacc cgctttgtga aatggccccg 180
ctatatcagg ttgcagcggc agagagccat cctctataag cggctgaaag tgcctcctgc 240
gattaaccag ttcacccagg ccctggaccg ccaaacagct actcagctgc ttaagctggc 300
ccacaagtac agaccagaga caaagcaaga gaagaagcag agactgttgg cccgggccga 360
gaagaaggct gctggcaaag gggacgtccc aacgaagaga ccacctgtcc ttcgagcagg 420
agttaacacc cgtcaccacc ttggtggaga acaagaaagc tcagctggtg gtgattgcac 480
acgacgtgga tcccatcgag ctggttgtct tcttgcctgc cctgtgtcgt aaaatggggg 540

tcccttactg cattatcaag ggaaaggcaa gactgggacg tctagtccac aggaagacct 600
gcaccactgt cgccttccac aggtgaactc 630

<210> 454
<211> 677
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(677)
<223> n = A,T,C or G

<400> 454
gaattcgaac cccttcgccc gcatgcggna catccccttg gccccagggt cagactggcg 60
cgatctgccc aacatcgagg tgcggctctc agacggcacc atggccagga agctgcggta 120
tacccaccat gacaggaaga acggccgcag cagctctggg gccctccgtg gggtctgctc 180
ctgcgtggaa gccggcaaag cctgcgaccc cgcagccagg cagttcaaca ccctcatccc 240
ctggtgcctg ccccacaccg ggaaccggca caaccactgg gctggcctct atggaaggct 300
cgagtgggac ggcttcttca gcacaaccgt caccaacccc gagcccatgg gcaagcaggg 360
ccgcgtgctc cacccagagc agcaccgtgt ggtgagcgtg cgggagtgtg cccgctccca 420
gggcttccct gacacctacc ggctcttcgg caacatcctg gacaagcacc ggcaggtggg 480
caatgccgtg ccaccgcccc tggcaaagcc attggcttgg agatcaagct ttgtattgtt 540
ggccaaagcc cgagagagtg cctcagctaa aataaaggag gaggaagctg ctaaggacta 600
gttctgcctt cccgtcaccc ctgtttctgg caccaggaat cccccacaat gcacttgatg 660
gtggggtttt aacatgt 677

<210> 455
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(598)
<223> n = A,T,C or G

<400> 455
ttttttggtt tataggagag atttatttga agaaatatta caacatataa aaactacata 60
aagtcttaat ttccactcat acagtggtag atttgatata atgcataata aaaaactttt 120
aaaatccaga atgcacaaag tactgcacaa tttgatcact aaatcattag ttgataagcg 180
aacctcacac aacagcttca tgtcagccaa ggccacaaac accatgtacc acacatgtga 240
acggacagat tgacatgtta aaaacacaac atcagtgcat gttggggatt cctggtgcca 300
gaaacagggg tgacgggagg gcagaactag tccttagcag cttcctcctc ctttatttta 360
gctgaggcac tctctcgggc tttggccaac atacaaagct tgatctccaa gccaatggct 420
ttggccaggg gcggtggcac ggcattgccc acctgccggt gcttngtcca ggatgttgcc 480
cgaagagccg gtaggtggtc aagggaagcc cctggggaag cgggcacact cccggacgct 540
naccacacgg tgctgntttt gggtggagca ccgcggcctt gcttgcccat gggctcgg 598

<210> 456
<211> 574
<212> DNA
<213> Homo sapiens

<400> 456
ggaattcgaa ccccttcggg gcggggagcc ccgtagaacc gagggggtcg gcccgggggt 60
cccgggggag gtggagatgg tgaaggggca gccgttcgac gtgggcccgc gctacacgca 120
gttgcagtac atcggcgagg gcgcgtacgg catggtcagc tcggcctatg accacgtgcg 180

caagactcgc gtggccatca agaagatcag ccccttcgaa catcagacct actgccagcg 240
cacgctccgg gagatccaga tcctgctgcg cttccgccat gagaatgtca tcggcatccg 300
agacattctg cgggcgtcca ccctggaagc catgagagat gtctacattg tgcaggacct 360
gatggagact gacctgtaca agttgctgaa aagccagcag ctgagcaatg accatatctg 420
ctacttcctc taccagatcc tgcggggcct caagtacatc cactccgcca acgtgctcca 480
ccgagatcta aagccctcca acctgcttca tcaacaccac ctggcgacct ttaaaatttg 540
tgaatttccg gcctggcccc cggattgccc gaat 574

<210> 457
<211> 546
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(546)
<223> n = A,T,C or G

<400> 457
tttttgaca catctctata tttatatatt agacgggtca gggaggtggc aggggcgccg 60
ggctctccac gccccccagc tccacttctg ctcaccacac acagaagcag cgagggcacg 120
cgaagtgaca gctttgacag ggaggggatt cggcccggcc tggctcctca gggatgctag 180
cccttgagac taaggaatgt tccttcaggg aaactagggt ggggtttgaa tganatgagg 240
ggggcaggca tggccctgag tccctactca gcgcccccca ccctccacct ctgcccttca 300
gcaggttggg gcagccagaa cccttccatt ccagaactgc cagagactgg gacgctgggg 360
aaggtaaggg cgcagcagca gcagcgggag attgaactgg ggccacctga gctcccgagg 420
ccccgtgggg agggcgggtg gggaggaaaa ggccttggcc tgcctgaagc tggaggcctc 480
agcaaaggag agaggtggcc aggcccatgc tccaccccgg cctgggctgc caanggtccc 540
gggctg 546

<210> 458
<211> 674
<212> DNA
<213> Homo sapiens

<400> 458
gaattcgaac cccttcggta ttattaagaa ctaagagaat agcttgccag atacaaatgg 60
aaacaccttc caaatgagtc ggagaaaatg tcttgcagta ttatgggtaa aatagcaaag 120
agcttgggaa tacagtttgc taatatcaag tccttaacaa cgaccattct tcattcaaga 180
ttagttgtgt ataaatacat gcttcttcag gagttgactt agaaaacaag caaacaaaca 240
aacatcagaa actatttaca actgggagca atccttgaag aacataaaga atataaatat 300
caacaaaggc tgaaaactct tttttagatt aaagatcaaa tggacatgtc atcggaatgt 360
attgtatggc tcttgattaa atcctggagc aaagtggaga gtgaggaaca actgtaaaga 420
atgtgaatac ggactgtgta ttagataaca gtaccataaa tttcctggat gggataatta 480
tgttgtgact atgtaagaga atattttgcc cttagaagat atatgatgaa gcatttagaa 540
gtaaagtatc atgacatctt gcaaataact ttcaagtgat tcagccagat atataaaaat 600
tatatataac acattatata atttatattt atataattat aatacattat ataatttata 660
cattataatt atat 674

<210> 459
<211> 682
<212> DNA
<213> Homo sapiens

<400> 459
ttttttaaa tccatggctt gttaattgtc atcccagtta tttacatgtg actatagaga 60
ctgcattctc ccagctgcca ggccgccagg gctttgccac tggtataatt tataacacga 120
ctaattaaaa tgaatttgct tgcaataagg ttctgtgtgc tatttgtggg agaggagtta 180

ttaaaatttt cagtacagta atagtaaact tgaatgcaaa gtaataataa tcatacattt 240
ttaattacat gtttaatacc catttggcta atgtagaact attctgaaaa ttacttggga 300
tcagcacaat gtctttttgt gcttagtagt atccaaagac atccttctga atgggcttag 360
caatatgcac tgtcatcaag atacagctgt ttgatgacag acacacagtg tgttcctatg 420
atactttgca caagatcagc tatgacaaat acaagttcat tttgcttatt gcaggcaaat 480
aatgtccttt gcaggaactt ggatggagcc agaggccatt attctaagtg aaatacctca 540
ggagtggaaa accaaatacc atatgttctc acttacaagt gggaactaag ctatgggtac 600
acaaacgcat atagagtaat ggactctggc gactcatact acatattgag tacaatgtac 660
actacttggg tgatgggtgc ac 682

<210> 460
<211> 663
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(663)
<223> n = A,T,C or G

<400> 460
gaattcgaac cccttcgcgg ggcgcgcgag cggcgccagc tcggggcagc ggaacccaga 60
gaagctgagg gggcggtagc ggcggcgacg gcgacgacga cgactcccgc gcgtgtgccc 120
agcctcttcc cgccgcagcc gccctttcc tccctccctt acgtccccga gtgcggcagt 180
accgcctcct tcccagccgc gcggcttcct ccagacctct cggcgcgggt gagccctatt 240
cccagaggca ggtggtgctg accctgtaac ccaaaggagg aaacagctgg ctaagctcat 300
cattgttact ggtgggcacc atgtccttga agcttcaggc aagcaatgta accaacaaga 360
atgaccccaa gtccatcaac tctcgagtct tcattggaaa cctcaacaca gctctggtga 420
agaaatcaga tgtggagacc atcttctcta agtatggccg tgtggccggc tgttctgtgc 480
acaagggcta tgcctttgtt cagtactcca atgagcgcca tgcccgggca gctgtgctgg 540
gagagaatgg gcgggtgctg gccgggcaga ccctggacat caacatggct ggagagccta 600
agcctgacag acccaagggg ctaaaganaa gcagcatctg gcatatacag gctcttcgac 660
tac 663

<210> 461
<211> 612
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(612)
<223> n = A,T,C or G

<400> 461
tttttgggga tccaatctnt ttattgtcag ggtcccctcc ctgnggcccc ccgccaaacc 60
tatagaaaaa acccaagcct gggagtgtcc tggggagggg aggtagtatg gggaaacccc 120
tgtgctctac cctntggcct gggcagtgca nacagggagg gctcatgggg aaggagtagg 180
ccagtaactc cacctgcana ggacatggca ctggctggga tgcgttgggg gaggaggcgc 240
ctgctgccag ctttcctntg gtacccgctg gggggtggca tccagggttg ggtgcccggc 300
ttgaggcctg gggcagcgat gcccttcacc tgctggnggc cattgctcct gtcaggctgc 360
ttactgcaag gccccatcat ccgcgtctgt gtcctggctg tgttccagct cttcctcgct 420
gngtgtcagg agcccttcct catcgccgtc gtctcgggtc cgtgcttccc cctggggcag 480
gcctgcctca naagttgtgt tctcttgggg ggctggtggc cggttgttgc caccgcaccg 540
caccaccact ggcaccggca ccgntgcacc accaccgccg ccgccgccgn tggngccacc 600
ttcatcaccc tt 612

<210> 462

<211> 672
<212> DNA
<213> Homo sapiens

<400> 462
gaattcgaac cccttcggat ggaaggggcc ggggcagcgt cggggaaagg aagggccgga 60
ggcgcggcgg cgggcggccg agaggggcgg cggcggcggc ggcggcgggg ttcccgcgcc 120
gcggagcccg gcccgagagc cgcgtccacg ttcctgcctc ctgctcccgc cgccctgggg 180
cgccgccatg acgcccgatc tgctcaactt cagccccaga tgtcaccaag ctctcggact 240
ctaacaagga gaacgcgctg cacagctaca gcacccagaa gggccccctg aaggcagggg 300
agcagcgggc gggctctgag gtcatcagcc ggggtggccc tcggaaggcg gacgggcagc 360
gtcaggcctt ggactacgtg gagctctcgc cgctgaccca ggcttccccg cagcgggccc 420
gcacccccagc ccgcactcct gaccgccctg gccaagcagg aggagctgga gcgggacctg 480
gcccagcgct ccgaggagcg gcgcaagtgg tttgaggcca cagacagcag gaccccagag 540
gtgcctgctg gtgaggggcc gcgccggggc ctgggtgccc cctgactgag gaccagcaaa 600
accggcttag tgaggagatc gagaagaagt ggcaggagct ggagaagctt gcccttgcgg 660
gagaataacc gg 672

<210> 463
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(562)
<223> n = A,T,C or G

<400> 463
tttttaaag tataaagtgt tttggaaaaa aaggaaaaan ntctatataa aaatctcttc 60
acatataaaa tcctgaagaa ggtgcaaggt gagacccagt gcgaggggcg tgctcagata 120
tgcagtgtgt gtgtgtgtgt gtgtgtgtgt gtatccgtgt gtacatgtgt gcacgtgtgt 180
gcgtatgtgt ctgtgtgtct gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt ggtgggtgca 240
agtgcacgtg tggcccacag agggtgggga gaaagcttgg ctttttactt ccatccagga 300
gggaaggagg gcggctggtc ctccagcctg gagggtctgc agctgggcgg gacctctact 360
cagccaggct gttgcgcatc gactccttct cctggagggc ggccatggca agacgcaggt 420
gctccttcag ctgctcgatc tcccgctcag accgtgtctt gatgtggctc aactccacat 480
agacgtcctg gtactttccc naggtgaagc gcttgtcctt ctgcatcatc tggagctcgt 540
cccggaggca ctgcaccttc ct 562

<210> 464
<211> 553
<212> DNA
<213> Homo sapiens

<400> 464
gaattcgaac cccttcggga ccaggaaccc aggagagcat ggccacgctg cgccggcttc 60
gggaggcgcc gcggcactta ctggtttgcg agaaatccaa cttcggcaac cacaagtcgc 120
gccaccggca tcttgtgcag acgcactact ataactacag ggtttcattt ctcattcctg 180
aatgtgggat actatcggaa gaactgaaaa acctggtcat gaacactgga ccctattact 240
ttgtgaagaa tttacctctt catgaattaa ttacacctga attcatcagt acctttataa 300
agaaaggttc ttgctatgca ctaacataca atacacatat tgatgaagat aatactgttg 360
ccctgctacc aaatgggaaa ttaattttgt cactggataa agacacttat gaagaaactg 420
gacttcaggg tcatccatct cagttttctg gcagaaaaat tatgaaattt agttcagaag 480
aatcgacaat gatgtcatat ttttccaagt accaaattca ggagcatcag ccaaaagtag 540
cactgagccc gtt 553

<210> 465

<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 465
tttttggaag aaaacacgat ttttaatttt tattttttat gggggacagn gatcatttgc 60
cccaacagcc atntgaagcc aatagtcctg attattaaaa atcacaaagt tatataaatg 120
ntctcctcct tttcgaaaac catgttcatt tttttcccaa naaacagggc tgtctgcaaa 180
gccttgaacg gacagngtaa cccatggagc taacttcggt tcatcaaagt agngacagan 240
atgttccaat agganacaga tcttntntgg aagtatgaag ccagngattg tacacaaata 300
agcttttgcc accactgtgc ttggctcagg acagcaatag gttgatatga aattattagg 360
ctcattattt aggncgacat tac 383

<210> 466
<211> 673
<212> DNA
<213> Homo sapiens

<400> 466
gaattcgaac cccttcgctc cctcctgcac gcaatggtgg cctatgatcc cgatgagaga 60
atcgccgccc accaggccct gcagcacccc tacttccaag aacagaggaa aacagagaag 120
cgggctctgg gcagccacag aaaagctggc tttccggagc accctgtggc accggaacca 180
ctcagtaaca gctgccagat ttccaaggag ggcagaaagc agaaacagtc cctaaagcaa 240
gaggaggacc gtcccaagag acgaggaccg gcctatgtca tggaactgcc caaactaaag 300
ctttcgggag tggtcagact gtcgtcttac tccagcccca cgctgcagtc cgtgcttgga 360
tctggaacaa atggaagagt gccggtgctg agacccttga agtgcatccc tgcgagcaag 420
aaggtagcgc ggaaccagct tctctgacgg cgctgctctt cgacccagcc caggccgcca 480
ctgaattttg tgtctgtaat ttttctttga cagacagatc cgcagaagga ccttaagcct 540
gccccgcagc agtgtcgcct gcccaccata gtgcggaaag gcggaagata actgagcagc 600
accgtcgtct cgacttcgga ggcaacacca agcccgaccg ggccaggcct gggtgatctg 660
ctgctgagac gcc 673

<210> 467
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(373)
<223> n = A,T,C or G

<400> 467
tttttactgg aacgacagct tattntttaa taaaagtcag gggngtcagc agngtcactg 60
gtaanacatg atggcgctcc acgactgacc agcagcgctg ggaagggaca cgcanaaccc 120
accttccaac cacgcccaac acatnacana aatgcctgct cgtttgtttt gattcatata 180
caaagttaca aagtatttcc tgccccaaat tnttaacgaa aatgaaagaa aaccctanaa 240
tgcgggggtt ttacaagtat attagcccan aacatcctag gcagctgcnc gggccgcggg 300
tgcggcaggg cgcagggcaa cacccaaagc cccggccagc gcgaaacgga cgcaggcgca 360
tccccagccc tcc 373

<210> 468
<211> 573

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(573)
<223> n = A,T,C or G

<400> 468
gaattcgaac cccttcgctg ctgtcctact tgatgcttgt cactgtcatg atgtggcccc 60
tngctgtgta ccaccgactg tgggatcgag catatgtgcg gctgaagcca gctctgcagc 120
ggctagactt cagtgtccgt ggctacatga tgtccaagca gagagagaga caattacgcc 180
gcagagctct ccacccagaa cgagccatgg acaaccacag tgacagcgaa gaggagcttg 240
ctgccttctg tcctcagctg gacgattcta ctgttgccag ggaattggcc atcacagact 300
ctgagcactc agacgctgaa gtctcctgta cagacaatgg cacattcaat ctttcaaggg 360
gccaaacacc tctaacggaa ggctctgaag acctagatgg tcacagtgat ccagaggaat 420
cctttgccag agaccttcca gacttccctt ccattaatat ggatcctgct ggcctggatg 480
atgangacga cactagcatt ggcatgccca gcttgatgta ccgttctccg ccaggggct 540
gaggagcccc aaggccccac ctgccagccc ggg 573

<210> 469
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(635)
<223> n = A,T,C or G

<400> 469
tcncgatcta gaactaggtt ggacaggctt gctcaagttt caccagagtt antactggcc 60
tctgttcgca gagtttttag ttnnacactg cagaattggc agactacacg gtttatggaa 120
gttgaagtag caataagatt gctgtatatg ttggcagaag ctcttccagt atctcatggt 180
gctcacttct caggtgatgt ttcaaaagct agtgctttgc aggatatgat gcgaactgta 240
agtatactgg agataatttt gaccataaat ttctgttttc agtataagct aatgggagtt 300
ccttaattgt tagagcttag tatatgttaa taccggggca ttttgatgtt gcaataaata 360
agaagaggtt tcctaacttt ttcctgatct agctggtaac atcaggagtc agttcctatc 420
agcatacatc tgtgacattg gagttcttcg aaactgttgt tagatatgaa aagtttttca 480
cagttgaacc tcagcacatt ccatgtgtac taatggcttt cttagatcac agaggtctgc 540
ggcattccag ngcaaaagtt cggagcagga cggcttacct gttttctaga tttgtcaaat 600
ctctcaataa gcaaatgaat cctttccttg aggat 635

<210> 470
<211> 593
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(593)
<223> n = A,T,C or G

<400> 470
gaattcgaac ccttcggtat taacaaatat ntacatttct atttttataa tccataagga 60
tatgcctgtt ttaaataaca tacatattaa caatatctat caggaaaacc ctcaagacag 120
cttctagtta aaaccttngn tgctgtcctc tcaaactata tttataaaaa tttgctaggg 180
ccaaatccat acttgcagaa taattcatca aattttattt ttaagngaaa agtaaccttt 240

caggcatttc agcagcatac attgacaatc tagggtatat atgtatgtat gtttcttatt 300
gtatgtctat atatgtatgt ggggaggaca ggagtgaatg ttcacacact tttcttgcgt 360
actcaactaa attggagaat gtttctgaag aaaattggat gaaattagct gctgagattg 420
agtttctgcc ttaaaatctg aaacaaaaaa agggacaaat tgctggtang atctactgac 480
tgtngccatc accagaacac ttagtttctt cccagacatg aatttcctga caggctctga 540
gccagaaaca cactgtgggc gtgcatntgg gtcaccctgg atatgcctcc act 593

<210> 471
<211> 581
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(581)
<223> n = A,T,C or G

<400> 471
tttttttaat cangggacat ttattaacat gcttcaaaag tgaccaaagt gtccagccag 60
cacaatagcc gaggcaatca acgttctctt agtgtgtgat ctcgtccaaa acaccaaata 120
aataggttta ggaataacct caaataaatt gtaatttaac ttcgcccaaa attatacatc 180
ctctactgct cttccctgct cctgtaaaga tactagcggg aggggagaaa gctcaaatga 240
ctctgtaatt tagaattaca accagagaag aaatacttca agcacaataa agacgttcca 300
ttgaagagcg acattcattc tggaatgttt gttttgaaaa caactcttnt gggggaattc 360
aaaaggtact gaacaaagca acataaagta agttttgggt tgttttgcaa aataaaaata 420
tacaattgag tggaccagat ggcaaaaaca taccaattac aatctgaatg ctatatttaa 480
aacccttaaa ttctgaaggc ctgaatatca acaaacctat ttatgtttat gatcctaaaa 540
agacattaaa tattattaaa cccccaactt ccaaaacata g 581

<210> 472
<211> 674
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(674)
<223> n = A,T,C or G

<400> 472
gaattcgaac cccttcggat ggcgtgatgt ntcacagaaa gttctccgct cccagacatg 60
ggtccctcgg cttcctgcct cggaagcgca gcagcaggca tcgtgggaag gtgaagagct 120
tccctaagga tgacccgtcc aagccggtcc acctcacagc cttcctggga tacaaggctg 180
gcatgactca catcgtgcgg gaagtcgaca ggccgggatc caaggtgaac aagaaggagg 240
tggtggaggc tgtgaccatt gtagagacac cacccatggt ggttgtgggc attgtgggct 300
acgtggaaac ccctcgaggc ctccggacct tcaagactgt ctttgctgag cacatcagtg 360
atgaatgcaa gaggcgtttc tataagaatt ggcataaatc taagaagaag gcctttacca 420
agtactgcaa gaaatggcag gatgaggatg gcaagaagca gctggagaag gacttcagca 480
gcatgaagaa gtactgccaa gtcatccgtg tcattgccca cacccagatg cgcctgcttc 540
ctctgcgcca gaagaagccc acctgatgga gatccaggtg aacggaggca ctgtggccga 600
gaagctggac tgggccccgc gagangcttg agcacaggta cctgtgaacc aagtgtttgg 660
gcaggatgaa aatg 674

<210> 473
<211> 646
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(646)
<223> n = A,T,C or G

<400> 473
tttttcagn ggaaaataac ttttattgan accccaccaa ctgcaaaatc tgttcctggc 60
attaagctcc ttnttccttt gcaattcggt ctttcttcag nggtcccatg aatgctttct 120
tctcctccat ggtctggaag cggccatggc caaacttgga ggnggtgtca atgaacttaa 180
ggtcaatctt ctccanagcc cgccgnttcg tctgcaccag caaggacttg cggagggtga 240
gcacccgctt cttggttccc accacacagc ctttcagcat gacaaagtca ttggtcactt 300
caccatagng gacaaagcca cccanagggt tgatgctctt gtcanatagg tcatagtcag 360
tggaggcatt gttcttgatc agcttgccgt ccttgataag gtagccctgg ccaatcttat 420
aaatcttctt gttgatctca gtgcggtgat ggtagccttt ctgcccagcg cgtgccacag 480
agaaggctac acgagcagga tgccatgccc caatacaggc caccttgcgc aggcctcggt 540
gggtcttgcg gggcagcttc ttggtgtgcc aacgactggt gacccctttg tagcctttgc 600
ccttggtcac cccgatgacg tcgatcatct catcctgccc aaacac 646

<210> 474
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(544)
<223> n = A,T,C or G

<400> 474
gaattcgaac cccttcggca gcacactccc antcggccgc agcctgacac gccgcgcggc 60
cccccagtct cccgcggctg ctccccagg catggcacag ggcctcgcct cactatggca 120
gcagcacggc acagcacgct cgacttcatg ctcggcgcca aagctgatgg tgagaccatt 180
ctaaaaggcc tccagtccat tttccaggag caggggatgg cggagtcggt gcacacctgg 240
caggaccatg gctatttagc aacctacaca aacaagaacg gcagctttgc caatttgaga 300
atttacccac atggattggt gttgctggac cttcagagtt atgatggtga tgcgcaaggc 360
aaagaagaga tcgacagtat tttgaacaaa gtagaggaaa gaatgaaaga attgagtcag 420
gacaagtact gggcgggtga aacgattacc acccatagtg cgaggaggag ccatcgacag 480
atactggccc accgncgacg ggcgccttgg ttgaatatga catagaatga agtggtatat 540
gacg 544

<210> 475
<211> 578
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(578)
<223> n = A,T,C or G

<400> 475
gaattcgaac cccttcggga gaaccccatg ngggaacttc gcatccgcaa actctgtctc 60
aacatctgtg ttggggagag tggagacaga ctgacgcgag cagccaaggt gttggagcag 120
ctcacagggc agacccctgt gttttccaaa gctagataca ctgtcagatc ctttggcatc 180
cggagaaatg aaaagattgc tgtccactgc acagttcgag gggccaaggc agaagaaatc 240
ttggagaagg gtctaaaggt gcgggagtat gagttaagaa aaaacaactt ctcagatact 300
ggaaactttg gttttgggat ccaggaacac atcgatctgg gtatcaaata tgacccaagc 360
attggtatct acggcctgga cttctatgtg gtgctgggta ggccaggttt cagcatcgca 420

gacaagaagc gcaggacagg ctgcattggg gccaaacaca gaatcagcaa agaggaggcc 480
atgcgctggt tccagcagaa gtatgatggg atcatccttc ctggcaaata aattcccgtt 540
tctatccaaa agagcaataa aaagttttca gtgaaaaa 578

<210> 476
<211> 619
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(619)
<223> n = A,T,C or G

<400> 476
ggaattcgaa ccccttcgct cctgcctgtc cgccatgttt tcaggncggg nctggcttgg 60
tcttcccccg taaggaaatg gccggggagc tccaggggac ccaggcgccg tcgcttcggc 120
ggagcctggg ctgaccagcc aggacagcgg ggtaaacccg aacaattctg cgcgaggtag 180
ggaggccatg gcgtccggca gtaactggct ctccggggtg aatgtcgtgc tggtgatggc 240
ctacgggagc ctggtgtttg tactgctatt tatttttgtg aagaggcaaa tcatgcgctt 300
tgcaatgaaa tctcgaaggg gacctcatgt ccctgtggga cacaatgccc ccaaggactt 360
gaaagaggag attgatattc gactctccag ggttcaggat atcaagtatg agccccagct 420
ccttgcagat gatgatgcta gactactaca actggaaacc cagggaaatc aaagttgcta 480
caactatctg tataggatga aagctctgga tgccattcgt acctctgaga tcccatttca 540
ttctgaaggc cggcatcccc gttccttaat gggcaagaat tttccgcttc taccttgctg 600
gatcttgcga aacactagt 619

<210> 477
<211> 674
<212> DNA
<213> Homo sapiens

<400> 477
gaattcgaac cccttcgggg tgttcgactg ctagagccga gcgaagcgat gcctaaatca 60
aaggaacttg tttcttcaag ctcttctggc agtgattctg acagtgaggt tgacaaaaag 120
ttaaagagga aaaagcaagt tgctccagaa aaacctgtaa agaaacaaaa gacaggtgag 180
acttcgagag ccctgtcatc ttctaaacag agcagcagca gcagagatga taacatgttt 240
cagattggga aaatgaggta cgttagtgtt cgcgatttta aaggcaaagt gctaattgat 300
attagagaat attggatgga tcctgaaggt gaaatgaaac caggaagaaa aggtatttct 360
ttaaatccag aacaatggag ccagctgaag gaacagattt ctgacattga tgatgcagta 420
agaaaactgt aaaattcgag ccatataaat aaaacctgta ctgttctagt tgttttaatc 480
tgtcttttta cattggcttt tgttttctaa atgttctcca agctattgta tgtttggatt 540
gcagaagaat ttgtaagatg aatacttttt tttaatgtgc attattaaaa atattgagtg 600
aagctaattg tcaactttat taaggattac tttgtctgcc cacccctagt gtaaaataaa 660
atcaagtaat acat 674

<210> 478
<211> 663
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(663)
<223> n = A,T,C or G

<400> 478
ttttttttaag ctttcacaat ttttattaaa tcctagtcta nttgaacaat atctgatgtt 60

acagacatca tcccatggtg aacatgttta ataagtgaaa gcaagtcaga catctcatct 120
aagtcattat tttctgcaga ctaagcaata actacacaga acactatggg taaacaaaca 180
cctgctcagt tttcacacaa gccatgttgt ttatcaaatt agatctgcta atattgaata 240
cagtagattc ggtgattgta gttctcatat aagtatctta ttgagataac attttgacag 300
tttcactgac tttccaaata agcataccat aatcaaagaa aagaataaag agtgaagtaa 360
aaactgaaca tgaagagatt aagttattaa aggaaaatga agtaaataaa aagagtgaaa 420
aaccattggg ggtggaagtc aaacaagcct agacatttga ttggaagaga aaagatcaaa 480
tatgaagttc acaaaccaaa agtttataaa ctcaatgcaa tacaaatcct ttttattgta 540
aaagctgagt tgaaactaaa agatctataa aaactgttac ttttggcctt aaacagtacc 600
aactcttatg atcaaaaaag gccacacagt taagattgna ttacttgatt ttattttaca 660
cta 663

<210> 479
<211> 673
<212> DNA
<213> Homo sapiens

<400> 479
gaattcgaac cccttcgaat gaagaactct ccagggatct agtgaataaa ctaaaaccct 60
acatgagctt cctgactcag tgccgtcccc tgtcagcgag catgcacaac gccatcaagt 120
tccttaacaa ggaaatcacc agtgtgggca gttccaagcg ggaagaggag gccaagtcag 180
aacttcgagc agccattgat cggtatgtgc aagagaagat tgtgctagca gctcaggcaa 240
tttcacgctt tgcttaccag aagatcagta atggagatgt gatcctggta tatggatgct 300
catctctggt atcacgaatt cttcaggagg cttggacaga gggccggcgg tttcgggtgg 360
tagtggtgga cagccggcca tggctggaag gaaggcacac actacgttct ctagtccatg 420
ctggtgtccc agcctcctac ctgctgattc ctgcagcctc ctatgtgctc ccagaggttt 480
ccaaggtgct attgggagct catgcactct tggccaacgg gtctgtgatg tcacgggtag 540
ggacagcaca gttagccctg gtggctcgag cccataatgt accagtgctg gtttgctgtg 600
aaacatacaa gttctgtgag cgtgtgcaga ctgatgcctt ttgtctctaa tgagctagat 660
gaccctgatg atc 673

<210> 480
<211> 203
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(203)
<223> n = A,T,C or G

<400> 480
gaattcgaac cccttcgggg ggaggaagag gaggtggagg aggagggtga tgttgatagt 60
gatgaagaag aggangaaga tganganance tcctcggagg gcttggaggc tgaggactgg 120
gcccagggag tagtggaggc cgntggcagc ttcggggctt atggtgccca ggaggaagcc 180
cantgcccta ctctgcattt cct 203

<210> 481
<211> 482
<212> DNA
<213> Homo sapiens

<400> 481
ccagacgctg cccatggagg cgtccagcga gccgccgctg gatgctaagt ccgatgtcac 60
caaccagctt gtagattttc agtggaaact gggtatggct gtgagctcag acacttgcag 120
atctcttaag tatccttacg ttgcagtgat gctaaaagtg gcagatcatt caggccaagt 180
aaagaccaag tgctttgaaa tgacgattcc acagtttcag aatttctaca gacagttcaa 240
ggaaattgct gcagttattg aaacggtgtg aagacggatt ctttggttga taaattgcta 300

tcattctaaa gtcatggact tcactttcgg caacaaaact aaataaggat ggaacattta 360
ttgaatgaaa aatgcacttt tgtttttcca tttttttaaa taataaaaat cagacaaaca 420
gaaaaaaaaa aaaaaaaggg cggccgctcg agtctagagg gcccgtttaa acccgctgat 480
ca 482

<210> 482
<211> 505
<212> DNA
<213> Homo sapiens

<400> 482
aaaatcttta gctgccaaga aagaagttaa gactctcagt gctgagagag actgaatcca 60
cctaggtgat aaggtgactg gacccagtaa accctttgtg tgctgggggg ttttatgcct 120
tgtagaaccc agtgtgagca agatttgggt accctacata cattcagtag ccaggaaagg 180
gtgattggat tgccagactc tgcctgctgg caaaaggatg agctgtagaa gctgaagtcc 240
taggtagtag atataaagaa gacaaattag gtggcacctt ctagactgtg caatgcatgg 300
atttggaatt gaatttttcc tctaattatt ctagggaaac cctgggctaa gaaaccaatg 360
taaaacctga tgaggtagtc tgtagtcaca ctgggtagag gtagaggcaa ccacaaaatt 420
attcttaaga atgcctccca ggcgcctgga agatgaaact ttctggtgaa tatgagctca 480
tggtaaaaat ttaggtcgga tgcag 505

<210> 483
<211> 501
<212> DNA
<213> Homo sapiens

<400> 483
tgcaaaaagg taacaaattc ataactggaa agcaaagaga agaacaagta tgatttggat 60
gataaagcat tgttttaatg gtgaaaactt cacagatcac taatgtttct agaggttaac 120
ttcaagtggg caagctgggg tttttaggta gtcagtggcc tagttcctaa agccacagta 180
taggatctgt taaactgaat gtctgttgaa agtttgtttt agctgcttgg aggcttcctt 240
ttaagacaaa ctgtatgtga ttaagttgtt ttgagggaac tgaagaacct gatgtagccc 300
ctggccagat aactgcctga tttctcagat attatttctc tgggaaacat tctacatagc 360
acaggagctt aagagtggca ttatcttctc gccttaattt ccagagatta tttctgtact 420
gagaatcctg gaactactat gctaggaaat ttaaagctgc atggtctgtc ttgttttcat 480
ttaattattg tgaataccta g 501

<210> 484
<211> 501
<212> DNA
<213> Homo sapiens

<400> 484
gcactaagac caccttctat gaggagcagg gtgactacta cagccagtac atccgggcct 60
gcctggacca cctggccccc gactccaaga gttctgggaa ggggaagaag cagccttctc 120
ttcattacac tgctgctcag ctcctggaaa agggtgtctt ggtggaaatt gaagatcttc 180
ccgcctctca cttcagaaac gtcatctttg acatcacgcc gggagatgag gcaggaaagt 240
ttgaagtaaa tgccaagttc ctgggtgtgg acatggagcg atttcagctt cactatcagg 300
atctcctgca gctccagtat gagggtgtgg ctgtcatgaa actcttcaac aaggccaaag 360
tcaatgtcaa ccttctcatc ttcctcctca acaagaagtt tttgcggaag tgacagaggc 420
aaagggtgct acccaagccc ctcttacctc tctggatgct ttctttaaca ctaactcacc 480
actgtgcttc cctgcagaca c 501

<210> 485
<211> 504
<212> DNA
<213> Homo sapiens

<400> 485
cgcactcttg gaacattctt tctttcaaca acccaaggca tgcttctatc tccttttgag 60
gtttccctct aagtgttacc tctaagatag gcttttcctg gacactctat gatggaacct 120
ctaggatttt ctctattgtt ttatgcttat tttgatattt gattcctaga attttaaata 180
cattatatat catataaaat aaacctttaa atattgaaat gaaaagataa aaatacatac 240
actaagtgaa taggtcaaaa gtgtgagatc atcttgaaca ttatcttgaa gagaagatac 300
caatttacct tctgctcaga tcatggtgta cgatatcaca acctgcctag aataactctc 360
cttttctgaa ccatttattc actactttg tcttccaatt aaatattagc ctgacttcaa 420
atatcataca ttagtttcct ttgtttatgt aattgaatta tataacatat attcattaga 480
gcctattttt tttaaaattt ttgt 504

<210> 486
<211> 501
<212> DNA
<213> Homo sapiens

<400> 486
gagaggtcac tatggcgcct ttctgcagga cgagtgggac ctgctccaaa gaatgatttt 60
gctggcccac gagaaactct ctgttcctgt cacgtgcaaa atccgtgtct tcccggagat 120
tgacaagacc gtgaggtacg cccagatgct ggagaaggcc ggctgccagt tgctgacggt 180
gcacggacgc accaaggagc agaaggggcc cctgtcgggt gcagcgtcct gggagcatat 240
caaggctgtg cggaaggctg tggccatccc tgtgtttgct aacgggaaca tccagtgcct 300
gcaggacgtg gagcgctgcc tccgggacac gggtgtgcag ggcgtcatga gcgcagaggg 360
caacctgcac aaccccgccc tgttcgaggg ccggagccct gccgtgtggg agctggccga 420
ggagtatctg gacatcgtgc gggagcaccc ctgccccctg tcctacgtcc gggcccacct 480
cttcaagctg tggcaccaca c 501

<210> 487
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(501)
<223> n = A,T,C or G

<400> 487
accattattt agcagcaaaa aggaaagttt gaagacatta acaggaactg gttaattgta 60
gtccttatct gaaaaggaca gattgaatgc agccaaatta tggcaaagaa atcagtagga 120
caacccctat aaagggtagt tcttttaaaa aaaatttctt tattggcaac aacataaaag 180
atatgaaaga atcactcata atttatcagc ataacatagc tattctcatt tttgcaattg 240
actttttagt tcttgaccaa atgtaatttt tattagttgt gattaactga ttttgtgctt 300
tttttaaaaa aaaaaaaaac ctagaataag acatttgttt tgttaattat tataaatgac 360
tgtattcatt ctgtttatgt accataattt tggatgttcc tacgatgtta aacttttagg 420
ttgtttttaa ttgtttgttc ttatagacaa ctctgtaagg gnttttaact gcttttatca 480
ggagaatgtc aaagaagtcc t 501

<210> 488
<211> 148
<212> DNA
<213> Homo sapiens

<400> 488
attctaagga tgaaatggct acagagcaaa ctgcagctga gagaaaactg cttggagttt 60
ggacagaggt ggaattgagt gtccacaggc cagctgagga ggtggtaccc agcactctat 120
gaacccttcg ctcaagtcag cctggagt 148

<210> 489
<211> 501
<212> DNA
<213> Homo sapiens

<400> 489
gctgtggatt cccctccaag tggaggagga tgggcaggct ggggatcctg gggcaaatct 60
ctgctgtcgt cagcatctgc cacagtaggt catggattga cggcagtcaa ggaaaaagca 120
ggagccactc tacggattca tggtgtaaat tctggatctt ctgaaggagc ccaaccaaat 180
actgaaaacg gagtccctga aataacagat gcagccacag atcagggccc tgcagaaagc 240
ccacccactt ccccttcatc agcctctcgg ggtatgctgt ctgccatcac caatgtggtt 300
caaaacacag gtaaaagtgt cttaactgga ggccttgatg cgttggaatt catcggcaag 360
aaaaccatga atgtccttgc agaaagtgac ccgggcttta agcggaccaa gacgctcatg 420
gagagaactg tttccttgtc tcagatgtta agggaagcta aggagaagga gaagcagaga 480
ctggcacagc agctcacgat g 501

<210> 490
<211> 482
<212> DNA
<213> Homo sapiens

<400> 490
attgcaaact gaaagtggac aaagacttaa ggtaaacctg ctcctcatgg tggaatgctt 60
ccaaatgctg gaaggaggac tttagggcag agttcactaa ggaggcttgt gcttatagat 120
cagtgggcct gaaagaagtt tctctaggtt ctggttgtgt gctgtacgag gtgtaggtag 180
taataatact cttgtcagcc acagtgaagc cccaagctag ccgggatagg ggactgacct 240
tgtacaggca gcatggagaa actaagacag agtgtcctgc ccaagtgatg gcactgggga 300
gcagtcactc aggtttattt ccaccagggc ccaagaaaaa aagaaatgag gcaacctaaa 360
attccatcaa gatagatacc aatatccaag gtgcttggtc ttagcggtgt gggacccacg 420
ttaaggctct tggtgggaag gtgggaggtg ttttcagcat gagatagggt tcaggctgtg 480
aa 482

<210> 491
<211> 483
<212> DNA
<213> Homo sapiens

<400> 491
cgcctctccc cgtgatccct ctctcgctaa ccgtaggcgc ttttcgtgaa ggcccgggtt 60
tttacagcac ttcgcttttc taaccacgaa cagtgctcgt tcgttcgcag ggccagcaag 120
gagagccccg cccccgcccg ccgcccgccg cccgccgccc gccgcctttg gatcccgcgg 180
actccgcccg gcccggcctc cccaggcatg gcgccgctgc gcttctccgc caatctgtcc 240
tggctattcc ccgagctccc cggcctcccc gcgcgggtgc gggccgcggg cagctcgggc 300
ttcgaggccg tcgaggtggc ctggccgtac gcggagacgc ctgaggcgct ggcgcgcgcc 360
gcgcgagaag cggggctgcg gcttgtactg atcaacacgc ccccgggaga ccaagagaag 420
ggggaaatgg ggctgggggc cgtccccggg agacaggcgg ccttccgaga gggactggag 480
cag 483

<210> 492
<211> 266
<212> DNA
<213> Homo sapiens

<400> 492
acctcatctg ctttgctttg gcatgtgagc cttgcctaag gggcatatc tgggtcccta 60
gaaggcccta gatgtggggc ttctagatta ccccctcctc ctgccatacc cgcacatgac 120
aatggaccaa atgtgccaca cgctcgctct tttttacacc cagtgcctct gactctgtcc 180
ccatgggctg gtctccaaag ctctttccat tgcccaggga gggaaggttc tgagcaataa 240

agtttcttag atcaatcaaa aaaaaa 266

<210> 493
<211> 483
<212> DNA
<213> Homo sapiens

<400> 493
gccgctcgcg ctaggagagc gggcttcggg cacttgacat ggcggcagtg gcggcgactg 60
cagcagcgaa ggggaatggg ggcggcggtg gcagggccgg ggccggggac gccagcggca 120
cgcggaagaa gaagggcccg gggcccctgg ccacggcgta cctggtcatc tacaatgtgg 180
tgatgacagc cgggtggctg gttatagcgg ttggtctggt ccgagcatac ctggctaagg 240
gtagctacca tagcctttat tattcaattg aaaagccttt gaaattcttt caaactggag 300
ccttattgga gattttacat tgtgctatag gaattgttcc atcttctgtt gtcctgactt 360
ctttccaggt gatgtcaaga gtttttctaa tatgggcagt aacacatagc gtcaaagagg 420
tacagagtga agacagtgtc ctcctgtttg ttattgcatg gacgatcacg gaaatcatcc 480
gtt 483

<210> 494
<211> 301
<212> DNA
<213> Homo sapiens

<400> 494
gtggctattt tcatggaata tcttttatca gcctttcagt tttaatttat ttgtgtcttt 60
ggatctaaag tcagtttgtt ttggacaatg tgtagtttga tcatgatttt aaaaaatcta 120
ttctgaagct gggtggttca cacctgtaat cccagcactt tgggaggatc tcttgagccc 180
aggagttgga gactagcctg gtctacaaag tgagactctg tttctacaaa aaaataaaat 240
aaatagttgg gtgtggtggt atgcgcttgt ggttccagct acttgggagg atgagggagg 300
a 301

<210> 495
<211> 496
<212> DNA
<213> Homo sapiens

<400> 495
cgaagtgaag gctaggggcc cgtacgcgcc cgcctgactg tcgccagcag ctcctcggcg 60
gccccaccgc agccgccgct ccctgaggcg cgggaggccc gcgccccgcg gctcgctgtg 120
cgtgggaggg cgcgagcgaa cgcgggcgag gagcggccga gccgctgaag aggagctggg 180
cgccggccgc ccggccgcgc tcggcccgcg gatcgcctcc gcccggtctt cgccggcccc 240
ggcccctggc gagatgccgt gtggggagga ttggctcagc cacccgctgg gaatcgtgca 300
gggattcttc gcccaaaatg gagttaatcc tgactgggag aagaaagtaa ttgagtattt 360
taaggaaaag ctgaaggaaa ataatgctcc taagtgggta ccatcactga acgaagttcc 420
ccttcattat ttgaaaccta atagttttgt gaaatttcgt tgcatgattc aggatatgtt 480
tgaccctgag ttttac 496

<210> 496
<211> 494
<212> DNA
<213> Homo sapiens

<400> 496
aaactatata aaaagtgatt tgtacagaac tttattttag ctctttttta aaaatgattt 60
gcatggttag aaaacggcga ggacagccag gggagggaag ggcctctagg gaactttgca 120
ctttctatac ctttgtacta tgcactgccc tattgattct acacccaata atgatattac 180
ttgaacccat ctgtaagaaa ctgcttcgga aattcatttg tgtgtatgta aataacacaa 240
catagaaaca ggaagggaaa aaagtctgca gtaatgcacg tattttttttt ctttcctgtt 300

tattttcggt tttgctttaa gtccttttat ttttaattcc ctttttgttt ttctttttgg 360
gttttggttc cttttgggtt tatgggtgcc ctgatactcc agcagagatc agaaggctac 420
agatccattc tatccatccg ttatgtggct ttgccatccc agcttggagt gtctttacaa 480
agataataac agtt 494

<210> 497
<211> 184
<212> DNA
<213> Homo sapiens

<400> 497
gcgcgccgcg gctggcaggg tgtgcgtgag tttggtggcg gccggctgtg cagagacgcc 60
atgtaccggc tcctgtcagc agtgactgcc cgggctgccg cccccggggg cttggcctca 120
agctgcggac gacgcggggt ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg 180
gtcg 184

<210> 498
<211> 471
<212> DNA
<213> Homo sapiens

<400> 498
tcttactaca aatggagatg gctattatga aacagcatga gcatgagcct tttatctttt 60
atacttagtg atatactttg cttgaaaatc actcagcaaa gtagttcaca tgatgtgtat 120
catatttgaa gtgtggtttt tctcaaaatc attgacttta aggagctcat ttctgaacaa 180
aaaggtttgc tctgtggaaa aatcaatcac tgccaggatt ctttcatttc tgtactattt 240
tgtataattg aatttgttca cttctctcac accagcaagt gttttacagg tgccttggat 300
taaaacaaaa ttgattttaa aatttttatg taagtcattg tgtctatgat gccactttta 360
aaaggaaaat gcaattgcgt aatggcttat atccttattt aatgtaccta tttgtgttct 420
aataattgtt tgaatgtttt attcagctta aaactttacc atgaagtcat a 471

<210> 499
<211> 478
<212> DNA
<213> Homo sapiens

<400> 499
aggtgggaaa agcggaggag gacgcccagg aggaggcggc ggcggcggcc gggaagtgaa 60
aggtctcgca aagttcagcg gcggctgcgg gcgccgagcc ccgggctagc ggcagacgag 120
cccgcagggc cgctccgcgg ggcagcgcag ccaggccggc tatggtcccg gggctcccgc 180
cgcccccag gtgcccggga cccgccaggc cggtgcgcga gggtcacccc acctccccgc 240
gcggtcccgg cccctggctc ccagctgccg gcgaccgctg accgagcccg gcgccccagg 300
aggaggaaga aaccagggcc ccgttccctc ccgaggacgg cggcgcttca tcccgcagcc 360
cagaggtctc ggctccctcc ggcacccgcc cggcccggct gctcccggct cctcccggcc 420
atggggagct gcgcgcggct gctgctgctc tggggctgca cggtggtggc cgcaagga 478

<210> 500
<211> 495
<212> DNA
<213> Homo sapiens

<400> 500
gggggcttct ggcttggtgt ggaccaggag ggggcagaag gcaccctgtc gtggctgggc 60
accgtcttcg gcgtgctggc tagcctctgt gtctcgctca acgccatcta caccacgaag 120
gtgctcccgg cggtggacgg cagcatctgg cgcctgactt tctacaacaa cgtcaacgcc 180
tgcgtcctct tcctgcccct gctcctgctg ctcggggagc ttcaggccct gcgtgacttt 240
gcccagctgg gcagtgccca cttctggggg atgatgacgc tgggcggcct gtttggcttt 300
gccatcggct acgtgacagg actgcagatc aagttcacca gtccgctgac ccacaatgtg 360

tcgggcacgg ccaaggcctg tgcccagaca gtgctggccg tgctctacta cgaggagacc 420
aagagcttcc tctggtggac gagcaacatg atggtgctgg gcggctcctc cgcctacacc 480
tgggtcaggg gctgg 495

<210> 501
<211> 494
<212> DNA
<213> Homo sapiens

<400> 501
ctgcggtgtg gttggtggtg agatgacgac cttagtgctg gataatggag cttacaacgc 60
caaaatcgtt acagccatga aaatgtgtcg gttattccta attgtcagtt ccggtcaaaa 120
acagcacgtc ttaaaacttt tactgccaac cagatagatg aaataaaaga cccttctgga 180
ctcttttaca tcctcccttt tcaaaagggc tacttggtga attgggatgt tcagagacaa 240
gtttgggatt acctttttgg aaaagaaatg tatcaggttg attttttaga tactaatatt 300
attatcactg aaccatactt taacttcact tcaattcaag aatcaatgaa tgaaattcta 360
tttgaagaat accagtttca agcagtatta agagtaaatg ctggggctct cagtgcacat 420
aggtatttcc gagataatcc ttccgaatta tgctgtatca ttgttgatag tggatattcc 480
tttacacata tagt 494

<210> 502
<211> 479
<212> DNA
<213> Homo sapiens

<400> 502
ttgtataatg ctgaatgtgt ccagagggac aagtttgcag aacctcatat tggtatatta 60
aagaaataat aaaataaaaa agcactttag gttattttat ctttaacccg attgctgcaa 120
tttcttttgt gtgtatatat acatatatat actttccaca aagttttatt ttttgctcag 180
aataaaaagt taaattgagg tgtgaaaaga aaagcactta ccttggtgca atatgtgtag 240
cttgatggtc gttgtcccat gtggccctgg cctggcagcg tttttccgct caatcagccc 300
tgtgctgtga gattgtccat agggaaacac tattatgcat tctcagcaac cgctcaatct 360
atgcaagcct tccctgtgtg ccccagggcg ccccctcagg ctctctgaag aactgctgtg 420
ggtcctgttt tctgctgact gttgaggccc tttttcatca cttcttggtc tctcgccat 479

<210> 503
<211> 451
<212> DNA
<213> Homo sapiens

<400> 503
ttgtgggccg ggtgggtttc ctaatctggt ttcgtctgcc tggttcatct gtgtgcgatg 60
gctccggact cggatccctt ccctgaaggg ccgctcttaa agctgctacc cttagacgct 120
agagaccggg gcacccagcg ctgccgcctg ggcccggccg ccctccacgc cctgggcgcg 180
cgcttgggct cggcagtgaa gatctcgcta cccgacggcg gctcctgcct ctgcactgcc 240
tggcctcggc gggacggagc ggacggcttt gtgcagctgg acccgctgtg cgcgagcccc 300
ggggcggcgg tcggggcgtc gagatcccgg aggagtctca gcctgaatcg cctcctccta 360
gtgccctgtc cgcccctgcg gcgcgtcgcc gtgtggccgg tgttgcgaga gcgggcaggc 420
gcgcccggtg cccggaatac agccgcggtg c 451

<210> 504
<211> 462
<212> DNA
<213> Homo sapiens

<400> 504
cagtggggaa ggggagagat gccgaggtgg tcagtatcct gactttcaga ggcctttttt 60
tgtttgtttt aatttttgct agattgatat taaaaactca tgtggaggaa ctcaaggaat 120

gtttagaaga ccaaaagtcc ccaatgacag gaacaaaagc aaccaatttt taactttctc 180
ttctcattcc tgttttcatt gatttcccac atgtagtcct tttgctcagg aagtctttgg 240
ggaaattaag gatctttgaa gctctgaaat aggtgatcag gttagtggtg tctgtcagct 300
gtctaagagg ttggaaaatg aactactcaa gatagtcacg aaaatactga aagtttgatt 360
tttctttcca tatttgaatt aatttttttct gtttgactgg aaggggtttt tgtataacta 420
aaacctcagc gcataaagga gatttaaaag gagcacatga tt 462

<210> 505
<211> 136
<212> DNA
<213> Homo sapiens

<400> 505
tcgattatat cacacatttc agttgggagg ttgtctcaac ctgtgaccac catctgagtt 60
agctggcaga cttctaggag gtcctgtctg aggtagaatc agaaatggct tccctccttc 120
tcccataaaa aaaaaa 136

<210> 506
<211> 466
<212> DNA
<213> Homo sapiens

<400> 506
ggggtacaga gacagcagcc tgcggagcgt tctaggcagg acagggcagc aaacctgaca 60
tgcggagctg ggggcagggg taatggggcc agggggtaat ggcaggtgag gccatggcct 120
agagggttgc catgcttggt gcaggggagg agaggcccag gtgtggctgc agtggcagca 180
ggagtcagtg tggctgtgcc cagtgggatg ttgtcagaga atggacctgg ctgctgggaa 240
aggtgattgt gtttgtctga gccacactgg actcttctct gaccagcaag cacattctgg 300
agatgcgggg cagagacgag gcctccgtga gaacctttga ggtgtgaggg ccttgatctg 360
gggtgcagcc tccagctttc tgcttacaga gcaggacctg caggagctcg ctgactgcct 420
gcacagtgga aggaagacct gtttctttta ctttccttga ggagaa 466

<210> 507
<211> 101
<212> DNA
<213> Homo sapiens

<400> 507
atgatttaat tttttaaact gtagcaattg gatagataat tttatttgaa attttacaca 60
ctgaaagctc taaataaaca gatacattca cattcaaaaa a 101

<210> 508
<211> 242
<212> DNA
<213> Homo sapiens

<400> 508
gacaatgcaa gtaacctcaa atgagagtgt ggaaaggcgg gaaagcagcc agagcttcat 60
tgttatgaaa aaagagtgaa atgtgctctg ttgaagagtt gaagaatgaa caaaggatat 120
ttagtttgaa tggaagctca gtaatgagaa atgagaatgg ttgagttctt aaaagaagca 180
agtaaagaag aggatttgtg ggctactatt ctcattcagt gaatctcatw ccacccttgc 240
ct 242

<210> 509
<211> 101
<212> DNA
<213> Homo sapiens

<400> 509
cctttgctcc ctttttccaa tttcttattg catatctttc tgtattacaa caaaatgata 60
tgcaataaga aattggaaaa agggagcaaa ggcgaagggg y 101

<210> 510
<211> 461
<212> DNA
<213> Homo sapiens

<400> 510
gcaggttcgg gaccatgagt tggattcctt ttaagattgg gcagcccaag aaacagattg 60
tgcccaaaac agtggagaga gactttgaaa gggagtatgg aaaacttcag caccatgtca 120
aaatctgccg tgaagatatc cttggactta ctctccaatc ccctctgtga gcaagaccag 180
gaccttctga acatggtgac ggccctggac acggccatga agcggatgga tgccttcaat 240
caggaaaagg tgaaccagat ccagaagact gtgatcgagc ccttaaaaaa gttcggcagt 300
gtcttcccga gcctcaacat ggctgtgaag aggcgggaac aggccttgca ggactacagg 360
aggctgcagg ccaaggtgga gaagtatgag gaaaaggaga agacggggcc agtgctggcc 420
aagctccacc aggcacgaga ggagctgcgg cctgtgcggg a 461

<210> 511
<211> 461
<212> DNA
<213> Homo sapiens

<400> 511
ggctttctga tatttctaaa attgacctgg aatcaaccat tgacatgtcc tgtgctaaat 60
atgaattcac tgatgccctg ctgtgccatg atgatgagct ggaagggcgc cggattgcct 120
tcatcctgta cctggttcct ccctgggaca ggagcatggg tggtaccctg gacctgtaca 180
gcattgatga acactttcag ccgaagcaga ttgtcaagtc tcttatccct tcgtggaaca 240
aactggtttt ctttgaagta tctcctgtgt cctttcacca ggtgtctgaa gtgctgtctg 300
aagaaaagtc acgtttgtct ataagtggct ggtttcatgg tccatcattg actcggcctc 360
ccaactactt tgaacccccc atacctcgga gccctcacat cccacaagat catgagattt 420
tgtatgattg gatcaaccct acttatctgg acatggatta c 461

<210> 512
<211> 686
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(686)
<223> n = A,T,C or G

<400> 512
actgacctga aggagaccta agagtccttt ccctttttga gtttgaatca tagccttgat 60
gtggtctctt gttttatgtc cttgttccta atgtaaaagt gcttaactgc ttcttggttg 120
tattgggtag cattgggata agattttaac tgggtattct tgaattgctt ttacaataaa 180
ccaattttat aatctttaaa tttatcaact ttttacattt gtgttatttt cagtcagggc 240
ttcttagatc tacttatggt tgatggagca cattgatttg gagtttcaga tcttccaaag 300
cactatttgt tgtaataact tttctaaatg tagtgccttt aaaggaaaaa tgaacacagg 360
gaagtgactt tgctacaaat aatgttgctg tgttaagtat tcatattaaa tacatgcctt 420
ctatatggaa catggcagaa agactgaaaa ataacagtaa ttaattgtgt aattcagaat 480
tcataccaat cagtgttgaa actcaaacat tgcaaaagtg ggtggcaata ttcagtgctt 540
aacacttttc tagcgttggt acctcgccgc gaccacgctg gaattccgga agggcctgtc 600

ctangatcca gtgtggtgga attctgcaga tatccagcac agtggcggnc gctcgagtct 660
aaanggcccg tttaacccgc tgatca 686

<210> 513
<211> 429
<212> DNA
<213> Homo sapiens

<400> 513
catgaacgac accgtaacta tccgcactag aaagttcatg accaaccgac tacttcagag 60
gaaacaaatg gtcattgatg tccttcaccc cgggaaggcg acagtgccta agacagaaat 120
tcgggaaaaa ctagccaaaa tgtacaagac cacaccggat gtcatctttg tatttggatt 180
cagaactcat tttggtggtg gcaagacaac tggctttggc atgatttatg attccctgga 240
ttatgcaaag aaaaatgaac ccaaacatag acttgcaaga catggcctgt atgagaagaa 300
aaagacctca agaaagcaac gaaaggaacg caagaacaga atgaagaaag tcagggggac 360
tgcaaaggcc aatgttggtg ctggcaaaaa gccgaaggag taaaggtgct gcaatgatgt 420
tagctgtgg 429

<210> 514
<211> 346
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(346)
<223> n = A,T,C or G

<400> 514
aaaactttct ctacttattt agttttntcc tctgagttca accgctgctg gattcgtttg 60
gcataacttt gtgccatgga gttaatgata gataggatga agtaacacac catgacaacg 120
accaactttt caaacatcca ggacaaccag ttttctccct gtggtgtgcc catttcgctt 180
ttgtggtgaa gcttctgccg ttgagcctcc aggtactcct gaaatggctt ctgcagagat 240
ggacctatgc cggggacagc actggaagca gggtacagta gcccaaagaa aaagacacat 300
ttgggaagaa aagcaggaaa aacgttaaag aaaatgtact taccac 346

<210> 515
<211> 549
<212> DNA
<213> Homo sapiens

<400> 515
ctgaccagga ctgtgaagat gcggttccgc tgcgaagatg gggagacatt ttccaggaac 60
gtcatgatga tccagtcctg caaatgcaac tacaactgcc cgcatgccaa tgaagcagcg 120
tttcccttct acaggctgtt caatgacatt cacaaattta gggactaaat gctacctggg 180
tttccagggc acacctagac aaacaaggga gaagagtgtc agaatcagaa tcatggagaa 240
aatgggcggg ggtggtgtgg gtgatggaac tcattgtaga aaggaagcct tgctcattct 300
tgaggagcat taaggtattt cgaaactgcc aagggtgctg gtgcggatgg acactaatgc 360
agccacgatt ggagaatact ttgcttcata gtattggagc acatgttact gcttcatttt 420
ggagcttgtg gagttgatga ctttctgttt tctgtttgta aattatttgc taagcatatt 480
ttctctaggc ttttttcctt ttggggttct acagtcgtaa aagagataat aagattagtt 540
ggacagttt 549

<210> 516
<211> 382
<212> DNA
<213> Homo sapiens

<400> 516
ccgctcgtca gactccagca gccaagatgg tgaagcagat cgagagcaag actgcttttc 60
aggaagcctt ggacgctgca ggtgataaac ttgtagtagt tgacttctca gccacgtggt 120
gtgggccttg caaaatgatc aagcctttct ttcattccct ctctgaaaag tattccaacg 180
tgatactcct tgaagtagat gtggatgact gtcaggatgt tgcctcagag tgtgaagtca 240
aatgcatgcc aacattccag tttttaaga agggacaaaa ggtgggtgaa ttttctggag 300
ccaataagga aaagcttgaa gccaccatta atgaattagt ctaatcatgt tttctgaaaa 360
tataaccagc cattggctat tt 382

<210> 517
<211> 323
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(323)
<223> n = A,T,C or G

<400> 517
acgagcgtag gacgatgctt ctcttntgtc agcctgcaac tgagtcagga ttgaatactt 60
ggaccccagg tctggagatt gggatactgt aatgcttctt tgttattata acataaaagc 120
accactgttc tgttcatttc ctagctgttc taattaagaa aactattaag atgagcaacc 180
acatttagaa atgtttattg acaggtcttt tcaaataatg cttttctaat taatagccaa 240
agatttcata tctaactttg taaccagaat tatacagtaa gttgacacca cttagattta 300
aaggcagaca gttttgcttt agt 323

<210> 518
<211> 605
<212> DNA
<213> Homo sapiens

<400> 518
ctggataccg aggctggggc cccacactgt ggaacaaacc cacagcttgc tcaggatcca 60
tcccagaatc agcagacatc aaatccaacg cacagttcag aagatgtgaa gccaaaaacc 120
ctcccgctgg ataaaagcat taaccatcag atcgagtctc ccagtgaaag gcggaagtct 180
ataagtggaa agaagctgtg ctcttcctgt gggcttcctt tgggtaaagg agctgcaatg 240
atcatcgaga ccctcaatct ctattttcac atccagtgtt tcaggtgtgg aatttgtaaa 300
ggccagcttg gagatgcagt gagtgggacg gatgttagga ttcgaaatgg tctcctgaac 360
tgtaatgatt gctacatgcg atccagaagt gccgggcagc ctacaacatt gtgacacggc 420
tttcaagctt ccggatcact caccatttct ttactgagag tgtcccctgg caactgctta 480
acaaaatccc aagctcaggg gcttctcagc atttacctaa tttctgaaag gctcttctga 540
aaggtggtat ctgttctttc gtagcacagt gtttatgttt ttcctgttta ttggtttggt 600
ttttt 605

<210> 519
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(462)
<223> n = A,T,C or G

<400> 519
ctgctggtca tgnccttggc agtcttttgt gcaaaataag gcatattnga gctccacatt 60
aaccttgcgg caggcgncta cttgctctgc atgctgtanc agngcacgtc ctccttcccc 120

ttggtggtgt agcctgngan aggctgccca tacttatcca cacaccagca naagccccgc 180
ttcctgcctt tggaagggcg acactgcttt ttcttataaa atcccttctt gtcacagttg 240
ggaatgtgna cacccctggg actcagcaca ttgaggaact tcaagtgatt cagtgtgnct 300
tccatttctc tacggcangn accatattct gtctcccgct tggactcgga ggagaagttc 360
tgggtatctg tgctctgaga ctcgtagtca actttgtagc gctggctgnc tttagcatgc 420
cctttcttga tgatgantat ctttgaatgg agggggtgga ac 462

<210> 520
<211> 565
<212> DNA
<213> Homo sapiens

<400> 520
actcgtaata aatatgcatc cggaaacaag ataaaaggct acacctcgtc aggcatccta 60
caaaaatgtc tcaagtttta tatactctgc agcatttctg tgcgggggca gaaggggctg 120
ttgtgtattt tctgaagtgc tgtgacaaaa ggtcctttca catttctttg gagcattttt 180
gaaattgctt aactataatt aaacaactta agaaaagtaa caccaagctt taaagccatt 240
tttgctttgc tgtcattggt ccttatccaa tacagatcaa catatcatcc agcacagcca 300
agcacccact gaggccaagc agccttgtgg gacatgggcc ctgtcagagc aggccctact 360
ttcagttaaa tactttggag agtccaggat tctgtctctc tccctcaaca agattaatgc 420
cataagggaa gttgcaagcg tgttagaaac atttttaacc tgaaagtaaa gtgaacagaa 480
atattttttt ttccgagacc tctgctatgc accataatat taccatatca gggtttttag 540
cttcaaagtt gaaaaacaga ttggt 565

<210> 521
<211> 127
<212> DNA
<213> Homo sapiens

<400> 521
acatggctga cgtcaccgtc cagtgcaaaa tcaaaaaaga aagaaagaaa aaccccaaag 60
aaagaggatt tttcagtgga gaacatggtg ggctgattag gcttctatta gattacattc 120
atttcac 127

<210> 522
<211> 642
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(642)
<223> n = A,T,C or G

<400> 522
actatgtttc gtaaattaaa taggtntggc ccagaagacc cactcaattg cctttgagat 60
taaaaaaaaa aaaaaaaaag aaagaaaaat gcaagtttct ttcaaaataa agagacattt 120
ttcctagttt caggaatccc ccaaatcact tcctcattgg cttagtttaa agccaggaga 180
ctgataaaag ggctcagggt ttgttcttta attcattaac taaacattct gcttttatta 240
cagttaaatg gttcaagatg taacaactag ttttaaaggt atttgctcat tggtctggct 300
tagagacagg aagacatatg agcaataaaa aaaagattct tttgcattta ccaatttagc 360
aaaaatttat taaaactgaa taaagtgctg ttcttaagtg cttgaaagac gtaaaccaaa 420
gtgcacttta tctcatttat cttatggngg aaacacagga acaaattctc taagagactg 480
tgtttcttta gttgagaaga aacttcattg agtagctgtg atatgttcga tactaaggaa 540
aaactaaaca gatcaccttt gacatgcgtt gtagagtggg aataagagag ggctttttat 600
tttttcgttc atacgagtat tgatgaagat gatactaaat gc 642

<210> 523

<211> 244
<212> DNA
<213> Homo sapiens

<400> 523
ctgaaggagc tgatccagaa ggagctcacc attggctcga agctgcagga tgctgaaatt 60
gcaaggctga tggaagactt ggaccggaac aaggaccagg aggtgaactt ccaggagtat 120
gtcaccttcc tgggggcctt ggctttgatc tacaatgaag ccctcaaggg ctgaaaataa 180
atagggaaga tggggacacc ctctgggggt cctctctgag tcaaatccag tggtgggtaa 240
ttgt 244

<210> 524
<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(407)
<223> n = A,T,C or G

<400> 524
acgttagtgg tgatgtcacc caccctnnng ctggggccga ggatgctctc attgtgcact 60
gcgtagatga ctctggccac tggggcagag gtggtttatt tacagctctg gaaaagcgat 120
ccgctgagcc aagaaaaata tatgagctgg ctgggaaaat gaaagacctg agtttgggag 180
gtgtcctttt atttcctgtt gatgataaag aatcaagaaa caaagggcaa gatttgttgg 240
ccttgattgt ggctcagcat cgtgatcgtt ccaatgtcct gtctggcatt aagatggcag 300
ccctagaaga gggcctgaag aagatatttt tagcagcaaa aaagaagaaa gcaagtgttc 360
atcttccacg tattggacat gccacgaaag gttttaactg gtatggt 407

<210> 525
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(276)
<223> n = A,T,C or G

<400> 525
acacaggagg caacgtgttt cacatnatag acttcacttc caactccttg gaatgttcat 60
ttctttggct tacaggagag actagacagg aaggccaggc aatgcttagg caactaaaat 120
gaggttgggg gtaatgctaa cgtcaccctc acagggatgg ccacggggac tgttattcgc 180
aagctggttt tctagacctg ttagctggaa gcatggtgag caccatttct ggacgctcag 240
gccgtgtcgg gcttcagtca tctccaccac acaggt 276

<210> 526
<211> 288
<212> DNA
<213> Homo sapiens

<400> 526
acaattaccc accactggat ttgactcaga gaggaccccc agagggtgtc tccatcttcc 60
ctatttattt tcagcccttg agggcttcat tgtagatcaa agccaaggcc cccaggaagg 120
tgacatactc ctggaagttc acctcctggt ccttgttccg gtccaagtct tccatcagcc 180
ttgcaatttc agcatcctgc agcttcgagc caatggtgag ctccttctgg atcagctcct 240
tcagctcctt cttgctcagg gtgtgcttgt caccctccct gccggagt 288

<210> 527
<211> 412
<212> DNA
<213> Homo sapiens

<400> 527
actttgagct tattgttttt attctgtatt aaatattttc agggttttaa acactaatca 60
caaactgaat gacttgactt caaaagcaac aaccttaaag gccgtcattt cattagtatt 120
cctcattctg catcctggct tgaaaaacag ctctgttgaa tcacagtatc agtattttca 180
cacgtaagca cattcggacc atttccgtgg tttctcatga gctgtgttca cagacctcag 240
cagggcatcg catggaccgc aggagggcag attcggacca ctaggcctga aatgacattt 300
cactaaaagt ctccaaaaca tttctaagac tactaaggcc ttttatgtaa tttctttaaa 360
tgtgtatttc ttaagaattc aaatttgtaa taaaactatt tgtgtaaaaa aa 412

<210> 528
<211> 489
<212> DNA
<213> Homo sapiens

<400> 528
aaatgcaaaa agtcaaagta ggtaacaggt tggtaattaa agtgtcagga agactggaag 60
aggcaaaaat caagcagagt tccaataagt gtatgaaaaa aaaaatcata actgaaggtt 120
taagaaaagt ccccaaaggc agaatcacaa tatgagcagg aggaataaaa agcttttgga 180
tataccaggc agctttctgt acgactcagg tttacaggtg aaattcctca gtttgagttc 240
agaagaattt gaacttattc cagcaaaata cttcaatctt tttattactg cctcctcccc 300
catcttcttt ctgggcaaag ggatgcttgg attaggtcca aagctcctgg caggggggagg 360
ggccatgtgt cacagcataa cagacggttg caagtgcttt actgagcagg ggtcaggttt 420
gcagcaactc tgataggctc acacaatggc ctccatttta cagcccctcc ttggaggccc 480
actgatcag 489

<210> 529
<211> 631
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 529
acttgcctaa agtttttata tctgnntctt ctgctgtaaa tcttcccttc ataaatgaaa 60
attttaataa aatcaactat gtggaaatat ataattaaag gaattcacta actgtgattt 120
tcataattta gggacattct cttctagtaa gcatggtgca ttatttacta gagatataat 180
atgcattaaa acaaaaaatg ttttctatca tcatagaaaa gtttgaggtc cagggataat 240
catctctgga tacattattt cctaccgtcg tggtacacac tgaacacatt tgaggcttat 300
gactggttct tttacttaca aatattgttt agacacattt tcaaatgtca caccaatcaa 360
taataataag gaatggattt tatctatatt gacagttctt tcaaccttaa gagtgaactg 420
ctacaggtaa gattcaatca catttttcag gagaaagcta ttgagaccaa tatgctttgg 480
ttatctaata ggggtggaat gacttataat gctatttact ccaggcaaag agaaaataca 540
acagacatag gatcttgatt tcaacgtagt tctcctccat gtgcatttct ctgtccgttt 600
aggcaatgcc aactggtcca ccagtgaaca t 631

<210> 530
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(316)
<223> n = A,T,C or G

<400> 530
acacatttaa atgactcacg agantnaagt ttttttcaaa tatattaaga tcacaccacc 60
ttgttgttta tcgaaagata ttcaaggaga aagatctgac tctccaaact gcatctgaga 120
ttgccacttt aaacagacct catttcaaac atgcaacaac gccactggta ataaagcttt 180
ggaatgggtg ctcattctat tatttcacta caaacagcat agaaagcaag agaagttggg 240
aatttattct aaaatagaat ggaggttgtc atctacagca gcactcctca ctcctctgtt 300
gccattttta gcaagt 316

<210> 531
<211> 296
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(296)
<223> n = A,T,C or G

<400> 531
aaagtatcat ttatttgaaa aacatacatt atcattntgt ttttgatatt tgataatgaa 60
aaaaatcttt gnttgtttat ttctgaaaaa gaactgtatt tagngattat tttagatagt 120
gatattatan cattcatctg tgtgtaaatt atttcatata gggaagagtt ctgatctgta 180
cctatggttc ttattgaaaa caacattgga tgtgcatttc tgtgatgtta tgaatacatt 240
tctactttat tttgaaacat ttgccaaact aaatactgta acactgtata acattt 296

<210> 532
<211> 266
<212> DNA
<213> Homo sapiens

<400> 532
acatatgcac caaattccat tttagaagtt tccatatcat tttcatagaa aacaaagttt 60
gaaaacaagt aacatttaaa cacagcacgg tattctacca caactgaaac ttttttcttc 120
ttcttcttta caggactcaa caaaatctaa aaatgaacta tgctgtagat ttacctcatg 180
caaagatctt tatgttatct ctgaaaatga aaaggatggc cttttaagca cattttactg 240
ttttatacta ttatggcaac ttgtgt 266

<210> 533
<211> 289
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(289)
<223> n = A,T,C or G

<400> 533
actcagaagt cacttttaat atcancgaca gaaatatttc actaattcaa ctgaggcaaa 60
tttcctttct agacaaagga cctagaaatt gagcatgcaa aacatccatc cattcattca 120
ttcaaataat tagccaattt taccgtcatt taattccacc agaagcaaat actagaatat 180
ctagaagtag tttgggtaaa gaaacattta cattttaata ttgtgtaatg tcataaattt 240

ggggctaaaa taacaccagg tcaaatttga tccctttgta tgtgagggt 289

<210> 534
<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(293)
<223> n = A,T,C or G

<400> 534
aaaataaaag gttctttaca agatgatacc ttaattacac tcccgcaaca cagccattat 60
tttattgtct anctccagtt atctgtattt tatgtaatgt aattgacagg atggctgctg 120
cagaatgctg gttgacacag ggattattat actgctattt ttccctgaat ttttttcctt 180
tgaattccaa ctgtggacct tttatatgtg ccttcacttt agctgtttgc cttaatctct 240
acagccttgc tctccggggn ggttaataaa atgcaacact tggcattttt atg 293

<210> 535
<211> 408
<212> DNA
<213> Homo sapiens

<400> 535
acttgaacac ttaaagagaa aaactctaaa taaagtcata gaggggatgg tagagatgac 60
cacagaaaat gaccacggag agtattatga agattgcaag attagacatt gatgatgtaa 120
attactccct ttctagataa aataatccat agatgtttat gaatcatatt tgtatgatta 180
ttgctgttac tattattttg acacattatt tattattatt gttgtcacta ttattaccat 240
taagatagca ggcgtaaaac tgtactggtt ccttcagtag tgagtatttc tcatagtgca 300
gctttattta tctccaggat gtttttgtgg ctgtatttga ttgatatgtg cttcttctga 360
ttcttgctaa tttccaacca tattgaataa atgtgatcaa gacaaaaa 408

<210> 536
<211> 184
<212> DNA
<213> Homo sapiens

<400> 536
acctctcatc aaggctctgc ctacaggcac attgtgatgt atctctgcac tgatcaccta 60
ggtcatgtaa ctttttctca ggctctacct acgatggcat tgtgacataa ctctgcacta 120
atcatccacg tgatgtaact cttgtctagg atgtgcctaa attaactttt tgacgtaacc 180
ctgt 184

<210> 537
<211> 311
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(311)
<223> n = A,T,C or G

<400> 537
ccacagttgt atcatatagc atctntaaca tttcatctag gattatctag tatagatctt 60
actatatttg ggctatgtt gtatacaatg ttaacaagaa catatcttct ctgcatatat 120
gtgtgaatta taaagaaaag catgagaatg actctaagtt caacaaacat gggtgaatct 180

ctatgtgctc ccagtgtcct ggatgggctc cccagcaagc cattcctcct tcctgttctg 240
atattactat tcttttttac attgtgctaa ggaggacaaa aggtgagaga tgaaaataaa 300
gccttgcctt t 311

<210> 538
<211> 302
<212> DNA
<213> Homo sapiens

<400> 538
aaaataaaaa agcaaaaact cttgtggtac ctagtcagat ggtagacgag ctgtctgctg 60
ccgcaggagc acctctatac aggacttaga agtagtatgt tattcctggt taagcaggca 120
ttgctttgcc ctggagcagc tattttaagc catctcagat tctgtctaaa ggggtttttt 180
gggaagacgt tttctttatc gccctgagaa gatctacccc agggagaatc tgagacatct 240
tgcctacttt tctttattag ctttctcctc attcatttct tttatacctt tcctttttgg 300
gg 302

<210> 539
<211> 396
<212> DNA
<213> Homo sapiens

<400> 539
actgtttatt tgctccttct cttcatgcct gtggctggat gtcccacaac actataagaa 60
atataagtca agccctttgt gttaagcaag aactacagac tccatctttt cacccaaatc 120
atgaatgacc aataaaaagc aagttattcc agaggaagaa gcagcccttg aaatgttaag 180
gcttaggctt gaaaggtgaa gagcaggaat tctctctttc aaatcctaga gcataaaccc 240
atgtgtggcc aagtgagatc agccctcaag ggcacatgcc aagggcagag cagcccatgt 300
agacagcttc ggagggcatg ggggtgtagg gagttcgggg tagctcctca ttaactattt 360
gttgggtgag taaaggggtg aggctcagtg gcaggt 396

<210> 540
<211> 634
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(634)
<223> n = A,T,C or G

<400> 540
ccaaaaacaa gatgaccaga tttgntttna gcctgatgac cctacaggtc gtgctatgat 60
atggagtcct catgggtaaa gcaggaagag agtgggaaag agaaccaccc cactctgtct 120
tcatatttgc atttcatgtt taacctccgg ctggaaatag aaagcattcc cttagagatg 180
aggataaaag aaagtttcag attcaacagg gggaagaaaa tggagattta atcctaaaac 240
tgtgacttgg ggaggtcagt catttacagt tagtcctgtg tctttcgact tctgtgatta 300
ttaaccccac tcactaccct gtttcagatg catttggaat accaaagatt aaatccttga 360
cataagatct catttgcaga aagcagatta aagaccatca gaaggaaatt atttaggttg 420
taatgcacag gcaactgtga gaaactgttg tgccaaaaat agaattcctt ctagtttttc 480
ttgttctcat ttgaaaggag aaaattccac tttgtttagc atttcaagct tttatgtatc 540
catcccatct aaaaactctt caaactccac ttgttcagtc tgaaatgcag ctccctgtcc 600
aagtgccttg gagaactcac agcagcacgc ctta 634

<210> 541
<211> 221
<212> DNA
<213> Homo sapiens

<400> 541
cacacaagca gcagagacca tgggaaccct ctcagcccct ccctgcacac agcgcatcaa 60
atggaagggg ctcctgctca cagcatcact tttaaacttc tggaacctgc ccaccactgc 120
ccaagtcacg attgaagccg agccaaccaa agtttccgag gggaaggatg ttcttctact 180
tgtccacaat ttgccccaga atcttaccgg ctacatctgg t 221

<210> 542
<211> 287
<212> DNA
<213> Homo sapiens

<400> 542
cctcttctac tatggcagga gatgtggcgt gctgttgcaa agttttcacg tcatcgtttc 60
ctggctagtt catttcatta agtggctaca tcctaacata tgcatttggt caaggttgca 120
gaagaggact gaagattgac tgccaagcta gtttgggtga agttcactcc agcaagtctc 180
aggccacaat ggggtggttt ggtttggttt ccttttaact ttccttttgt tatttgcttt 240
tctcctccac ctgtgtggta tattttttaa gcagaatttt atttttt 287

<210> 543
<211> 274
<212> DNA
<213> Homo sapiens

<400> 543
acttgtgaaa cacagctgtt cttctgttct gcagacacgc cttcccctca gccacaccca 60
ggcacttaag cacaagcaga gtgcacagct gtccactggg ccattgtggt gtgagcttca 120
gatggtgaag cattctcccc agtgtatgtc ttgtatccga tatctaacgc tttaaatggc 180
tactttggtt tctgtctgta agttaagacc ttggatgtgg tttaattgtt tgtcctcaaa 240
aggaataaaa cttttctgct gataagataa aaaa 274

<210> 544
<211> 307
<212> DNA
<213> Homo sapiens

<400> 544
ccaggtggtt gtcttattgc accatactcc ttgcttcctg atgctgggca atgaggcaga 60
tagcactggg tgtgagaatg atcaaggatc tggaccccaa agaatagact ggatggaaag 120
acaaactgca caggcagatg tttgcctcat aatagtcgta agtggagtcc tggaatttgg 180
acaagtgctg ttgggatata gtcaacttat tctttgagta atgtgactaa aggaaaaaac 240
tttgactttg cccaggcatg aaattcttcc taatgtcaga acagagtgca acccagtcac 300
actgtgg 307

<210> 545
<211> 570
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(570)
<223> n = A,T,C or G

<400> 545
accttagaaa tttgcaacca cctccctgaa agtcttctcc cacgttatta agtgcaatgt 60
ttatggtaaa tgtagaagca tcatgatgag gacgaagaga acgctgtcgt tcaggggagt 120
attttactac aaaattcagt agtgcaaatc ccttcgtata atagcctgca aagaccttca 180

gtgtaactgg ngcaatgaac tcccggataa aatgaagcca tacattctcc agatcaactt 240
gcttcatgtg gatatcatca gttgggacat tttcataacc accagatata cggctatcat 300
gatgttttcc cccagaccat ttgccgtaat gttccatttc ttctaccaat tcatcacagg 360
ctttttcaga aaatatgggg aaccaaaaga catctggaca gggctgttca actatatttt 420
cagtgaaaat ctttgaataa tcacggttta tatacttttc cttccagtcc acaggatttt 480
caaaaatctg ccagaggtca ttgttataat gggaagtatt gtaattagca gtggataata 540
gccttccaaa ttcatgtcta ttagaaatgt 570

<210> 546
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(589)
<223> n = A,T,C or G

<400> 546
aaaaatactt tttaccaaag gtgctatttc tctgtaaaac actttttttt ggcaagttga 60
ctttattctt caattattat cattatatta ttgtttttta atattttatt ttcttgacta 120
ggtattaagc ttttgtaatt atttttcagt agtcccacca cttcataggt ggaaggagtt 180
tggggttctt cctggtgcag ggctgaaat aacccagatg cccccaccct gccacatact 240
agatgcagcc catagttggc ccccctagct tccagcagtc cactatctgc cagaggagca 300
agggtgcctt agaccgaagc caggggaaga agcatcttca taaaaaactt tcaagatcca 360
aacattaatt tgtttttatt tattctgaga agttgaggca aatcagtatt cccaaggatg 420
gcgacaaggg cagccaagca gggcttagga tatcccagcc taccaatatg ctcattcgac 480
taactaggag ggtgagttgg ccctgtctct tctttttctt ggacctcagt ttccttcagt 540
ggagcttggt aaaaatgcac taccntttga tttgataagg tataaatct 589

<210> 547
<211> 293
<212> DNA
<213> Homo sapiens

<400> 547
actcctatta ttgactgtag tcaatcaaac ataaaaaggt gaaagtaaaa tttaattttt 60
taccccttatt ttactgacca atatggaagt tcttggtatc tttaaggctg accttcctgg 120
tattgtgtaa tgattgaatg tatctaaact gtaataattt gaaactgaca aacataacct 180
tctcagactt acaaaactat gttctttcta aagatacaga tttttattat tttattttga 240
ctaggaagga tttataaata aatgtaatga aaaatctttg atcttaataa agt 293

<210> 548
<211> 98
<212> DNA
<213> Homo sapiens

<400> 548
aaacaaaggt tgagatgtaa aaggtattaa attgatgttg ctggactgtc atagaaatta 60
cacccaaaga ggtatttatc tttacttttt tttgtaca 98

<210> 549
<211> 121
<212> DNA
<213> Homo sapiens

<400> 549
acatgcatat ttcaaagacc tgttaatggc gtccactttg gattcttaca tgaaacgatt 60

cagtgcacat tgtaagccta aggaccacgc aaaagggttt cccacatatt aagtattcag 120
t 121

<210> 550
<211> 509
<212> DNA
<213> Homo sapiens

<400> 550
acaatagtat acattttata atgatgaact tataatgatt aagggacatt tctataaaaa 60
tactacaata gttttatgca caacttccca ttaaaaatga gatttcttat ttgtttgtct 120
gtttttactc tgggagtaat actttttaaa ttacctttac atatatagtc actggcatac 180
tgagaatata caatgatcct ggaaattgca gtaacaaaag cacacaacga ttatagtaac 240
tataagatac aataaaacaa ataaatgtga aagtagattc atgaaaatgt attcctttaa 300
aatattgttt tcctacaggc ctatttaaca agatgtttca ttttactgta tatttgtag 360
ttaatataaa tgttgctcta atcagattgc ttaaaagcat ttttattata tttatgttgt 420
tgaactaata tatgaaataa gtaaatgtag ctcccacaag gtaaacttca ttggtaagat 480
tgcactgttc tgattatgta agcatttgt 509

<210> 551
<211> 427
<212> DNA
<213> Homo sapiens

<400> 551
accatggtta tatgattaat cttgggacaa agaattttat agaaattttt aaacatctgg 60
aaaagaagct taagttttat catccttttt tttctcgtga attcttaaag gattatgctt 120
taatgctgtt atctatctta ttgttcttga aaatacctgc atttttttggt atcatgttca 180
accaacatca ttatgaaatt aattagattc ccatggccat aaaatggctt taaagaatat 240
atatatattt ttaaagtagc ttgagaagca aattggcagg taatatttca tacctaaatt 300
aagactctga cttggattgt gaattataat gatatgcccc ttttcttata aaaacaaaaa 360
aaaaaataat gaaacacagt gaatttgtag agtgggggta tttgacatat tttacagggt 420
ggagtgc 427

<210> 552
<211> 340
<212> DNA
<213> Homo sapiens

<400> 552
cctcaaggcg gtccaattat ccacttgcag attctacaga aagagtgttt caaaactgct 60
ctgtcaagag aaatggtcca ccgtgtgtgt ggaatgcagc catcacacat tagtttctga 120
gattgcttct gtcttggttt tatggggaga tatttccatt tctagcatag gcttcaaggc 180
gctctaaata tccgcttgga aatactacaa aaacagtgtt tcaaaactgc tgtatccaaa 240
ggaaggtgcc actcgctgag ttgaatgcac acatcacaag gaagtttctg agaattcttc 300
tgtctagatt catacgaaga aatcccgttt ccaacgaagg 340

<210> 553
<211> 549
<212> DNA
<213> Homo sapiens

<400> 553
acttgagctg tgaggtcatc ggaatcccga cacctgtcct catctggaac aaggtaaaaa 60
ggggtcacta tggagttcaa aggacagaac tcctgcctgg tgaccgggac aacctggcca 120
ttcagacccg gggtggccca gaaaagcatg aagtaactgg ctgggtgctg gtatctcctc 180
taagtaagga agatgctgga gaatatgagt gccatgcatc caattcccaa ggacaggctt 240
cagcatcagc aaaaattaca gtggttgatg ccttacatga aataccagtg aaaaaaggtg 300

aaggtgccga gctataaacc tccagaatat tattagtctg catggttaaa agtagtcatg 360
gataactaca ttacctgttc ttgcctaata agtttctttt aatccaatcc actaacactt 420
tagttatatt cactggtttt acacagagaa atacaaaata aagatcacac atcaagacta 480
tctacaaaaa tttattatat atttacagaa gaaaagcatg catatcatta aacaaataaa 540
atactttttt 549

<210> 554
<211> 321
<212> DNA
<213> Homo sapiens

<400> 554
acctaataat atgttaacat aaacataaca acacacatat tatttttcta ccccttggca 60
actgaaaatg aagttaccat tcctaggcca aatttttaga caaagctttc taaaaccatc 120
tttataaagt aaattcagat atgcttacaa taaaaagaca taaaagattc atcctgagat 180
gaattctgag tcaataacta aaaaccattt ctaccagtgc atcactacca tgtaatccat 240
tctacgcaag ctctacaaat attgagtcaa atcctgtctg tcagaaaatg aagacccaat 300
aagtttgccg aagtattcag t 321

<210> 555
<211> 322
<212> DNA
<213> Homo sapiens

<400> 555
ctggatcccg agaatactgg aacaatagag ctcgacctta tctcttggct ctgtttctca 60
gtactttgaa gttataacta atctgcctga agacttctca tgatggaaaa tcagccaagg 120
actaagcttc catagaaata cactttgtat ctggacctca aaattatggg aacatttact 180
taaacggatg atcatagctg aaaataatga tactgtcaat ttgagatagc agaagtttca 240
cacatcaaag taaaagattt gcatatcatt atactaaatg caaatgagtc gcttaaccct 300
tgacaaggtc aaagaaaact tt 322

<210> 556
<211> 286
<212> DNA
<213> Homo sapiens

<400> 556
aaaaaatatg tatctaagaa tgttctaggg cactctggga acctataaag gcaggtattt 60
cgggccctcc tcttcaggaa tcttcctgaa gacatggccc agtcgaaggc ccaggatggc 120
ttttgctgcg gccccgtggg gtaggaggga cagagagaca gggagagtca gcctccacat 180
tcagaggcat cacaagtaat ggcacaattc ttcggatgac tgcagaaaat agtgttttgt 240
agttcaacaa ctcaagacga agcttatttc tgaggataag ctcttt 286

<210> 557
<211> 459
<212> DNA
<213> Homo sapiens

<400> 557
acagaagatg aataataatg aaaaactgtg atttttttgac tatcacatac attgtgttaa 60
aaaacaggta aatataatga ctattactgt taagaaagac aaggaggaaa actgtttcaa 120
tgttcaggtt taaatactaa gcacaaaaat ataacaaatt ctgtgtctac aataattttt 180
gaagtgtata caagtgcatt gcaaatgagc tctttaaaat ttaaagtcca tttccccttt 240
agccaagcat atgtctacat ttatgatttc tttctcttat tttaaagtct cttctggttt 300
agtttttttaa aaagtttcat catggctgtc atcttggaat ctagcctcca gctcaaagct 360
gagacttcac gcatacatat tctcctttct gggtgcatct tcacctagtt tctccaagta 420
ttcagagtta aatagcacaa cttcttttat atgttccct 459

<210> 558
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 558
aaaaaataaa aaacaagaca acaatttagt agaagtaccn ctgggaggga ggggagggga 60
aaaaaggata tacaggggca ggngtattct ctgtacagag gtgcananaa aatttcacat 120
anctttanag aatgccttgt ggaaaaaaaa aaataggccc caatacttgt tactgccctt 180
tatcaaaact gtgtgcatga cctgcacaaa taaaatcaca aaacagtgtt gccacattct 240
tcaaggaaac aaagcaaaat ttagggggnt tcttttccct ctccttgtta aaagtcattt 300
ttt 303

<210> 559
<211> 232
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(232)
<223> n = A,T,C or G

<400> 559
aaagcattta ttaagaattt actcaggcat gatggcccat acttgtaatc ccagctattg 60
ggaaggatga gatgggagga tggcttgagg ccagaggttt gagaccgacc agccagggca 120
acacagtgag acccccttctc aaaaaaaaaa aaaaaaaaag agagagtgtg tgattagaag 180
ctaaatagga aagttttgag cttcaagtca gngaggagta aaaaagattt tt 232

<210> 560
<211> 336
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(336)
<223> n = A,T,C or G

<400> 560
ctctgcaaaa ataannataa aaaaataaat aaaattttaa aaataataaa attcactata 60
tacacatata aagaaataaa aagaagtctc agttgcagct atttgtcaaa attaatatcc 120
atttcttttt atatacggtg aatattgcgc aattatagat ctggattttg aaccacttaa 180
tgaagcggca acaccaggtg ttttgaggtg ttggcattct tcgctgattt ggctgttccc 240
aatgtttaca ttatttaatc ttgcaaaaat ggttctgtgc acttggatgn gaaatgctgn 300
ccagntttat ttttttatg ttgntatcct tggatg 336

<210> 561
<211> 636
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(636)
<223> n = A,T,C or G

<400> 561
acattatggg ttttattgct ttcttttatg gtagacctgt taatggggaa aaaatacatc 60
aaatcaaata gaatcttata tctgtatgtt aaaatagagc acttacctga agtcagtggc 120
ctggatcata gccctggatc atttcccagt ctgtcctgtg ctgtgtgacc ttggacaagg 180
cgcttcatct ctctgggcct ctatttctcc atttgtaaaa caagtggctg cagtagatga 240
tggctgagag cccttcctgt tcccagatgc cttggtccaa agaccccacc cctctgctgg 300
tcctgccaac gtgttggtgc tataagctgc ttcagatata aaattggttt atctataatg 360
tttgttcatt taatagcttc taaaaggcct ttttgttata cagtgctttt tttctagttt 420
tatggacttg gttactgtaa taatgtcttg tttttagcca tgtaactaca aacagatatt 480
ctcttgatgt cttagtaaat ttgcatttga tatatcattg atgagatttt gttgttatgt 540
aatattcttt ggctacgcat ctgtccagca tcttattaac cataatactg ngatcattat 600
ttggaaatat gtcctatgga aagaataaaa gcatgt 636

<210> 562
<211> 708
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(708)
<223> n = A,T,C or G

<400> 562
acagtccacc ttttgataca tgccatgcct ttgatcaaag aacaggacat aaaaacaaag 60
tcacaatgac attccatagt aaatttggaa tcagaactcc aaatgcaact tcgggctcgc 120
tggagaacaa ctaaggggca ccaaaccctc tgaggtttta ctttaaggtt cgctgtatgt 180
ttgccttgga caaaaaggct acctaccacg tgctatccag taatatactt aaataagcca 240
atacttagat ctactgtaag gcagatgcta attataaggc attaagtaag caaatagtgc 300
cctcagctac tgcagaagaa aagtcccact gaggaaaaga aagtcttgtg atttttaaag 360
gcaagttttc aagtgctctc atagttctat cctctaattc cattaaatcc atactaggag 420
cgtcagtgag ggttttcata gcttttggaa atactttggt ctctgaactg taattagcaa 480
gaagtaaaaa cagaaacgtc aaacgtcaaa tgtttgcttt gttacctgga ggactaaatg 540
tagatgtctt tagtatactt tgtatgttct taatattgga agataatttt gtgaatctgt 600
agattttatt ttttcagtct taccttacaa atttcttttc tatgaataat agaggactta 660
cngcactctg ccatttgtta atgaaaggaa ggcngangat ttagaaag 708

<210> 563
<211> 290
<212> DNA
<213> Homo sapiens

<400> 563
ccagatgctc atccactttc agactttcat ctcttctgcc atctgccaaa gtcaacagag 60
ctttccggaa gtcaccagat gtttcggaac taatgtcatc tccaagactc ttcttgtata 120
ctgtataata ggcttgagag atatccttca tttgcctgct tgtcctggta gttaagattt 180
caatcaaggc atcttcgttt gttcccgcgc ccttcatgga tttctttagc tgctttgcat 240
caaagactgc tggtggagtc actagggcca ccatgagatg ctcaaagtgg 290

<210> 564
<211> 530
<212> DNA
<213> Homo sapiens

<400> 564
accaccagat acttaaagct tcaaaaagac tgcccctacc accacaggag gaccagccta 60
accatacgct ccaaaagatg gctgtgatag atcttgtgaa gcaattactg agcagatcaa 120
gatctttggg aaggaacact aaagatgttt tgaatgaatt atagtccact ggcattttag 180
tgtatttttt tttcttttta gaaacacaca tttctaaaaa tgtcatgtta cattcctgca 240
tgtccctttt gatagcatta gtggatccat tggatttctt ttttcttttt gtgagacagc 300
ttttagtctt acctgaattt atgtgtgttt ttccgacagt ggttaataat tatattggtg 360
atgtagcagc aattgtgttg gcagggtttt catatattat tagtaattaa cactaactgt 420
tggactgact tgtgtcgata gcgctcacgc aagcatggtt aacgtcccta aaacccgccg 480
gactttctgt aagaagtgtg gcaagcacca accccataaa gtgacacagt 530

<210> 565
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(450)
<223> n = A,T,C or G

<400> 565
ctgcttacgg aagcgctgnn tgactaggat gtgatttatt aacgaccaac ttctgttatt 60
gtgtgttaag tttttcatct gtgcatcaaa tcacaaaaag aataaataga gctttttcct 120
ttatcagtcc cttgggcaca gcaggtcctg aacaccctgc tctacaatgt tgcatcaaga 180
gttcaaacaa caaaataaaa aatattaaga ggaaatcccc atcctgtgac ttgagtccct 240
taagtctaca ggggctggtg acctcttttt gctaatagga aaatcacatt actacaaaat 300
ggggagaaaa ctgtttgcct gtggtagaca cctgcacgca taggattgaa gacagtacag 360
gctgctgtac agagaagcgc ctctcacatc tgaactgcat actgagcggg caagtcggtt 420
gtaagttcag taaaaccctc tgatgatgcc 450

<210> 566
<211> 563
<212> DNA
<213> Homo sapiens

<400> 566
acttgagctg tgaggtcatc ggaatcccga cacctgtcct catctggaac aaggtaaaaa 60
ggggtcacta tggagttcaa aggacagaac tcctgcctgg tgaccgggac aacctggcca 120
ttcagacccg ggtggcccca gaaaagcatg aagtaactgg ctgggtgctg gtatctcctc 180
taagtaagga agatgctgga gaatatgagt gccatgcatc caattcccaa ggacaggctt 240
cagcatcagc aaaaattaca gtggttgatg ccttacatga aataccagtg aaaaaaggtg 300
aaggtgccga gctataaacc tccagaatat tattagtctg catggttaaa agtagtcatg 360
gataactaca ttacctgttc ttgcctaata agtttctttt aatccaatcc actaacactt 420
tagttatatt cactggtttt acacagagaa atacaaaata aagatcacac atcaagacta 480
tctacaaaaa tttattatat atttacagaa gaaaagcatg catatcatta aacaaataaa 540
atacttttta tcacaaaaaa aaa 563

<210> 567
<211> 424
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(424)
<223> n = A,T,C or G

<400> 567
ccagtgagca aattgaaaac caactgaaag caaatccaaa tgaggaagat tttaataaag 60
gaataccctt ctccatagca ggtgcaatgc tgactgctca aggcgtgcgt gcgcgcgcac 120
acacacacac acacacacac atacatactc tcacacacnc atctttccaa ttaaactgca 180
ggtagaatga gattttgtgt tattcaaaaa atttgtaagt gatcaaaanc actgctatgg 240
aatgcctgtt tatctgcctt tgntctggtt aaaatctcat aaaaatacat tcaacaggaa 300
aacatanatt gtatgtgtat aaatatatat gtatatatat atattatata cacatgcaca 360
caaatacttt tgtttttttga agcataagat agttacataa atactcctat aattgctaaa 420
gttt 424

<210> 568
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 568
actggctcac tcagagagga cgtccttcaa ctatgccatg aaggaggctg ctgcagcggc 60
tttgaagaag aaaggatggg aggtggtgga gtcggacctc tatgccatga acttcaatcc 120
catcatttcc agaaaggaca tcacaggtaa actgaaggac cctgcgaact ttcagtatcc 180
tgccgagtct gttctggctt ataaagaagg ccatctgagc ccagatattg tgggttganc 240
aaaagaaagc ttggaagccn caagaacctt gtgatattcc agttccccct gcantgggtt 300
tgggaagtcc ctgccntttt gaaagctggt ttgaagcgaa tgttcatagg aaagtttgct 360
taccacttac cctgcccatg gtangacaaa ag 392

<210> 569
<211> 559
<212> DNA
<213> Homo sapiens

<400> 569
aaagagattt attaaatcat cttatcacaa agatggaaac atatacaaac tagaaacatg 60
caaccatcat cttccacagt caagtcacaa tgtcaaatat ttttcttgcc tctgcagatg 120
aaaagttcag atcttatacc caactactta ctcaccccga atatttaagt cagtcttcct 180
gaaagtactc agggtagcaa gtaacaaaat gcaaacgatt atataaagaa agtgcagtta 240
aaaaggaaac tatgtggcaa gtaccctctt tcccttccca ccccccaatt aaaggcaaac 300
aatggcactt tgctcttgct taacctagat tgtcttcaaa aactattaaa atgtaaaaga 360
cttaacaaaa aaacaaaaag acgtttaaca gatgtcaaaa agctccttag tgtttgaaaa 420
taaatgctta aacaaaagac aacatatttt atatcaaaca agtttgaaga gccctgaatt 480
gcagcattct gtaacataaa caaacaaaaa gctggtatag gatttattgg caaaggcaga 540
atttcttcaa gcagggtaa 559

<210> 570
<211> 368
<212> DNA
<213> Homo sapiens

<400> 570
agccgccgct ggatgctaag tccgatgtca ccaaccagct tgtagatttt cagtggaaac 60
tgggtatggc tgtgagctca gacacttgca gatctcttaa gtatccttac gttgcagtga 120
tgctaaaagt ggcagatcat tcaggccaag taaagaccaa gtgctttgaa atgacgattc 180
cacagtttca gaatttctac agacagttca aggaaattgc tgcagttatt gaaacggtgt 240
gaagacggat tctttggttg ataaattgct atcattctaa agtcatggac ttcactttcg 300

gcaacaaaac taaataagga tggaacattt attgaatgaa aaatgcactt ttgtttttcc 360
attttttt 368

<210> 571
<211> 261
<212> DNA
<213> Homo sapiens

<400> 571
acacgattgc tgcttccgct atatttgtga tataggaatt aagaggatac acacgtttgt 60
ttcttcgtgc ctgttttatg tgcacacatt aggcattgag acttcaagct tttctttttt 120
tgtccacgta tctttgggtc tttgataaag aaaagaatcc ctgttcattg taagcacttt 180
tacggggctg gtggggaggg gtgctctgct ggtcttcaat taccaagaat tctccaaaac 240
aattttctgc aggatgattg t 261

<210> 572
<211> 488
<212> DNA
<213> Homo sapiens

<400> 572
ctctcagctc tcggcgcacg gcccagcttc cttcaaaatg tctactgttc acgaaatcct 60
gtgcaagctc agcttggagg gtgatcactc tacacccccca agtgcatatg ggtctgtcaa 120
agcctatact aactttgatg ctgagcggga tgctttgaac attgaaacag ccatcaagac 180
caaaggtgtg gatgaggtca ccattgtcaa cattttgacc aaccgcagca atgcacagag 240
acaggatatt gccttcgcct accagagaag gaccaaaaag gaacttgcat cagcactgaa 300
gtcagcctta tctggccacc tggagacggt gattttgggc ctattgaaga cacctgctca 360
gtatgacgct tctgagctaa aagcttccat gaaggggctg ggaaccgacg aggactctct 420
cattgagatc atctgctcca gaaccaacca ggagctgcag gaaattaaca gagtctacaa 480
ggaaatgt 488

<210> 573
<211> 619
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(619)
<223> n = A,T,C or G

<400> 573
actttactga aagaacacta ntgttctttc ctttccgttg tgaaaaaagt tgtttctgag 60
gaattgaaac cccagaagat aactacaaca aaaacatgtt aatttttttt taaaaatgat 120
gattcaaagg cagatttgaa gggaagtaat atttaggtgg cagaagaagg caaatgcagc 180
ctctgaaggg aactgttcta attattacct aaaaaataaa gttacacaac tatattcaag 240
gacatgagat aaagcactgc ttgaaaacca gaatgactga acagttaggt gaaaaggaac 300
agctgaaata ggaaggggaa atggactgaa gaataatttg aatcgggaca gtgatccatc 360
agtcctagat gcttctggta tgtaaatatc ttgaatcaca ttgtttcctt tcttctgaaa 420
tctcaaagga gaattctcac agcactacat taaggttgcc attttgttag gattcaaaat 480
ttcaatccag tagccatcag gatcttgaat aaatgccagg cctttcattt taccatcatc 540
aggtttcttc acaaatttga ctccagtctt caaccttttc aagcctgatc atcaggaaca 600
caattccata tgaccgatc 619

<210> 574
<211> 202
<212> DNA
<213> Homo sapiens

<400> 574
acatccaccc cactatttct tcacataccg aatcaggatt gaaatgtcaa aagatgcact 60
tcctgagaag gcctgtcagt tggacagtcg ctattggaga ataacaaatg ctaagggtga 120
cgtggaagaa gttcaaggac ctggagtagt tggtgaattt ccaatcatca gcccaggtcg 180
ggtatatgaa tacacaagct gt 202

<210> 575
<211> 311
<212> DNA
<213> Homo sapiens

<400> 575
ccacagttgt atcatatagc atctctaaca tttcatctag gattatctag tatagatctt 60
actatatttg ggactatgtt gtatacaatg ttaacaagaa catatcttct ctgcatatat 120
gtgtgaatta taaagaaaag catgagaatg actctaagtt caacaaacat gggtgaatct 180
ctatgtgctc ccagtgtcct ggatgggctc cccagcaagc cattcctcct tcctgttctg 240
atattactat tctttttttac attgtgctaa ggaggacaaa agatgagaga tgaaaataaa 300
gctttgcctt t 311

<210> 576
<211> 134
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(134)
<223> n = A,T,C or G

<400> 576
ttttttgcat caaaaagctt tatttccatt tggnccaagg cttgttagga tagttaaaaa 60
agctgcctat tggctggagg ganaggctta ggcaaaancc ctattacttt gcaaggggcc 120
cttcaaaagt cgct 134

<210> 577
<211> 488
<212> DNA
<213> Homo sapiens

<400> 577
ctgatcagtg ggcctccaag gaggggctgt aaaatggagg ccattgtgtg agcctatcag 60
agttgctgca aacctgaccc ctgctcagta aagcacttgc aaccgtctgt tatgctgtga 120
cacatggccc ctccccctgc caggagcttt ggacctaatc caagcatccc tttgcccaga 180
aagaagatgg gggaggaggc agtaataaaa agattgaagt attttgctgg aataagttca 240
aattcttctg aactcaaact gaggaatttc acctgtaaac ctgagtcgta cagaaagctg 300
cctggtatat ccaaaagctt tttattcctc ctgctcatat tgtgattctg cctttgggga 360
cttttcttaa accttcagtt atgatttttt tttcatacac ttattggaac tctgcttgat 420
ttttgcctct tccagtcttc ctgacacttt aattaccaac ctgttaccta ctttgacttt 480
ttgcattt 488

<210> 578
<211> 476
<212> DNA
<213> Homo sapiens

<400> 578
accatgcatt aagagcttcc tgattgagat tcagtgcatc agccgtgtct attccatcta 60

cgtccacacc gtctgtgacc cactctttga agctgttggg aaaatattca gcaatgtccg 120
catcaacttg cagaaagaaa tataaatgac atttcaagga tagaagtata cctgattttt 180
ttccttttaa ttttcctggt gccaatttca agttccaagt tgctaataca gcaacaattt 240
atgaattgaa ttatcttggt tgaaaataaa aagatcactt tctcagtttt cataagtatt 300
atgtctcttc tgagctattt catctatttt tggcagtctg aatttttaaa acccatttaa 360
atttttttcc ttaccttttt atttgcatgt ggatcaacca tcgctttatt ggctgagata 420
tgaacatatt gttgaaaggt aatttgagag aaatatgaag aactgaggaa aaaaaa 476

<210> 579
<211> 246
<212> DNA
<213> Homo sapiens

<400> 579
ctggtgctca ctgagatggt aggttttcct attttcctgc tacatctgca caagctacat 60
ctagaatgaa gccaccaatt tcaatgtgac caggcaatgg cagccagcac tgccttacac 120
tggtttgatt ctgattccct aattctggcc actgcaggtg atgagtaagg gtggggatca 180
gggaggaagt ccagaagcca gtctttgtct ccctttcctg cttatattta agtgcctatt 240
tacatg 246

<210> 580
<211> 615
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(615)
<223> n = A,T,C or G

<400> 580
gtcttcacag taataactaa tggtggatcc taaggtgaaa ttatttcctt caaaatagnc 60
atgaactgna ttcccaggag ggncacagtc cctacttttg canatgggaa agggaggtgc 120
ccaggtgtgg tcctctagac actggctccg attgctgccc ttgaggatgt agtggtcatt 180
gcacataaac gtgattttgt cacttacatt cacaggccct gaagaactga actctccatt 240
caccagcaca ggatcaggac agtggcccaa gcggcactca gtagtggtgt tatcccactc 300
cttagaggca ttgcaaaaaa gggtcttctt tcctaccagg tggtagccct tgatacaaac 360
gtaagtcccc agaatctgtc cttccacctc ctttgcgaca aatatgctat tgtccactgg 420
aggaagctct ggacagtgct catctgaagc agaaactcgc cacgcaacca taagacagca 480
cgcacaccaa aaaaacatct ggtgatcaaa gtcctctccc caggctggaa ttcacccagc 540
tcagacacct tacctgtctc tgtccctcca gagttagggc ttcccancaa ggaactgggc 600
ttaactgact tccaa 615

<210> 581
<211> 576
<212> DNA
<213> Homo sapiens

<400> 581
actcttgttg agttctgtag agccttctga tgtctctaaa gcactaccga ttctttggag 60
ttgtcacatc agataagaca tatctctaat tccatccata aatccagttc tactatggct 120
gagttctggt caaagaaaga aagtttagaa gctgagacac aaagggttgg gagctgatga 180
aactcacaaa tgatggtagg aagaagctct cgacaatacc cgttggcaag gagtctgcct 240
ccatgctgca gtgttcgagt ggattgtagg tgcaagatgg aaaggattgt aggtgcaagc 300
tgtccagaga aaagagtcct tgttccagcc ctattctgcc actcctgaca gggtgacctt 360
gggtatttgc aatattcctt tgggcctctg cttctctcac ctaaaaaaag agaattagat 420
tatattggtg gttctcagca agagaaggag tatgtgtcca atgctgcctt cccatgaatc 480
tgtctcccag ttatgaatca gtgggcagga taaactgaaa actcccattt acgtgtctga 540

atcgagtgag acaaaatttt agtccaaata acaagt 576

<210> 582
<211> 939
<212> DNA
<213> Homo sapiens

<400> 582
atgagcatcg gcctcctgtg ctgtgcagcc ttgtctctcc tgtgggcagg tccagtgaat 60
gctggtgtca ctcagacccc aaaattccag gtcctgaaga caggacagag catgacactg 120
cagtgtgccc aggatatgaa ccatgaatac atgtcctggt atcgacaaga cccaggcatg 180
gggctgaggc tgattcatta ctcagttggt gctggtatca ctgaccaagg agaagtcccc 240
aatggctaca atgtctccag atcaaccaca gaggatttcc cgctcaggct gctgtcggct 300
gctccctccc agacatctgt gtacttctgt gccagcagtt actcagtcgg ggagggcggg 360
gattcacccc tccactttgg gaatgggacc aggctcactg tgacagagga cctgaacaag 420
gtgttcccac ccgaggtcgc tgtgtttgag ccatcagaag cagagatctc ccacacccaa 480
aaggccacac tggtgtgcct ggccacaggc ttcttccctg accacgtgga gctgagctgg 540
tgggtgaatg ggaaggaggt gcacagtggg gtcagcacgg acccgcagcc cctcaaggag 600
cagcccgccc tcaatgactc cagatactgc ctgagcagcc gcctgagggt ctcggccacc 660
ttctggcaga acccccgcaa ccacttccgc tgtcaagtcc agttctacgg gctctcggag 720
aatgacgagt ggacccagga tagggccaaa cccgtcaccc agatcgtcag cgccgaggcc 780
tggggtagag cagactgtgg ctttacctcg gtgtcctacc agcaaggggt cctgtctgcc 840
accatcctct atgagatcct gctagggaag gccaccctgt atgctgtgct ggtcagcgcc 900
cttgtgttga tggccatggt caagagaaag gatttctga 939

<210> 583
<211> 828
<212> DNA
<213> Homo sapiens

<400> 583
atgaactatt ctccaggctt agtatctctg atactcttac tgcttggaag aacccgtgga 60
aattcagtga cccagatgga agggccagtg actctctcag aagaggcctt cctgactata 120
aactgcacgt acacagccac aggataccct tccctttttct ggtatgtcca atatcctgga 180
gaaggtctac agctcctcct gaaagccacg aaggctgatg acaagggaag caacaaaggt 240
tttgaagcca cataccgtaa agaaaccact tctttccact tggagaaagg ctcagttcaa 300
gtgtcagact cagcggtgta cttctgtgct ccgaaccctt ctcttcaggg cggatctgaa 360
aagctggtct ttggaaaggg aacgaaactg acagtaaacc catatatcca gaaccctgac 420
cctgccgtgt accagctgag agactctaaa tccagtgaca agtctgtctg cctattcacc 480
gattttgatt ctcaaacaaa tgtgtcacaa agtaaggatt ctgatgtgta tatcacagac 540
aaaactgtgc tagacatgag gtctatggac ttcaagagca acagtgctgt ggcctggagc 600
aacaaatctg actttgcatg tgcaaacgcc ttcaacaaca gcattattcc agaagacacc 660
ttcttcccca gcccagaaag ttcctgtgat gtcaagctgg tcgagaaaag ctttgaaaca 720
gatacgaacc taaactttca aaacctgtca gtgattgggt tccgaatcct cctcctgaaa 780
gtggccgggt ttaatctgct catgacgctg cggctgtggt ccagctga 828

<210> 584
<211> 275
<212> PRT
<213> Homo sapiens

<400> 584
Met Asn Tyr Ser Pro Gly Leu Val Ser Leu Ile Leu Leu Leu Leu Gly
5 10 15
Arg Thr Arg Gly Asn Ser Val Thr Gln Met Glu Gly Pro Val Thr Leu

20 25 30
Ser Glu Glu Ala Phe Leu Thr Ile Asn Cys Thr Tyr Thr Ala Thr Gly
35 40 45
Tyr Pro Ser Leu Phe Trp Tyr Val Gln Tyr Pro Gly Glu Gly Leu Gln
50 55 60
Leu Leu Leu Lys Ala Thr Lys Ala Asp Asp Lys Gly Ser Asn Lys Gly
65 70 75 80
Phe Glu Ala Thr Tyr Arg Lys Glu Thr Thr Ser Phe His Leu Glu Lys
85 90 95
Gly Ser Val Gln Val Ser Asp Ser Ala Val Tyr Phe Cys Ala Pro Asn
100 105 110
Pro Ser Leu Gln Gly Gly Ser Glu Lys Leu Val Phe Gly Lys Gly Thr
115 120 125
Lys Leu Thr Val Asn Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val Tyr
130 135 140
Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr
145 150 155 160
Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val
165 170 175
Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys
180 185 190
Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala
195 200 205
Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser
210 215 220
Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr
225 230 235 240
Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile
245 250 255
Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu
260 265 270
Trp Ser Ser
275

<210> 585
<211> 312
<212> PRT
<213> Homo sapiens

<400> 585
Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
5 10 15
Gly Pro Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu
20 25 30
Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
35 40 45
Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
50 55 60
Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
65 70 75 80
Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
85 90 95
Leu Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110
Ser Tyr Ser Val Gly Glu Gly Gly Asp Ser Pro Leu His Phe Gly Asn
115 120 125
Gly Thr Arg Leu Thr Val Thr Glu Asp Leu Asn Lys Val Phe Pro Pro

130 135 140
Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln
145 150 155 160
Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val
165 170 175
Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
180 185 190
Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
195 200 205
Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
210 215 220
Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
225 230 235 240
Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
245 250 255
Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser
260 265 270
Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
275 280 285
Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
290 295 300
Ala Met Val Lys Arg Lys Asp Phe
305 310

<210> 586
<211> 97
<212> PRT
<213> Homo sapiens

<400> 586
Glu Val Glu Val Ser Arg Asp His Ala Ser Leu Gly Asp Ser Glu Thr
5 10 15
Leu Ser Gln Thr Glu Leu Arg Lys Lys Glu Arg Lys Lys Lys Arg Glu
20 25 30
Arg Lys Phe Gln Ala Asn Cys Gly Ile Asp Phe Ile Ile Phe Trp Ile
35 40 45
Phe Trp Ile Leu Leu Phe Ser His His Trp Ile Gln Glu Ser Leu Leu
50 55 60
Cys Pro Pro Ser Pro Lys Glu Val Thr Cys Arg Glu Met Leu Thr Gly
65 70 75 80
Gly Cys Leu Pro Trp Ala Thr Arg Ser His Leu Gly Arg Arg Lys Cys
85 90 95
Ser

<210> 587
<211> 16
<212> PRT
<213> Homo sapiens

<400> 587
Phe Gln Ala Asn Cys Gly Ile Asp Phe Ile Ile Phe Trp Ile Phe Trp
1 5 10 15